



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 161552

TO: Louis V Wollenberger
Location: rem/3B61/2C18
Art Unit: 1635
Friday, August 19, 2005
Case Serial Number: 10/774721

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *psb*

barbara.obryen@uspto.gov

Search Notes

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	13.8	65.7	20	1	US-08-136-811-24	Sequence 24, Appl
C 2	13.8	65.7	20	1	US-08-835-770-24	Sequence 24, Appl
C 3	13.8	65.7	20	1	US-08-828-731-24	Sequence 24, Appl
C 4	13.2	62.9	19	3	US-08-637-732A-26	Sequence 26, Appl
C 5	13.2	62.9	21	1	US-08-271-942A-57	Sequence 57, Appl
C 6	13.2	62.9	21	1	US-08-779-916A-57	Sequence 57, Appl
C 7	13.2	62.9	21	5	PCT-US95-08604-57	Sequence 57, Appl
C 8	12.8	61.0	19	1	US-08-271-946A-13	Sequence 13, Appl
C 9	12.8	61.0	19	1	US-08-271-942A-13	Sequence 13, Appl
C 10	12.8	61.0	19	3	US-08-779-916A-13	Sequence 13, Appl
C 11	12.8	61.0	19	3	US-08-750-233-13	Sequence 13, Appl
C 12	12.8	61.0	19	5	PCT-US95-08604-13	Sequence 13, Appl
C 13	12.8	61.0	19	5	PCT-US95-08606-13	Sequence 13, Appl
C 14	12.4	59.0	20	4	US-09-657-346A-126	Sequence 126, Appl
C 15	12.2	58.1	17	3	US-09-275-680-7	Sequence 7, Appl
C 16	12.2	58.1	20	3	US-09-366-257-38	Sequence 38, Appl
C 17	12.2	58.1	20	3	US-09-844-634-62	Sequence 62, Appl
C 18	12.2	58.1	21	4	US-09-762-195-8	Sequence 8, Appl
C 19	12.2	58.1	21	4	US-09-762-195-17	Sequence 17, Appl
C 20	11.8	56.2	17	3	US-09-375-318-50	Sequence 50, Appl
C 21	11.8	56.2	20	4	US-10-177-573-15	Sequence 15, Appl
C 22	11.6	55.2	18	2	US-08-897-340-26	Sequence 26, Appl
C 23	11.6	55.2	18	3	US-08-757-024-823	Sequence 823, Appl
C 24	11.6	55.2	18	3	US-09-252-329-26	Sequence 26, Appl
C 25	11.6	55.2	18	4	US-09-093-972C-823	Sequence 823, Appl
C 26	11.6	55.2	19	3	US-08-757-024-809	Sequence 809, Appl
C 27	11.6	55.2	19	3	US-08-757-024-822	Sequence 822, Appl


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; REFERENCE/DOCKET NUMBER: 147-155P (PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer T60"
US-08-637-732A-26

Query Match 62.9%; Score 13.2; DB 3; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 UGCCUGUCGGGAACUGG 19
Db 2 TGCCAGTCGGGAACGGC 19

RESULT 5
US-08-271-942A-57/c
; Sequence 57, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,942A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
US-08-779-916A-57

Query Match 62.9%; Score 13.2; DB 3; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GUGCCUGUCGGGAACUGG 18
Db 21 GCGTCTGTGGGAACG 4

RESULT 6
US-08-779-916A-57/c
; Sequence 57, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; APPLICANT: Hui, May
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
US-08-779-916A-57

Query Match 62.9%; Score 13.2; DB 3; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GUGCCUGUCGGGAACUGG 18
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Db 21 GCGTCTGTGGGGAAC TGG 4

RESULT 7
PCT-US95-08604-57/c
; Sequence 57, Application PC/TUS9508604
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: HSC Research and Development Limited Partnership
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
; PCT-US95-08604-57
; Sequence 57, Score 13.2; DB 5; Length 21;
; Query Match 62.9%;
; Best Local Similarity 66.7%; Pred. No. 2.3e+03;
; Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
; QY 1 GUGCCUGUCGGGAACUGG 18
; Db 21 GCGTCTGTGGGGAAC TGG 4
; Sequence 13, Application US/08271946A
; Patent No. 5545527
; APPLICANT: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
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; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
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; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
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; ANTI-SENSE: no
; FRAGMENT TYPE: internal
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; ORGANISM: human
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; NAME/KEY: primer for exon 1 of human Rb1 gene
; US-08-271-946A-13
; Sequence 13, Score 12.8; DB 1; Length 19;
; Query Match 61.0%;
; Best Local Similarity 68.8%; Pred. No. 3.5e+03;
; Matches 11; Conservative 3; Mismatches 2; Indels 0;
; QY 3 GCGUGUCGGGAACUGG 18
; Db 19 GTCGTGTGGGGAAC TGG 4
; Sequence 13, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
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; CLASSIFICATION: 435
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
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; TELEX:
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; TYPE: nucleic acid
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; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
; US-08-271-946A-13
; Sequence 13, Score 12.8; DB 1; Length 19;
; Query Match 61.0%;
; Best Local Similarity 68.8%; Pred. No. 3.5e+03;
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; QY 3 GCGUGUCGGGAACUGG 18
; Db 19 GTCGTGTGGGGAAC TGG 4
; Sequence 13, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
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; PRIOR APPLICATION DATA:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
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; MOLECULE TYPE: genomic DNA
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; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
; US-08-271-946A-13
; Sequence 13, Score 12.8; DB 1; Length 19;
; Query Match 61.0%;
; Best Local Similarity 68.8%; Pred. No. 3.5e+03;
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; QY 3 GCGUGUCGGGAACUGG 18
; Db 19 GTCGTGTGGGGAAC TGG 4
; Sequence 13, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
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; SOFTWARE: Word Perfect
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; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
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; ANTI-SENSE: no
; FRAGMENT TYPE: internal
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; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
; US-08-271-946A-13
; Sequence 13, Score 12.8; DB 1; Length 19;
; Query Match 61.0%;
; Best Local Similarity 68.8%; Pred. No. 3.5e+03;
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; Sequence 13, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
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; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
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; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human Rb1 gene
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; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
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; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
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; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
; US-08-779-916A-13
;
Query Match 61.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels
;
QY 3 GCCTGUCGGGAACUGG 18
| | | | | | | | | |
;
Db 19 GTCGTGGGGAACTGG 4
;
;
RESULT 11
; US-08-750-232-13/c
; Sequence 13, Application US/08750232
; Patent No. 6270963
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,946
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038

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us-10-774-721-37.rn1

Fri Aug 19 08:52:57 2005

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; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
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; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
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US-08-750-232-13
Query Match 61.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGCGGGAACUGG 18
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Db 19 GTCTGTGGGGAACCTGG 4

RESULT 12
PCT-US95-08604-13/c
; Sequence 13, Application PC/TUS9508604
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
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; COMPUTER: IBM Compatible
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; SOFTWARE: Word Perfect
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
;
PCT-US95-08604-13
Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGCGGGAACUGG 18
| | | | | | | | | | | | | | | |
Db 19 GTCTGTGGGGAACCTGG 4

RESULT 13
PCT-US95-08606-13/c
; Sequence 13, Application PC/TUS9508606
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,946
; APPLICATION NUMBER: 08-JUL-1994
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:

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; NAME/KEY: primer for exon 1 of human RB1 gene
PCT-US95-08606-13

Query Match          61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCCUGUCGGGAACUGG 18
Db 19 GTCTGTGGGAACTGG 4

RESULT 14
US-09-657-346A-126/c
; Sequence 126, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-346A-126

Query Match          59.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 78.6%; Pred. No. 5.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GUCGGGAACUGGCT 20
Db 16 GTCGGGAACGCT 3

RESULT 15
US-09-275-680-7
; Sequence 7, Application US/09275680
; Patent No. 6221630
; GENERAL INFORMATION:
; APPLICANT: Hopper, James E
; TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
; TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
; TITLE OF INVENTION: Yeast
; FILE REFERENCE: 98428
; CURRENT APPLICATION NUMBER: US/09/275,680
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7

Query Match          58.1%; Score 12.2; DB 3; Length 17;
Best Local Similarity 64.7%; Pred. No. 7e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCUGUCGGGAACUGGC 19
Db 1 GCCTGTTGACAACTGGC 17

Search completed: August 18, 2005, 07:58:54
Job time : 76.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 05:29:57 ; Search time 842 Seconds
(without alignments)
1208.503 Million cell updates/sec

Title: US-10-774-721-37
Perfect score: 21
Sequence: 1 GUGCCUGCGGGAACUGGCTT 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	6	CQ860125 Sequence
2	19	90.5	21	6	CQ860126 Sequence
3	18.4	87.6	20	6	CQ860119 Sequence
4	13.8	65.7	20	6	AR037349 Sequence
5	13.8	65.7	20	6	AR040632 Sequence
6	13.8	65.7	20	6	AR040632 Sequence
7	13.4	63.8	16	6	AX471987 Sequence
8	13.2	62.9	21	6	AX471987 Sequence
9	12.8	61.0	16	6	CQ858638 Sequence
10	12.8	61.0	19	6	AR163030 Sequence
11	12.8	61.0	19	6	AR163030 Sequence
12	12.8	61.0	19	6	I25226 Sequence
13	12.8	61.0	21	6	CQ848735 Sequence
14	12.4	59.0	20	6	AR271882 Sequence
15	12.2	58.1	20	6	AR215747 Sequence
16	12.2	58.1	21	6	BD190401 Phosphati
17	12.2	58.1	21	6	BD190410 Phosphati
18	12.2	58.1	21	6	AR452563 Sequence
19	12.2	58.1	21	6	AR452572 Sequence

C	20	12.2	58.1	21	6	AX024461 Sequence
	21	12.2	58.1	21	6	AX024470 Sequence
	22	12.2	58.1	21	6	AX614231 Sequence
	23	11.8	56.2	17	6	AR240883 Sequence
	24	11.8	56.2	20	6	AX708916 Sequence
	25	11.8	56.2	20	6	AX708918 Sequence
	26	11.6	55.2	18	6	AR075066 Sequence
	27	11.6	55.2	18	6	AR141884 Sequence
	28	11.6	55.2	18	6	E15984 Oligonucleo
	29	11.6	55.2	20	6	AR020500 Sequence
	30	11.6	55.2	20	6	AR044730 Sequence
	31	11.6	55.2	20	6	AR052377 Sequence
	32	11.6	55.2	20	6	AR053223 Sequence
	33	11.6	55.2	20	6	AR055175 Sequence
	34	11.6	55.2	20	6	AR158046 Sequence
	35	11.6	55.2	20	6	I15822 Sequence 50
	36	11.6	55.2	20	6	I92526 Sequence 50
	37	11.6	55.2	20	6	AR222696 Sequence
	38	11.6	55.2	20	6	AR399783 Sequence
	39	11.6	55.2	20	6	AX449014 Sequence
	40	11.6	55.2	20	6	AX785895 Sequence
	41	11.6	55.2	20	6	BD070977 Novel hum
	42	11.6	55.2	21	6	AR529567 Sequence
	43	11.6	55.2	21	6	AX095592 Sequence
	44	11.6	55.2	21	8	ZAMRRN04
	45	11.6	55.2	21	8	ZAMRRNA03

ALIGNMENTS

RESULT 1	CQ860125	Sequence 37 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
LOCUS	CQ860125	Sequence 37 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
DEFINITION	CQ860125	Sequence 37 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
ACCESSION	CQ860125	Sequence 37 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
VERSION	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
KEYWORDS	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
SOURCE	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
ORGANISM	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
REFERENCE	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
AUTHORS	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
TITLE	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
JOURNAL	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
FEATURES	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
source	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
ORIGIN	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
Query Match	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
Best Local Similarity	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
Matches	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
Oy	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
Db	CQ860125.1	GI:51982013	21 bp	DNA	linear	PAT 10-SEP-2004
RESULT 2	CQ860126/c	Sequence 38 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
LOCUS	CQ860126/c	Sequence 38 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
DEFINITION	CQ860126/c	Sequence 38 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004
ACCESSION	CQ860126/c	Sequence 38 from Patent WO2004072293.	21 bp	DNA	linear	PAT 10-SEP-2004

Q0860126.1	GI:51982014				
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
synthetic construct					
other sequences; artificial sequences.					
REFERENCE					
AUTHORS	Jockers,R., Couturier,C. and Uhlmann,E.				
TITLE	Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor				
JOURNAL	Patent: WO 2004072293-A 38 26-AUG-2004;				
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)					
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source	Location/Qualifiers				
1..21	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
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	/note="Artificial"				
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Query Match	90.5%; Score 19; DB 6; Length 21;				
Best Local Similarity	78.9%; Pred. No. 2.4e+02;				
Matches	15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 GUGCCUUCGGGAACUGGC 19				
Db	19 GTGCTGTGCGGAATGCC 1				
RESULT 3					
LOCUS	Q0860119/c	20 bp	DNA	linear	PAT 10-SEP-2004
DEFINITION	Sequence 31 from Patent WO2004072293.				
ACCESSION	Q0860119				
VERSION	Q0860119.1 GI:51982007				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE					
AUTHORS	Jockers,R., Couturier,C. and Uhlmann,E.				
TITLE	Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor				
JOURNAL	Patent: WO 2004072293-A 31 26-AUG-2004;				
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)					
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source	Location/Qualifiers				
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Query Match	87.6%; Score 18.4; DB 6; Length 20;				
Best Local Similarity	75.0%; Pred. No. 4.8e+02;				
Matches	15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;				
Qy	2 UGCUCUGCGGAACUGGCTT 21				
Db	20 TGCTGTGCGGAATGCCAT 1				
RESULT 4					
LOCUS	AR037349/c	20 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 24 from patent US 5801154.				
ACCESSION	AR037349				
VERSION	AR037349.1 GI:59552005				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE					
AUTHORS	Baracchini,E., Bennett,C.Frank, and Dean,N.M.				
TITLE	Antisense oligonucleotide modulation of multidrug resistance-associated protein				
JOURNAL	Patent: US 5801154-A 24 01-SEP-1998;				
Location/Qualifiers					
FEATURES					
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Query Match	65.7%; Score 13.8; DB 6; Length 20;				
Best Local Similarity	76.5%; Pred. No. 9.8e+04;				
Matches	13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
Qy	4 CCUGUCGGGAACUGGCT 20				
Db	20 CCTGCTGTGGAATGGCT 4				
RESULT 5					
LOCUS	AR040632/c	20 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 24 from patent US 5807838.				
ACCESSION	AR040632				
VERSION	AR040632.1 GI:5959995				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE					
AUTHORS	Baracchini,E. Jr. and Bennett,C.Frank.				
TITLE	Oligonucleotide modulation of multidrug resistance-associated protein				
JOURNAL	Patent: US 5807838-A 24 15-SEP-1998;				
Location/Qualifiers					
FEATURES					
source	1..20				
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ORIGIN					
Query Match	65.7%; Score 13.8; DB 6; Length 20;				
Best Local Similarity	76.5%; Pred. No. 9.8e+04;				
Matches	13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
Qy	4 CCUGUCGGGAACUGGCT 20				
Db	20 CCTGCTGTGGAATGGCT 4				
RESULT 6					
LOCUS	I19643/c	20 bp	DNA	linear	PAT 07-OCT-1999
DEFINITION	Sequence 24 from patent US 5510239.				
ACCESSION	I19643				
VERSION	I19643.1 GI:1599998				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE					
AUTHORS	Baracchini,E. Jr. and Bennett,C.F.				
TITLE	Oligonucleotide modulation of multidrug resistance-associated protein				
JOURNAL	Patent: US 5510239-A 24 23-APR-1996;				
Location/Qualifiers					
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Query Match          65.7%; Score 13.8; DB 6; Length 20;
Best Local Similarity 76.5%; Pred. No. 9.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCUGCGGGAACUGGCT 20
Db 20 CCGTCTGTGGGAACCTGG 4

RESULT 7
AX471987
LOCUS          AX471987          16 bp      DNA          linear          PAT 09-AUG-2002
DEFINITION     Sequence 6 from Patent WO2053171.
ACCESSION      AX471987
VERSION        AX471987.1 GI:22207038
KEYWORDS
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL        Alzheimer,C., Goppelt,A. and Koegel,H.
FEATURES       Use of intermediate-conductance potassium channels and modulators
                for the diagnosis and treatment of illnesses having disturbed
                keratinocyte activity
                Patent: WO 02053171-A 6 11-JUL-2002;
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Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CUGUCGGGAACUGGC 19
Db 1 CTGGCGGGAACCTGG 15

RESULT 8
125270/c
LOCUS          125270/c          21 bp      DNA          linear          PAT 07-OCT-1996
DEFINITION     Sequence 57 from patent US 5550020.
ACCESSION      125270
VERSION        125270.1 GI:1605140
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE          Method, reagents and kit for diagnosis and targeted screening for
                retinoblastoma
                Patent: US 5550020-A 57 27-AUG-1996;
                Location/Qualifiers
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Query Match          62.9%; Score 13.2; DB 6; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCUCUGCGGGAACUGG 18
Db 19 GTCTGTGTGGGAACCTGG 4

RESULT 11
124629/c
LOCUS          124629/c          19 bp      DNA          linear          PAT 07-OCT-1996
DEFINITION     Sequence 13 from patent US 5545527.
ACCESSION      124629
VERSION        124629.1 GI:1604499
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E.
TITLE          Method for testing for mutations in DNA from a patient sample
                Patent: US 5270963-A 13 07-AUG-2001;
                Location/Qualifiers
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Query Match          61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GUGCCUGCGGGAACUGG 18
Db 21 GCCTCTGTGGGAACCTGG 4

RESULT 9
CQ858638/c
LOCUS          CQ858638/c          16 bp      DNA          linear          PAT 31-AUG-2004
DEFINITION     Sequence 100 from Patent WO2004069991.
ACCESSION      CQ858638
VERSION        CQ858638.1 GI:51852605
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Hansen,B., Thruue,C.A., Petersen,K.D., Westergaard,M. and
                Wissenbach,M.
TITLE          Oligomeric compounds for the modulation of survivin expression
                Patent: WO 2004069991-A 100 19-AUG-2004;
                Santaris Pharma A/S (DK)
                Location/Qualifiers
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Qy 5 CUGUCGGGAACUGGCT 20
Db 16 CTGTGTGGGAACCTGGCT 1

RESULT 10
ARI63030/c
LOCUS          ARI63030/c          19 bp      DNA          linear          PAT 17-OCT-2001
DEFINITION     Sequence 13 from patent US 6270963.
ACCESSION      ARI63030
VERSION        ARI63030.1 GI:16233504
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E.
TITLE          Method for testing for mutations in DNA from a patient sample
                Patent: US 6270963-A 13 07-AUG-2001;
                Location/Qualifiers
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Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCUCUGCGGGAACUGG 18
Db 19 GTCTGTGTGGGAACCTGG 4

RESULT 11
124629/c
LOCUS          124629/c          19 bp      DNA          linear          PAT 07-OCT-1996
DEFINITION     Sequence 13 from patent US 5545527.
ACCESSION      124629
VERSION        124629.1 GI:1604499
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E.
TITLE          Method for testing for mutations in DNA from a patient sample
                Patent: US 5270963-A 13 07-AUG-2001;
                Location/Qualifiers
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ORIGIN
Query Match          61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GUGCCUGCGGGAACUGG 18
Db 21 GCCTCTGTGGGAACCTGG 4
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Fri Aug 19 08:52:56 2005

us-10-774-721-37.rge

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Stevens,J.K. and Dunn,J.M.
TITLE       Method for testing for mutations in DNA from a patient sample
JOURNAL     Patent: US 5545527-A 13 13-AUG-1996;
FEATURES    Location/Qualifiers
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Query Match      61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACUGG 18
    |||:|||||:|
Db 19 GTCTGTGGGGAACCTGG 4

RESULT 12
LOCUS      125226/c          19 bp      DNA          linear      PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5550020.
ACCESSION 125226
VERSION   125226.1 GI:1605096
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE     Method, reagents and kit for diagnosis and targeted screening for
          retinoblastoma
JOURNAL   Patent: US 5550020-A 13 27-AUG-1996;
FEATURES  Location/Qualifiers
          1..19
          /organism="unknown"
          /mol_type="unassigned DNA"

ORIGIN
Query Match      61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACUGG 18
    |||:|||||:|
Db 19 GTCTGTGGGGAACCTGG 4

RESULT 13
LOCUS      CQ848735          21 bp      DNA          linear      PAT 19-AUG-2004
DEFINITION Sequence 195 from Patent WO2004065628.
ACCESSION  CQ848735
VERSION   CQ848735.1 GI:51470163
KEYWORDS  .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Fu,G.
TITLE     Quantitative multiplex detection of nucleic acids
JOURNAL   Patent: WO 2004065628-A 195 05-AUG-2004;
          Fu, Guoliang (GB)
FEATURES  Location/Qualifiers
          1..21
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Bennett,C.F. and Watt,A.T.
TITLE       Antisense modulation of tumor necrosis factor receptor 2 expression
JOURNAL     Patent: US 6410324-A 62 25-JUN-2002;
FEATURES    Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      58.1%; Score 12.2; DB 6; Length 20;
Best Local Similarity 70.6%; Pred. No. 6.2e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCUGUCGGGAACUGGCT 20
    |||:|||||:|
Db 17 CCTGTAGGGAACGGGT 1

Search completed: August 18, 2005, 06:53:19
Job time : 851 secs
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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Zhang,H. and Wyatt,J.
TITLE       Antisense modulation of BH3 interacting domain death agonist
          expression
JOURNAL     Patent: US 6503754-A 126 07-JAN-2003;
FEATURES    Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 4.9e+05;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GUCGGGAACUGGCT 20
    |||:|||||:|
Db 16 GTCGGGAACCTGCCT 3

RESULT 15
LOCUS      AR215747/c          20 bp      DNA          linear      PAT 25-SEP-2002
DEFINITION Sequence 62 from patent US 6410324.
ACCESSION  AR215747
VERSION   AR215747.1 GI:23314003
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Bennett,C.F. and Watt,A.T.
TITLE     Antisense modulation of tumor necrosis factor receptor 2 expression
JOURNAL   Patent: US 6410324-A 62 25-JUN-2002;
FEATURES  Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      58.1%; Score 12.2; DB 6; Length 20;
Best Local Similarity 70.6%; Pred. No. 6.2e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCUGUCGGGAACUGGCT 20
    |||:|||||:|
Db 17 CCTGTAGGGAACGGGT 1

Search completed: August 18, 2005, 06:53:19
Job time : 851 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 04:18:21 ; Search time 229 Seconds
(without alignments)
542.858 Million cell updates/sec

Title: US-10-774-721-37

Perfect score: 21

Sequence: 1 gugccugcgggaacugcgtt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

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Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.4	87.6	20	13 ADR27688	Adr27688 OB-RGRP a
C 2	13.8	65.7	20	2 Aq86849	Aq86849 Antisense
C 3	13.8	65.7	20	2 AAV53600	Aav53600 Nucleotid
C 4	13.4	63.8	16	6 ABQ78935	Abq78935 Mouse int
5	13.2	62.9	19	2 Aq88255	Aq88255 Neisseria
C 6	13.2	62.9	21	2 AAT11420	Aat11420 Retinobla
C 7	12.8	61.0	16	13 ADR70031	Adr70031 Human sur
C 8	12.8	61.0	18	12 ADP66743	Adp66743 Mouse KIA
C 9	12.8	61.0	19	2 AAT11532	Aat11532 Retinobla
C 10	12.8	61.0	19	2 AAT12851	Aat12851 PCR 5' pr
C 11	12.8	61.0	21	13 ADQ31737	Adq31737 Multiplex
C 12	12.4	59.0	20	6 AAL38283	Aal38283 Mouse BH3
C 13	12.4	59.0	21	12 ADP46888	Adp46888 Human c-C
14	12.2	58.1	17	4 AAT24024	Aat24024 Yeast GAL
15	12.2	58.1	20	3 AAZ95350	Aaz95350 Human mtp
C 16	12.2	58.1	20	6 ABL52426	Ab152426 Human FLI
C 17	12.2	58.1	20	6 ABL52442	Ab152442 Human FLI
C 18	12.2	58.1	20	6 ABQ74812	Abq74812 Human TNF
C 19	12.2	58.1	20	10 ABZ86558	Abz86558 Human oli
C 20	12.2	58.1	20	11 ABD2788	Abd2788 Human myo

21	12.2	58.1	20	12 ADG72431	Adg72431 Human E2-
C 22	12.2	58.1	20	12 ADG72397	Adg72397 Human E2-
C 23	12.2	58.1	21	3 AAZ88957	Aaz88957 Human MDR
24	12.2	58.1	21	3 AAZ88966	Aaz88966 Human MDR
C 25	11.8	56.2	15	4 AAF53027	Aaf53027 IGF-I oli
C 26	11.8	56.2	19	1 AAN80323	Aan80323 Synthetic
C 27	11.8	56.2	20	10 ADG32645	Adg32645 Murine pr
C 28	11.8	56.2	20	10 ADG32643	Adg32643 PCR prime
C 29	11.8	56.2	20	12 ADI27267	Adi27267 Antisense
C 30	11.8	56.2	20	12 ADJ86220	Adj86220 Nucleic a
C 31	11.8	56.2	20	12 ADJ53366	Adj53366 Human G p
C 32	11.8	56.2	20	12 ADJ53437	Adj53437 Human GPC
33	11.8	56.2	20	12 ADJ22606	Adj22606 Human end
34	11.8	56.2	20	12 ADJ22882	Adj22882 Human end
35	11.8	56.2	20	12 ADJ22087	Adj22087 Human end
36	11.8	56.2	20	12 ADJ22300	Adj22300 Human end
37	11.8	56.2	20	12 ADJ22833	Adj22833 Human end
38	11.8	56.2	20	12 ADJ23216	Adj23216 Human end
C 39	11.8	56.2	21	4 AAF96883	Aaf96883 Human gen
40	11.8	56.2	21	6 ABK65513	Abk65513 Human 6in
41	11.8	56.2	21	6 ABS97799	Abs97799 Human NAD
42	11.8	56.2	21	12 ADM57172	Adm57172 Murine mo
C 43	11.8	56.2	21	12 ADM57173	Adm57173 Murine mo
44	11.8	56.2	21	12 ADM70133	Adm70133 Plant gen
C 45	11.6	55.2	18	2 AAV11871	Aav11871 Mus muscu

ALIGNMENTS

RESULT 1

ADR27688/c

ID ADR27688 standard; DNA; 20 BP.

XX ADR27688;

AC ADR27688;

XX ADR27688;

DT 04-NOV-2004 (first entry)

XX 04-NOV-2004 (first entry)

DE OB-RGRP antisense oligonucleotide, AS 10.

XX OB-RGRP antisense oligonucleotide, AS 10.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

XX Leptin receptor related protein; OB-RGRP; lepin receptor;

XX Leptin receptor related protein; OB-RGRP; lepin receptor;

XX anorexia; sexual maturity disorder; osteoporosis; calcification; diabetes;

XX thrombus formation; immunity; inflammation; fetal development; cancer;

XX antisense; ss.

XX Synthetic.

OS Synthetic.

Key Location/Qualifiers

modified_base 1..20

/*tag= b

/mod_base= OTHER

/note= "Optional thioester"

modified_base 1..5

/*tag= a

/mod_base= OTHER

/note= "2' O-methylation"

modified_base 16..20

/*tag= c

/mod_base= OTHER

/note= "2' O-methylation"

modified_base 20

/*tag= d

/mod_base= OTHER

/note= "3' triethyleneglycol spacer"

FR2850971-A1.

13-AUG-2004.

10-FEB-2003; 2003FR-00001543.

us-10-774-721-37.rng

Fri Aug 19 08:52:56 2005

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XX 10-FEB-2003; 2003FR-00001543.
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis; thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 87.6%; Score 18.4; DB 13; Length 20;
Best Local Similarity 75.0%; Pred. NO. 24;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2 UGCGUCUGGGAAACUGGCTT 21
Db 20 TGCCTGTCGGAACTGGCAT 1
XX
RESULT 2
AAQ86849/c
ID AAQ86849 standard; DNA; 20 BP.
XX
XX AAQ86849;
XX
XX 13-DEC-1995 (first entry)
XX
XX Antisense oligonucleotide ISIS 8363 hybridises to MRP gene.
XX
XX Untranslated region; coding sequence; chemotherapeutic drug treatment;
XX antisense; modulation; multidrug resistance protein; drug; cancer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..20
XX FT /*tag= a
XX FT /note= "contains phosphorothioate internucleotide
XX FT linkages"
XX
XX WO9510938-A1.
XX
XX 27-APR-1995.

```

```

XX 23-SEP-1994; 94WO-US010827.
XX 18-OCT-1993; 93US-00136811.
XX (ISIS-) ISIS PHARM INC.
XX Baracchini E, Bennett CF;
XX WPI; 1995-169974/22.
XX
XX New oligonucleotide cpds., esp. for cancer therapy - which are
XX specifically hybridisable with nucleic acid encoding multi:drug
XX resistance-associated protein.
XX
XX Claim 7; Page 11; 36pp; English.
XX
XX Oligonucleotides AAQ86826-50 are antisense oligonucleotides used to
XX modulate the expression of the multidrug resistance protein (MRP) by
XX hybridising with the multidrug resistance (MDR) gene or its RNA message.
XX This sequence is targeted to the 3' untranslated region (3'UTR) of the
XX MDR gene. The oligonucleotides can be used to improve the efficacy of
XX chemotherapeutic drug treatment of a disease such as cancer or to prevent
XX multidrug resistance developing during drug treatment of a disease
XX
XX Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match 65.7%; Score 13.8; DB 2; Length 20;
Best Local Similarity 76.5%; Pred. NO. 4.9e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4 CTGUCGGGAACUGGCT 20
Db 20 CCTGCTGGAACUGGCT 4
XX
RESULT 3
AAV53600/c
ID AAV53600 standard; DNA; 20 BP.
XX
XX AAV53600;
XX
XX 25-MAR-2003 (revised)
XX 20-NOV-1998 (first entry)
XX
XX Nucleotide sequence of a phosphorothioate oligonucleotide 24.
XX
XX Phosphorothioate oligonucleotide; antisense; inhibition; cancer;
XX multidrug resistance; multiresistant protein; MRP; chemotherapy; human;
XX leukotriene; inflammatory condition; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX FT /*tag= a
XX FT /note= "phosphorothioate backbone"
XX
XX US5801154-A.
XX
XX 01-SEP-1998.
XX
XX 08-APR-1997; 97US-00835770.
XX
XX 18-OCT-1993; 93US-00136811.
XX 16-APR-1996; 96US-00628731.
XX
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dean NM, Baracchini E;
XX WPI; 1998-494825/42.

```


XX Anti-sense oligo:nucleotide(s) inhibiting multi:drug resistance protein
 PT expression - useful for increasing the efficacy of drugs that certain
 PT conditions have become resistant to e.g. small cell lung cancer.
 XX
 PS Claim 11; Col 12; 29pp; English.
 XX
 CC This is the nucleotide sequence of the phosphorothioate oligonucleotide
 CC used in the method of the invention, involving the use of antisense
 CC oligonucleotides to inhibit multidrug resistance. The oligonucleotides
 CC are used for the antisense inhibition of multiresistant proteins (MRPs).
 CC These proteins are commonly found in some cancers which initially respond
 CC to chemotherapy, but overexpression of the protein leads to chemotherapy
 CC drug resistance. They are administered with the drugs to attempt to
 CC enhance efficacy of the drugs. MRPs are also expressed in other ailments,
 CC as well. The oligonucleotides can be used to treat these conditions
 CC as well. The sequences are based on the human MRP and are used to treat
 CC conditions such as cancers, especially small-cell lung cancer, prevention
 CC of development of multidrug resistance during chemotherapy, and treatment
 CC of conditions characterised by leukotriene production, especially
 CC inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 65.7%; Score 13.8; DB 2; Length 20;
 Best Local Similarity 76.5%; Pred. No. 4.9e+03;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 4 CCUGUGGGGAACUGGCT 20
 ||:|||||:|||||
 DB 20 CCTGCTGGACTGGCT 4
 RESULT 4
 ID ABQ78935 standard; DNA; 16 BP.
 XX
 AC ABQ78935;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
 XX
 KW Mouse; intermediate-conductance potassium channel; dermatological;
 KW antiinflammatory; keratolytic; vulnerary; antipsoriatic; atopic eczema;
 KW contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose;
 KW hyperrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIK1;
 KW PCR; primer; 88.
 XX
 OS Mus musculus.
 XX
 XX WO200253171-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 27-DEC-2001; 2001WO-EP015317.
 XX
 XX 28-DEC-2000; 2000DE-01065475.
 PR 20-MAR-2001; 2001US-0277453P.
 XX
 XX (SWIT-) SWITCH BIOTECH AG.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 XX
 PI Goppelt A, Alzheimer C, Koegel H;
 XX
 DR WPI; 2002-643295/69.
 XX
 XX Use of intermediate-conductance potassium channel proteins for the
 PT diagnosis, prevention and treatment of disorders associated with
 PT disturbed keratinocyte activity, especially psoriasis.
 XX
 PS Example 3; Page 119; 121pp; German.
 XX

CC The invention relates to a novel use of intermediate-conductance
 CC potassium channel proteins. The proteins of the invention have
 CC dermatological, antiinflammatory, keratolytic, vulnerary, and
 CC antipsoriatic activity. The method is used especially in the field of
 CC damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo,
 CC hyperkeratosis, actinic keratosis, hypertrophic scars, keloids, lentigo,
 CC aged skin, ulcers and especially psoriasis. The sequence represents a PCR
 CC primer for the mouse potassium channel protein mIK1 of the invention
 XX
 SQ Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 63.8%; Score 13.4; DB 6; Length 16;
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 5 CUGUGGGGAACUGGC 19
 ||:|||||:|||||
 DB 1 CTGGCGGGAACTGGC 15
 RESULT 5
 ID AAQ88255 standard; DNA; 19 BP.
 XX
 AC AAQ88255;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-DEC-1995 (first entry)
 XX
 DE Neisseria pilC gene constant region probe TR60.
 XX
 KW pilC protein; pilin; pathogenic type 4 pilus bacteria; vaccine;
 KW detection; bacterial adhesin; phase variation; constant region; probe;
 KW Neisseria gonorrhoeae; Neisseria meningitidis; Pseudomonas aeruginosa;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN DE4336530-Cl.
 XX
 PD 13-APR-1995.
 XX
 PF 26-OCT-1993; 93DE-04336530.
 XX
 PR 26-OCT-1993; 93DE-04336530.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Meyer TFF, Rudel T, Rylf RR, Scheuerpflug IB;
 XX
 DR WPI; 1995-140328/19.
 XX
 PT Recombinant pilC-proteins derived from Neisseria gonorrhoeae - and their
 PT prodn. methods; useful for immunisation against pathogen type 4 pilus
 PT carrying bacteria or their detection.
 XX
 PS Claim 5; Page 12; 29pp; German.
 XX
 CC Sequences coding for pilin pilC proteins from Neisseria spp. have been
 CC isolated (see AAQ88239-Q88241). The pilC1 and pilC2 genes from
 CC N.gonorrhoeae have 84% identity. Probes were designed based on regions of
 CC shared homology (see AAQ88242-88261) and these constant region probes
 CC were used in Southern hybridisations to identify other pilC genes in
 CC N.gonorrhoeae strain MS11 and N.meningitidis strain A1493. Also, the same
 CC probes were used to screen a Pseudomonas aeruginosa strain and identified
 CC a pilC-like sequence. Gene sequences which hybridise with any of the
 CC constant region probes are claimed. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 2; Length 19;
 Best Local Similarity 72.2%; Pred. No. 9.7e+03;

of a medicament for the treatment of atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis. (I), (II) or a pharmaceutical (III) containing (I) is useful for treating cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder carcinoma, recurrent superficial bladder cancer, stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid tumours. The malignant melanoma is chosen from superficial spreading melanoma, nodular melanoma, lentigo maligna melanoma, acral melanoma, amelanotic melanoma, and desmoplastic melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma, chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's sarcoma. The treatment further involves administration of a chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or Docetaxel. (I), (II) or (III) is also useful for preventing or limiting apoptosis or for preventing cellular proliferation. This sequence corresponds to an antisense oligonucleotide targeted to the human survivin gene.

XX SQ Sequence 16 BP; 4 A; 8 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 13; Length 16;

Best Local Similarity 68.8%; Pred. No. 1.5e+04;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 5 CUGUCGGGACUGGCT 20

||: ||| ||: |||
16 CTGTGGGGACTGGCT 1

RESULT 8

ADP66743

ID ADP66743 standard; cDNA; 18 BP.

AC ADP66743;

DT 09-SEP-2004 (first entry)

DE Mouse KIAA0377 forward primer.

XX ss; acid phosphatase; BT42-I; BT42; histidine acid phosphatase;
KW hydrolysis; phosphate ester; BT42-II; deletion; fasting;
KW genetically induced; obesity; isoform; metabolic disease; dysfunction;
KW metabolic syndrome; obesity; diabetes; eating disorder; cachexia;
KW hypertension; coronary heart disease; hypercholesterolaemia;
KW dyslipidemia; osteoarthritis; gallstone; liver fibrosis; primer.

XX Mus sp.

XX WO2004050007-A2.

XX 17-JUN-2004.

XX 01-DEC-2003; 2003WO-EP013521.

XX 29-NOV-2002; 2002EP-00026693.

XX (DEVE-) DEVELOGEN AG.

XX Schreiter K;

XX WPI; 2004-460971/43.

XX New pharmaceutical composition comprising a BT-42 homologous protein or nucleic acid, and carriers, diluents or/and additives, useful for treating obesity, hyperlipidemia, osteoarthritis, cell masses.

XX Example 4; Page 39; 79pp; English.

XX This sequence is a primer which was used in the amplification of the mouse KIAA0377 coding sequence. KIAA0377 is homologous to human BT42.

CC BT42 contains the central signature of a histidine acid phosphatase, which are known to hydrolyze phosphate ester at low pH and are able to use a wide spectrum of substrates. The two BT42 isoforms of the invention, BT42-I hypercholesterolaemia of 40 amino acids compared to mouse BT42. Also BT42-II contains an additional exon of 40 amino acids. BT42 is regulated by fasting and by genetically induced obesity. BT42, and the disclosed isoforms, may be used for the manufacture of an agent for detecting or/and verifying, for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including metabolic syndrome, obesity or/and diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolaemia, dyslipidemia, osteoarthritis, gallstones, or liver fibrosis, in cells, cell masses, organs and/or subjects in vivo or in vitro. The BT42 nucleic acid molecule and polypeptide are useful for the manufacture of a medicament for the treatment of obesity, diabetes, or/and metabolic syndrome for controlling the function of a gene or/and a gene product, which is influenced or/and modified by a BT42 homologous polypeptide, for identifying substances capable of interacting with a BT42 homologous polypeptide, and for the production of a non-human transgenic animal which over- or under-expresses the BT42.

XX SQ Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 12; Length 18;

Best Local Similarity 68.8%; Pred. No. 1.5e+04;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 CCUGUCGGGAAACUGGC 19

||: ||| ||: |||
1 CCTGTGGGAGACTGGC 16

RESULT 9

AAT11532/c

ID AAT11532 standard; DNA; 19 BP.

AC AAT11532;

DT 10-SEP-1996 (first entry)

DE Retinoblastoma gene, RBL, exon 1 PCR 5' primer.

XX Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;
KW mutation; polymerase chain reaction; PCR; ss.

XX Synthetic.

XX WO9601908-A1.

XX 25-JAN-1996.

XX 07-JUL-1995; 95WO-US008604.

XX 08-JUL-1994; 94US-00271942.

XX (VISI-) VISIBLE GENETICS INC.

XX (HSCR-) HSC RES & DEV LP.

XX Gallie BL, Dunn JM, Stevens JK, Hui M;

XX WPI; 1996-097637/10.

XX Identifying mutation(s) in RBL exons by quantitative amplification - and by comparing length of amplification products and sequencing, for diagnosis and genetic screening of retinoblastoma.

XX Claim 12; Page 14; 48pp; English.

XX AAT11532 is a PCR amplification primer used for the amplification of exon 1 of the human retinoblastoma RBL gene. This primer and many other primers (see AAT11420-T11473) are used to amplify RBL exons for use in a method of diagnosing mutations in the RBL gene. By comparing the lengths of amplification products of RB exons from a suspected RB patient with

Query Match 61.0%; Score 12.8; DB 13; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.6e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACUGG 18
DB 1 GCCTGTGGTAACTGG 16

RESULT 12
ID AAL38283/c
XX AAL38283 standard; DNA; 20 BP.
AC AAL38283;
XX
DT 29-AUG-2003 (revised)
DT 15-AUG-2002 (first entry)
XX
DE Mouse BH3 interacting domain death mRNA agonist inhibitor SEQ ID 126.
XX
KW Hepatotropic; immunomodulatory; cytostatic; antiinflammatory; hepatitis;
KW haemostatic; BH3 interacting domain death agonist; liver disease;
KW haematopoietic disorder; developmental disorder; immunological disorder;
KW hyperproliferative disorder; apoptosis; mouse; chimeric; 2'-methoxyethyl;
KW 2'-MOE; phosphorothioate backbone; murine; ds.
XX
OS Mus musculus.
OS Chimeric.
XX
PN WO200220547-A1.
XX
PD 14-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-US027316.
XX
PR 07-SEP-2000; 2000US-00557346.
PR 07-MAR-2001; 2001US-00800631.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Zhang H, Wyatt JR;
XX
DR WPI; 2002-393838/42.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding the
PT BH3 interacting domain death agonist, useful for treating animals with
PT diseases associated with BH3 interacting domain death agonist, e.g.
PT hepatitis.
XX
PS Claim 3; Page 89; 171pp; English.
XX
CC The invention relates to a compound 8 to 50 nucleotides in length
CC targeted to a nucleic acid molecule encoding a BH3 interacting domain
CC death agonist, where the compound specifically hybridises with and
CC inhibits the expression of the BH3 interacting domain death agonist. The
CC compound of the invention is useful for inhibiting the expression of the
CC BH3 interacting domain death agonist in cells or tissues. The compound is
CC also useful for treating an animal having a disease or condition
CC associated with the BH3 interacting domain death agonist, e.g.
CC haematopoietic disorder, hyperproliferative disorder, a developmental
CC disorder, immunological disorder, or a disease or condition of the liver
CC e.g., hepatitis, or a condition associated with apoptosis. The compound
CC is useful for diagnostics, therapeutics, prophylaxis and as research
CC reagents and kits. This polynucleotide sequence represents an antisense
CC oligonucleotide inhibitor of the DNA from mouse BH3 interacting domain
CC death agonist RNA of the invention. NOTE: This sequence is a chimeric
CC oligonucleotide 20 nucleotides in length, which is flanked on both sides
CC by five-nucleotide 'wings'. The wings are composed of 2'-methoxyethyl (2'
CC -MOE) nucleotides. The internucleoside (backbone) linkages are
CC phosphorothioate (P-S) throughout the oligonucleotide. (Updated on 29-AUG
CC -2003 to standardise OS field)

Sequence 20 BP; 5 A; 8 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 2.5e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GUCGGGAACUGGCT 20
DB 16 GTCGGGAACGCTCCT 3

RESULT 13
ID ADP46888 standard; DNA; 21 BP.
XX
AC ADP46888;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human c-Cbl siRNA antisense strand, SEQ ID 224.
XX
KW Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour;
KW fat deposition; metabolic rate; lean muscle mass; body fat; Cbl;
KW multi-adaptor protein; feeding disorder; glucose uptake disorder;
KW metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl;
KW siRNA; short interfering RNA; ds; RNA interference; gene silencing.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004055181-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-AU001676.
XX
PR 16-DEC-2002; 2002AU-00953393.
PR 14-NOV-2003; 2003AU-00906285.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Molero JC, James D;
XX
DR WPI; 2004-488065/46.
XX
PT Identifying compounds capable of modulating feeding behavior, fat
PT deposition, metabolic rate, or the ratio of lean muscle mass to body fat
PT by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity
PT and hypolipidemia.
XX
PS Claim 86; SEQ ID NO 224; 213pp; English.
XX
CC The present invention relates to a method for identifying a compound that
CC is capable of modulating feeding behaviour, fat deposition, metabolic
CC rate, or the ratio of lean muscle mass to body fat in a subject. The
CC method comprises performing an assay to measure a metabolism-associated
CC phenotype that has been determined for a genetically modified non-human
CC animal that comprises a genetic modification within an allele of its Cbl
CC locus, and determining the effect of the compound on the phenotype. The
CC genetic modification reduces or prevents expression of a functional
CC endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
CC protein that is involved in ligand-induced down regulation of receptor
CC tyrosine kinases. The method of the invention is useful in the treatment
CC of feeding disorders or disorders of glucose uptake and metabolism, such
CC as diabetes, obesity and hyperlipidaemia. The present sequence is the
CC antisense strand for a human c-Cbl siRNA. The siRNA is useful in
CC modulating a metabolism-associated phenotype in a cell, tissue or animal
CC subject.

Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 59.0%; Score 12.4; DB 12; Length 21;
Best Local Similarity 71.4%; Pred. No. 2.5e+04;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCCUGCGGAACU 16
||||:|||||:
Db 7 GCCTCTCGGAACT 20

RESULT 14
AAH24024
ID AAH24024 standard; DNA; 17 BP.
XX AC AAH24024;
XX DT
XX 29-AUG-2001 (first entry)
XX DE Yeast GAL7 gene upstream UASgal site, SEQ ID NO:7.
XX XW UASgal site; cis-acting transcription control element; Gal4; Gal3; Gal80;
KW stochiometrically balanced expression; yeast;
KW galactose-inducible expression; expression construct; promoter; GAL7; ds.
XX OS Saccharomyces cerevisiae.
XX PN US6221630-B1.
XX PD
XX 24-APR-2001.
XX PF 24-MAR-1999; 99US-00275680.
XX PR 24-MAR-1999; 99US-00275680.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Hopper JE;
XX WPI; 2001-307557/32.
XX Expression construct for inducing and sustaining high level recombinant
PT polypeptide production in yeast, comprises nucleic acids encoding a trans
PT -acting transcription factor, selectable marker and yeast origin of
PT replication.
XX Disclosure; Col 15; 22pp; English.
XX The invention relates to high copy number expression constructs for high
XX level polypeptide expression in yeast. The yeast expression constructs
XX comprise a nucleic acid sequence encoding a set of trans- acting
XX transcription factors, a nucleic acid encoding a yeast selectable marker
XX providing an inefficiently or efficiently selected phenotype, a nucleic
XX acid encoding a yeast or bacterial origin of replication (ori), and a
XX unique restriction site downstream of a promoter containing a cis- acting
XX transcription control element that is regulated by the transcription
XX factors which are encoded by the expression construct. In a specific
XX embodiment of the invention, the expression construct provides for
XX galactose-inducible protein expression. Such constructs contain DNA
XX encoding the transcription factors Gal3, Gal4 and Gal80, and a UASgal cis
XX -acting control element within the promoter which drives expression of
XX the inserted gene of interest. The vector-encoded transcription factors
XX are expressed in stoichiometrically-balanced amounts, which is
XX particularly important for a galactose-inducible system, as Gal4, when
XX not balanced by stoichiometric levels of Gal3 and Gal80, becomes a
XX constitutive transcription factor, and can become toxic to the cell. The
XX constructs of the invention express the transcription factors at levels
XX higher than those found in native yeast cells, thereby ensuring
XX expression of the gene of interest. The expression constructs provide
XX robust, high level expression of a gene of interest (which can encode an
XX endogenous or heterologous polypeptide) in yeast. Sequences AAH24019-
XX AAH24035 represent actual UASgal sites found within the promoters of
XX various yeast galactose-inducible genes which may be used as the cis-
XX acting control element in a galactose-inducible expression construct of
XX the invention
XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 58.1%; Score 12.2; DB 4; Length 17;
Best Local Similarity 64.7%; Pred. No. 3e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCUGCGGAACUGGC 19
||||:|||||:
Db 1 GCCTGTTGACAACTGGC 17

RESULT 15
AAZ95350
ID AAZ95350 standard; DNA; 20 BP.
XX AC AAZ95350;
XX 31-MAY-2000 (first entry)
XX DT Human mtPEPCK phosphorothioate antisense oligonucleotide SEQ ID NO:38.
XX DE Human mtPEPCK phosphorothioate antisense oligonucleotide; modulation;
XX XW Human mitochondrial phosphoenolpyruvate carboxykinase; PEPCK-M; PCK2;
KW PEPCK-mitochondrial; mtPEPCK; antisense oligonucleotide; modulation;
KW phosphorothioate; inhibition; diagnosis; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX US6030837-A.
XX PD 29-FEB-2000. 99US-00366257.
XX PF 03-AUG-1999; 99US-00366257.
XX PR 03-AUG-1999; 99US-00366257.
XX PA (ISIS-) ISIS PHARM INC.
XX PI McKay R, Cowse LM, Butler MM;
XX WPI; 2000-205209/18.
XX New antisense compound targeted to a nucleic acid molecule encoding human
XX mitochondrial phosphoenolpyruvate carboxykinase useful for treating a
XX human with a mitochondrial phosphoenolpyruvate carboxykinase-associated
XX disease.
XX Claim 3; Col 39; 32pp; English.
XX AAZ95320 to AAZ95359 represent antisense oligonucleotides targeted to a
XX nucleic acid molecule encoding human mitochondrial phosphoenolpyruvate
XX carboxykinase (also known as PEPCK-mitochondrial; PEPCK-M; PCK2 and
XX mtPEPCK), where the oligonucleotide specifically hybridize with and
XX inhibit the expression of human mtPEPCK. The antisense oligonucleotides
XX can be used for inhibiting the expression of mtPEPCK in human cells or
XX tissues in vitro and can also be used for treating an animal,
XX particularly a human suspected of having or being prone to a condition or
XX disease associated with expression of mtPEPCK. They can also be used in
XX diagnostics and as research reagents in sandwich and other assays
XX Sequence 20 BP; 1 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 58.1%; Score 12.2; DB 3; Length 20;
Best Local Similarity 58.8%; Pred. No. 3.1e+04;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GUGCCUCGCGGAACUG 17
|:|:|:|:|:|:|:
Db 4 GTGTCTCTCGGCACTG 20

Search completed: August 18, 2005, 06:25:06
Job time : 238 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:17:36 ; Search time 1765 Seconds
(without alignments)
452.889 Million cell updates/sec

Title: US-10-774-721-37

Perfect score: 21
Sequence: 1 guggcugcggaacuggctt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.2	53.3	19	8	AZ763411
2	9.8	46.7	17	9	AJ589126
3	9.8	46.7	19	8	AZ486389
4	9.8	46.7	20	8	AZ593689
5	9.6	45.7	16	1	AL039794
6	9.6	45.7	18	1	AL039892
7	9.6	45.7	18	1	AL043072
8	9.6	45.7	19	1	AL042746
9	9.6	45.7	19	8	AZ466725
10	9.6	45.7	19	8	AZ589446
11	9.6	45.7	20	1	AL039677
12	9.6	45.7	20	1	AL043331
13	9.6	45.7	20	1	AL043349
14	9.6	45.7	20	1	AL045408
15	9.6	45.7	21	8	AZ794033
16	9.4	44.8	17	9	AJ589127
17	9.4	44.8	20	8	AZ827586
18	9.4	44.8	21	7	C0785256
19	9.2	43.8	15	1	AL039409
20	9.2	43.8	21	9	AG195343
21	9.2	43.8	18	6	CA851577
22	9.2	43.8	20	8	AZ318416
23	9.2	43.8	21	7	C0788185
24	9.2	43.8	21	8	AZ806008

25	8.8	41.9	20	5	BX563610
26	8.8	41.9	20	8	AZ309156
27	8.8	41.9	20	8	AZ386570
28	8.8	41.9	20	8	AZ823352
29	8.8	41.9	21	1	AL043263
C 30	8.8	41.9	21	8	AZ436036
C 31	8.8	41.9	21	1	AA876113
C 32	8.6	41.0	19	1	AI049374
33	8.6	41.0	20	8	AZ616822
34	8.6	41.0	20	9	AG204980
35	8.4	40.0	18	9	AJ588001
C 36	8.4	40.0	19	4	BM399863
C 37	8.4	40.0	20	8	AZ309592
38	8.4	40.0	20	8	AZ803105
39	8.4	40.0	21	5	BQ593572
C 40	8.4	40.0	21	8	AZ665199
41	8.2	39.0	13	1	AL043127
42	8.2	39.0	14	1	AL039339
43	8.2	39.0	15	1	AL043135
44	8.2	39.0	15	1	AL043264
45	8.2	39.0	15	1	AL043298

ALIGNMENTS

RESULT 1
AZ763411
LOCUS
DEFINITION
1M0558B24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0558B24 R, genomic survey sequence.
19 bp DNA linear GSS 16-FEB-2001
AZ763411
AZ763411.1 GI:12874413
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0558 row: B column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0558B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

Fri Aug 19 08:52:57 2005

/note="T-DNA flanking sequence
left border"

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 19;
Best Local Similarity 68.8%; Pred. No. 7.6e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CUGCGGACUGGCT 20

Db 4 CTGTGGGTACAGCT 19

RESULT 2

AJ589126/c 17 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 545A02, genomic survey sequence.

ACCESSION AJ589126.1 GI:37938750

VERSION GSS; left border; T-DNA flanking sequence.

KEYWORDS Arabidopsis thaliana (Chale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, P.,
Chauvin, S., Bechold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M., and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBL Rep. 3 (12), 1152-1157 (2002)

JOURNAL

MEDLINE 22363535

PUBMED 12446565

REFERENCE 2 (bases 1 to 17)

AUTHORS Balzergue, S.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES

source

1. .17

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Wassiliewskija"

/db_xref="taxon:3702"

/clone="545A02"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature 1. .17

ORIGIN

Query Match 46.7%; Score 9.8; DB 9; Length 17;
Best Local Similarity 69.2%; Pred. No. 3.8e+06;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 UGCUCUGCGGAA 14

Db 17 TACCGGTCCGGAA 5

RESULT 3

AJ486389

LOCUS

DEFINITION

AZ486389 19 bp DNA linear GSS 05-OCT-2000
1M0314E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0314E21 F, genomic survey sequence.

ACCESSION AZ486389

VERSION AZ486389.1 GI:10653117

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0314 row: E column: 21

Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

1. .19
/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0314E21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor-mouse DNA was annealed to
adaptor vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 19;
Best Local Similarity 69.2%; Pred. No. 3.8e+06;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 UGCCUGCGGAA 14
:|||||
Db 4 TGCCTGATGGAA 16

RESULT 4
AZ593689
LOCUS
DEFINITION AZ593689 20 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0405C21 F, genomic survey sequence.

ACCESSION
VERSION AZ593689.1 GI:11715879
KEYWORDS
SOURCE GSS.

ORGANISM
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 20)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Igiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0405 row: C column: 21
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

1..20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0405C21"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 20;
Best Local Similarity 61.5%; Pred. No. 3.9e+06;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CUGUCGGGAACUG 17
:|||||
Db 5 CTGTTGGTAACTG 17

RESULT 5
AL039794
LOCUS
DEFINITION AL039794 16 bp mRNA linear EST 06-JUL-2004
DKFZp434B1612 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1612, mRNA sequence.

ACCESSION
VERSION AL039794.1 GI:49682336
KEYWORDS
SOURCE EST.

ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)

REFERENCE
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source

1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434B1612"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="vector: pSport1; Site_1: NotI; Site_2: SalI"

Query Match 45.7%; Score 9.6; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 4.8e+06;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GUGCCUGCGGAACU 16
:|||||
Db 1 GTACCGTCCGGAATT 16

RESULT 6
AL039892
LOCUS
DEFINITION AL039892 18 bp mRNA linear EST 06-JUL-2004
DKFZp434G1212 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434G1212, mRNA sequence.

ACCESSION
VERSION AL039892.1 GI:49682352
KEYWORDS
SOURCE EST.

ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)

REFERENCE
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS

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SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE           EST (Blum, et al.)
JOURNAL         Unpublished (1999)
COMMENT         Contact: MIPS
                MIPS
FEATURES        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
                Location/Qualifiers
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                    /tissue_type="testis"
                    /dev_stage="adult"
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ORIGIN
Query Match      45.7%; Score 9.6; DB 1; Length 18;
Best Local Similarity 56.2%; Pred. No. 4.8e+06;
Matches          9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy              1 GUGCCUUCGGGAACU 16
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Db              1 GTACCGGTCCGGAATT 16

RESULT 7
AL043072
LOCUS            DKFZp34B1823_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION      DKFZp34B1823, mRNA sequence.
ACCESSION       AL043072
VERSION         AL043072.1 GI:49682480
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 18)
AUTHORS         Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE           EST (Blum, et al.)
JOURNAL         Unpublished (1999)
COMMENT         Contact: MIPS
                MIPS
FEATURES        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
                Location/Qualifiers
                source
                  1..18
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                    /dev_stage="adult"
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                    /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      45.7%; Score 9.6; DB 1; Length 18;
Best Local Similarity 56.2%; Pred. No. 4.8e+06;
Matches          9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy              1 GUGCCUUCGGGAACU 16
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Db              3 GTACCGGTCCGGAATT 18

RESULT 8
AL042746
LOCUS            DKFZp34C1822_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION      DKFZp34C1822, mRNA sequence.
ACCESSION       AL042746
VERSION         AL042746.1 GI:49682451
KEYWORDS        EST.

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/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 19;
 Best Local Similarity 62.5%; Pred. No. 4.8e+06;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CUGUGGGGAACUGGCT 20
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 Db 2 CTGTGGGGAACCTACT 17

RESULT 10
 AZ858446 19 bp DNA linear GSS 21-FEB-2001
 LOCUS 2M0163D08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION clone UUC2M0163D08 R, genomic survey sequence.

ACCESSION AZ858446
 VERSION AZ858446.1 GI:13051622
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
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 Location/Qualifiers
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 /organism="Mus musculus"
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FEATURES

source
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 /mol_type="genomic DNA"
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Query Match

Best Local Similarity 45.7%; Score 9.6; DB 1; Length 20;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GUGCCUGCGGGAACU 16
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 Db 5 GTACCGGTCGGAATT 20

/sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 19;
 Best Local Similarity 56.2%; Pred. No. 4.8e+06;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCUGCGGGAACUGGC 19
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 Db 4 CCTGTAGATCCTGGC 19

RESULT 11
 AL039677 20 bp mRNA linear EST 06-JUL-2004
 LOCUS DKFP3434H0411_r1 434 (synonym: htes3) Homo sapiens cDNA clone
 DEFINITION DKFP3434H0411, mRNA sequence.

ACCESSION AL039677
 VERSION AL039677.1 GI:49682316
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS

FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
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 /clone_lib="434 (synonym: htes3)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

[illegible]

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0047 row: D column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

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/db_xref="taxon:10090"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 21;
Best Local Similarity 62.5%; Pred. No. 4.9e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 3 GCCTGCGGAGCTGG 18
|:| | | | | | | | | |
Db 4 GCCTGCGGAGCTGG 19

Search completed: August 18, 2005, 07:56:22
Job time : 1773 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:53:53 ; Search time 1790 Seconds
(without alignments)
76.221 Million cell updates/sec

Title: US-10-774-721-37

Perfect score: 21

Sequence: 1 gugcugcuggggaacuggctt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 2032376

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	21	US-10-774-721-37
2	19	90.5	21	21	Sequence 37, Appl
3	18.4	87.6	20	21	Sequence 38, Appl
4	13.4	63.8	16	20	US-10-774-721-31
5	13	61.9	21	20	US-10-451-805-6
6	12.8	61.0	16	21	US-10-792-280-281
7	12.8	61.0	16	21	US-10-776-934-100
			16	21	US-10-776-934-540

c	8	12.8	61.0	16	21	US-10-776-934-541	Sequence 541, App
c	9	12.8	61.0	16	21	US-10-776-934-542	Sequence 542, App
c	10	12.8	61.0	16	21	US-10-776-934-543	Sequence 543, App
c	11	12.8	61.0	21	20	US-10-751-736-36589	Sequence 36589, A
c	12	12.8	61.0	21	20	US-10-751-736-37093	Sequence 37093, A
c	13	12.8	61.0	21	22	US-10-349-780A-195	Sequence 195, App
c	14	12.6	60.0	21	22	US-10-736-892-1	Sequence 1, Appli
c	15	12.4	59.0	20	9	US-09-800-631-126	Sequence 126, App
c	16	12.4	59.0	20	15	US-10-293-783-126	Sequence 126, App
c	17	12.4	59.0	20	17	US-10-388-263-778	Sequence 778, App
c	18	12.2	58.1	20	17	US-10-173-240-36	Sequence 36, Appl
c	19	12.2	58.1	20	17	US-10-173-240-70	Sequence 70, Appl
c	20	12.2	58.1	20	19	US-10-476-021-62	Sequence 62, Appl
c	21	12.2	58.1	20	20	US-10-695-568-104	Sequence 104, App
c	22	12.2	58.1	20	20	US-10-695-568-120	Sequence 120, App
c	23	12.2	58.1	21	20	US-10-751-736-46727	Sequence 46727, A
c	24	12	57.1	21	20	US-10-792-280-279	Sequence 279, App
c	25	12	57.1	21	20	US-10-751-736-25592	Sequence 25592, A
c	26	11.8	56.2	17	16	US-10-180-781-50	Sequence 50, Appl
c	27	11.8	56.2	17	19	US-10-712-672-1359	Sequence 1359, Ap
c	28	11.8	56.2	17	19	US-10-712-672-1360	Sequence 1360, Ap
c	29	11.8	56.2	17	19	US-10-712-672-1361	Sequence 1361, Ap
c	30	11.8	56.2	20	16	US-10-171-319-98	Sequence 98, Appl
c	31	11.8	56.2	20	16	US-10-171-319-100	Sequence 100, App
c	32	11.8	56.2	20	17	US-10-177-573-15	Sequence 15, Appl
c	33	11.8	56.2	20	17	US-10-210-479-26	Sequence 26, Appl
c	34	11.8	56.2	20	17	US-10-210-479-97	Sequence 97, Appl
c	35	11.8	56.2	20	19	US-10-619-739-1288	Sequence 1288, Ap
c	36	11.8	56.2	21	9	US-09-765-081-133	Sequence 133, App
c	37	11.8	56.2	21	20	US-10-751-736-37094	Sequence 37094, A
c	38	11.6	55.2	21	21	US-10-847-918-3427	Sequence 3427, App
c	39	11.6	55.2	18	10	US-09-093-972C-823	Sequence 823, App
c	40	11.6	55.2	18	21	US-10-758-451-823	Sequence 823, App
c	41	11.6	55.2	19	9	US-09-986-632-27	Sequence 27, Appl
c	42	11.6	55.2	19	10	US-09-093-972C-809	Sequence 809, App
c	43	11.6	55.2	19	10	US-09-093-972C-822	Sequence 822, App
c	44	11.6	55.2	19	16	US-10-251-117-189	Sequence 189, App
c	45	11.6	55.2	19	16	US-10-251-117-438	Sequence 438, App

ALIGNMENTS

RESULT 1

US-10-774-721-37
; Sequence 37, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-37

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3;

Fri Aug 19 08:52:57 2005

us-10-774-721-37.rnpb

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Db 1 GUGCCUGUGGGGAACUGGCTT 21

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; Publication No. US20050009042A1
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; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-38

Query Match 90.5%; Score 19; DB 21; Length 21;
Best Local Similarity 78.9%; Pred. No. 13;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGCCUGUGGGGAACUGGC 19
Db 19 GTGCTGTGCGGAACCTGCG 1

RESULT 3
US-10-774-721-31/c
; Sequence 31, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS10
US-10-774-721-31

Query Match 87.6%; Score 18.4; DB 21; Length 20;

Best Local Similarity 75.0%; Pred. No. 26;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 UGCCUGUGGGGAACUGGCTT 21
Db 20 TGCCTGTGCGGAACCTGCGAT 1

RESULT 4
US-10-451-805-6
; Sequence 6, Application US/10451805
; Publication No. US20040248099A1
; GENERAL INFORMATION:
; APPLICANT: Goppelt, Andreas
; APPLICANT: Alzheimer, Christian
; APPLICANT: Kogel, Heidi
; TITLE OF INVENTION: Use of Intermediate-Conductance
; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity
; FILE REFERENCE: 50125/080001
; CURRENT APPLICATION NUMBER: US/10/451,805
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/15317
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/277,453
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: DE 10065475.4
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-451-805-6

Query Match 63.8%; Score 13.4; DB 20; Length 16;
Best Local Similarity 80.0%; Pred. No. 8.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGC 19
Db 1 CTGCGCGGAACCTGCG 15

RESULT 5
US-10-792-280-281
; Sequence 281, Application US/10792280
; Publication No. US20040234517A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Bowman, Michael
; APPLICANT: Follettie, Maximillian
; APPLICANT: Chen, Heng
; APPLICANT: Williams, Cara
; APPLICANT: Ellis, Debra
; APPLICANT: Winkler, Aaron
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR
; TITLE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES
; FILE REFERENCE: AM101023-2
; CURRENT APPLICATION NUMBER: US/10/792,280
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 1535
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 281
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-792-280-281

Query Match 61.9%; Score 13; DB 20; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.3e+04;

Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GUGGUCUGGGGAACUGGCTT 21
 |||||
 Db 1 GUGGUCUCUGGGACACUGCUU 21
 |||||

RESULT 6

US-10-776-934-100/c
 ; Sequence 100, Application US/10776934
 ; Publication No. US20050014712A1

GENERAL INFORMATION:
 ; APPLICANT: HANSEN, BO
 ; APPLICANT: THRUUE, CHARLOTTE ALBAEK
 ; APPLICANT: WESTERGAARD, MAJKEN
 ; APPLICANT: PETERSEN, KAMILLE DUMONG
 ; APPLICANT: WISENBACH, MARGIT

TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: 58610(71432)
 ; CURRENT APPLICATION NUMBER: US/10/776,934
 ; CURRENT FILING DATE: 2004-02-10
 ; PRIOR APPLICATION NUMBER: 60/446,372
 ; PRIOR FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: 60/523,591
 ; PRIOR FILING DATE: 2003-11-19
 ; NUMBER OF SEQ ID NOS: 741
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 100
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence

FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 US-10-776-934-100

Query Match 61.0%; Score 12.8; DB 21; Length 16;
 Best Local Similarity 68.8%; Pred. No. 1.7e+04;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CUGUCGGGAACUGGCT 20
 |:::|
 Db 16 CTGTGGGGGACTGGCT 1
 |:::|

RESULT 7

US-10-776-934-540/c
 ; Sequence 540, Application US/10776934
 ; Publication No. US20050014712A1

GENERAL INFORMATION:
 ; APPLICANT: HANSEN, BO
 ; APPLICANT: THRUUE, CHARLOTTE ALBAEK
 ; APPLICANT: WESTERGAARD, MAJKEN
 ; APPLICANT: PETERSEN, KAMILLE DUMONG
 ; APPLICANT: WISENBACH, MARGIT

TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: 58610(71432)
 ; CURRENT APPLICATION NUMBER: US/10/776,934
 ; CURRENT FILING DATE: 2004-02-10
 ; PRIOR APPLICATION NUMBER: 60/446,372
 ; PRIOR FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: 60/523,591
 ; PRIOR FILING DATE: 2003-11-19
 ; NUMBER OF SEQ ID NOS: 741
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 540
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence

FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(4)

OTHER INFORMATION: beta-D-oxy-LNA modified base

FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (13)..(16)

OTHER INFORMATION: beta-D-oxy-LNA modified base

FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(16)

OTHER INFORMATION: phosphothioate linkage

US-10-776-934-540

Query Match 61.0%; Score 12.8; DB 21; Length 16;
 Best Local Similarity 68.8%; Pred. No. 1.7e+04;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CUGUCGGGAACUGGCT 20
 |:::|
 Db 16 CTGTGGGGGACTGGCT 1
 |:::|

RESULT 8

US-10-776-934-541/c
 ; Sequence 541, Application US/10776934
 ; Publication No. US20050014712A1

GENERAL INFORMATION:
 ; APPLICANT: HANSEN, BO
 ; APPLICANT: THRUUE, CHARLOTTE ALBAEK
 ; APPLICANT: WESTERGAARD, MAJKEN
 ; APPLICANT: PETERSEN, KAMILLE DUMONG
 ; APPLICANT: WISENBACH, MARGIT

TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: 58610(71432)
 ; CURRENT APPLICATION NUMBER: US/10/776,934
 ; CURRENT FILING DATE: 2004-02-10
 ; PRIOR APPLICATION NUMBER: 60/446,372
 ; PRIOR FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: 60/523,591
 ; PRIOR FILING DATE: 2003-11-19
 ; NUMBER OF SEQ ID NOS: 741
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 541
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence

FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(4)

OTHER INFORMATION: beta-D-oxy-LNA modified base

FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (13)..(15)

OTHER INFORMATION: beta-D-oxy-LNA modified base

FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(16)

OTHER INFORMATION: phosphothioate linkage

US-10-776-934-541

Query Match 61.0%; Score 12.8; DB 21; Length 16;
 Best Local Similarity 68.8%; Pred. No. 1.7e+04;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CUGUCGGGAACUGGCT 20
 |:::|
 Db 16 CTGTGGGGGACTGGCT 1
 |:::|

RESULT 9

US-10-776-934-542/c
 ; Sequence 542, Application US/10776934
 ; Publication No. US20050014712A1

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; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRU, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 542
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(13)
; OTHER INFORMATION: phosphothioate linkage
; US-10-776-934-542

Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
Db 16 CTGTGGGGAGTGGCT 1

RESULT 10
US-10-776-934-543/c
; Sequence 543, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRU, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature

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; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphothioate linkage
; US-10-776-934-543

Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
Db 16 CTGTGGGGAGTGGCT 1

RESULT 11
US-10-751-736-36589/c
; Sequence 36589, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AML00927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36589
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-751-736-36589

Query Match 61.0%; Score 12.8; DB 20; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 UGUCGGGAACUGGCTT 21
Db 16 TGTCGTGAAGTGGCTT 1

RESULT 12
US-10-751-736-37093/c
; Sequence 37093, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AML00927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37093
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-751-736-37093

Query Match 61.0%; Score 12.8; DB 20; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy 6 UGUCGGGAACUGGCTT 21
Db 17 TGCTGTGAAGTGGCTT 2

RESULT 13

US-10-349-780A-195
; Sequence 195, Application US/10349780A
; Publication No. US20040146866A1
; GENERAL INFORMATION:
; APPLICANT: Pu, Guoliang
; TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
; FILE REFERENCE: patent1
; CURRENT APPLICATION NUMBER: US/10/349,780A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-780A-195

Query Match 61.0%; Score 12.8; DB 22; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GCCUGUCGGGAACUGG 18
Db 1 GCCTGTGGTAACTGG 16

RESULT 14

US-10-736-892-1
; Sequence 1, Application US/10736892
; Publication No. US20050148505A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: JI, Tai
; TITLE OF INVENTION: GENES AND AGENTS TO REGULATE FOLLICULAR DEVELOPMENT, OVULATION
; FILE REFERENCE: 050229-0424
; CURRENT APPLICATION NUMBER: US/10/736,892
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: 60/437,729
; PRIOR FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-10-736-892-1

Query Match 60.0%; Score 12.6; DB 22; Length 21;
Best Local Similarity 63.2%; Pred. No. 2.1e+04;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 UGCCUGUCGGGAACUGGCT 20
Db 2 TGACTGGCGAGAACTGGAT 20

RESULT 15

US-09-800-631-126/c
; Sequence 126, Application US/09800631
; Patent No. US20020082228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang

; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPRESSION
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/09/800,631
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-800-631-126

Query Match 59.0%; Score 12.4; DB 9; Length 20;
Best Local Similarity 78.6%; Pred. No. 2.7e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GUCGGGAACUGGCT 20
Db 16 GTCGGGAACGCT 3

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Job time : 1797 secs

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:53:53 ; Search time 1790 Seconds

(without alignments)
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Title: US-10-774-721-38

Perfect score: 21

Sequence: 1 gccaguccgacagcactt 21

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Searched: 7316285 seqs, 3248459403 residues

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Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	21	US-10-774-721-38
2	19	90.5	21	21	Sequence 38, Appl
3	18	85.7	20	21	Sequence 37, Appl
4	13.4	63.8	16	20	Sequence 31, Appl
5	13	61.9	21	20	US-10-451-805-6
6	12.8	61.0	21	20	Sequence 6, Appl
7	12.6	60.0	19	9	Sequence 280, App
					Sequence 195, App
					Sequence 27, Appl
					Sequence 38, Appl
					Sequence 37, Appl
					Sequence 31, Appl
					Sequence 6, Appl
					Sequence 280, App
					Sequence 195, App
					Sequence 27, Appl

8	12.6	60.0	19	18	US-10-189-359-16	Sequence 16, Appl
9	12.6	60.0	20	19	US-10-688-706-1896	Sequence 1896, Ap
10	12.6	60.0	20	19	US-10-688-706-1896	Sequence 2734, Ap
11	12.4	59.0	18	22	US-10-499-544-15	Sequence 15, Appl
12	12.2	58.1	20	17	US-10-173-240-36	Sequence 36, Appl
13	12.2	58.1	20	17	US-10-173-240-36	Sequence 70, Appl
14	12.2	58.1	20	19	US-10-671-395-382	Sequence 382, App
15	12.2	58.1	20	19	US-10-671-395-455	Sequence 455, App
16	12.2	58.1	20	19	US-10-671-395-537	Sequence 537, App
17	12.2	58.1	20	19	US-10-671-395-730	Sequence 730, App
18	12.2	58.1	20	20	US-10-695-568-104	Sequence 104, App
19	12.2	58.1	20	20	US-10-695-568-120	Sequence 120, App
20	12.2	58.1	21	22	US-10-736-892-1	Sequence 1, Appli
21	12	57.1	21	20	US-10-751-736-14876	Sequence 14876, A
22	12	57.1	21	20	US-10-751-736-25591	Sequence 25591, A
23	12	57.1	21	20	US-10-751-736-39050	Sequence 39050, A
24	12	57.1	21	20	US-10-751-736-39053	Sequence 39053, A
25	11.8	56.2	16	21	US-10-776-934-100	Sequence 100, App
26	11.8	56.2	16	21	US-10-776-934-540	Sequence 540, App
27	11.8	56.2	16	21	US-10-776-934-541	Sequence 541, App
28	11.8	56.2	16	21	US-10-776-934-542	Sequence 542, App
29	11.8	56.2	16	21	US-10-776-934-543	Sequence 543, App
30	11.8	56.2	17	16	US-10-180-781-50	Sequence 50, Appl
31	11.8	56.2	17	19	US-10-712-672-1359	Sequence 1359, Ap
32	11.8	56.2	17	19	US-10-712-672-1360	Sequence 1360, Ap
33	11.8	56.2	17	19	US-10-712-672-1361	Sequence 1361, Ap
34	11.8	56.2	18	18	US-10-280-183A-215	Sequence 215, Ap
35	11.8	56.2	20	16	US-10-171-319-98	Sequence 98, Appl
36	11.8	56.2	20	16	US-10-171-319-100	Sequence 100, App
37	11.8	56.2	20	17	US-10-177-573-15	Sequence 15, Appl
38	11.8	56.2	20	17	US-10-210-479-26	Sequence 26, Appl
39	11.8	56.2	20	17	US-10-210-479-97	Sequence 97, Appl
40	11.8	56.2	20	19	US-10-619-739-1288	Sequence 1288, Ap
41	11.8	56.2	20	19	US-10-476-021-62	Sequence 62, Appl
42	11.8	56.2	21	9	US-09-765-081-133	Sequence 133, App
43	11.8	56.2	21	21	US-10-847-918-3427	Sequence 3427, Ap
44	11.6	55.2	19	16	US-10-251-117-46	Sequence 46, Appl
45	11.6	55.2	19	16	US-10-251-117-189	Sequence 189, App

ALIGNMENTS

RESULT 1

US-10-774-721-38
; Sequence 38, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774, 721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-38

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2;

us-10-774-721-38.rnpb

Fri Aug 19 08:52:58 2005

Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAGGCA 18
| | | | | : | | | | | | | | | |
Db 3 GCCAGTCCGACAGGCA 20

RESULT 4

US-10-451-805-6/c
; Sequence 6, Application US/10451805
; Publication NO. US2004024809A1
; GENERAL INFORMATION:
; APPLICANT: Goppelt, Andreas
; APPLICANT: Alzheimer, Christian
; APPLICANT: Kogel, Heidi
; TITLE OF INVENTION: Use of Intermediate-Conductance
; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity
; FILE REFERENCE: 50125/080001
; CURRENT APPLICATION NUMBER: US/10/451,805
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/15317
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/277,453
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: DE 10065475.4
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-451-805-6

Query Match 63.8%; Score 13.4; DB 20; Length 16;
Best Local Similarity 80.0%; Pred. No. 8.3e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAG 15
| | | | | : | | | | | | | | | |
Db 15 GCCAGTCCGACAG 1

RESULT 5

US-10-792-280-280
; Sequence 280, Application US/10792280
; Publication NO. US20040234517A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Bowman, Michael
; APPLICANT: Pollettie, Maximilian
; APPLICANT: Chen, Heng, Cara
; APPLICANT: Williams, Cara
; APPLICANT: Ellis, Debra
; APPLICANT: Winkler, Aaron
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR
; TITLE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES
; FILE REFERENCE: AM101023-2
; CURRENT APPLICATION NUMBER: US/10/792,280
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 1535
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 280
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Rnai-sense strand
US-10-792-280-280

Query Match 61.9%; Score 13; DB 20; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.3e+04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAGGCACTT 21
| | | | | : | | | | | | | | | |
Db 1 GCCAGUUCGACAGGCACTT 21

RESULT 2

US-10-774-721-37/c
; Sequence 37, Application US/10774721
; Publication NO. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-37

Query Match 90.5%; Score 19; DB 21; Length 21;
Best Local Similarity 89.5%; Pred. No. 12;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAGGCA 19
| | | | | : | | | | | | | | | |
Db 19 GCCAGTCCGACAGGCA 1

RESULT 3

US-10-774-721-31
; Sequence 31, Application US/10774721
; Publication NO. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS10
US-10-774-721-31

Query Match 85.7%; Score 18; DB 21; Length 20;

Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCAGUCCCGACAGGCCTT 21
|||:|||||
Db 1 GCAAGUCCAGAGCCACUU 21

RESULT 6

US-10-349-780A-195/c
; Sequence 195, Application US/10349780A
; Publication No. US20040146866A1

; GENERAL INFORMATION:

; APPLICANT: Fu, Guoliang

; TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS

; FILE REFERENCE: patent1

; CURRENT APPLICATION NUMBER: US/10/349,780A

; CURRENT FILING DATE: 2003-01-24

; NUMBER OF SEQ ID NOS: 284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 195

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-349-780A-195

Query Match 61.0%; Score 12.8; DB 22; Length 21;

Best Local Similarity 75.0%; Pred. No. 1.6e+04;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGC 17

|||:|||||
Db 16 CCAGTTACCCACAGC 1

RESULT 7

US-09-986-632-27/c

; Sequence 27, Application US/09986632

; Patent No. US20020119944A1

; GENERAL INFORMATION:

; APPLICANT: AGUERA, Michelle

; TITLE OF INVENTION: Modulation of Ulp1/CRMP activity for the prevention or

; FILE REFERENCE: treatment of myelin disorders

; CURRENT APPLICATION NUMBER: US/09/986,632

; CURRENT FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: US 60/246,751

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-986-632-27

Query Match 60.0%; Score 12.6; DB 9; Length 19;

Best Local Similarity 68.4%; Pred. No. 2.1e+04;

Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGCCT 20

|||:|||||
Db 19 CCAGTTACCCAGGAGC 1

RESULT 8

US-10-189-359-16

; Sequence 16, Application US/10189359

; Publication No. US20040039187A1

; GENERAL INFORMATION:

; APPLICANT: MARTIN, Annette

; APPLICANT: SANGAR, DAVID V.

; APPLICANT: LEMON, STANLEY M.
; TITLE OF INVENTION: Chimeric GB Virus B (GBV-B)

; FILE REFERENCE: UTSG:258US

; CURRENT APPLICATION NUMBER: US/10/189,359

; CURRENT FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: 10/189,359

; PRIOR FILING DATE: 2002-07-03

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Primer

US-10-189-359-16

Query Match 60.0%; Score 12.6; DB 18; Length 19;

Best Local Similarity 68.4%; Pred. No. 2.1e+04;

Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGCCT 20

|||:|||||
Db 1 CCAGTTCCGGCAGAGACT 19

RESULT 9

US-10-688-706-1896/c

; Sequence 1896, Application US/10688706

; Publication No. US20040102412A1

; GENERAL INFORMATION:

; APPLICANT: Brochacat, Kay

; APPLICANT: Pharmacia Corp.

; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

; FILE REFERENCE: 01393/1

; CURRENT APPLICATION NUMBER: US/10/688,706

; CURRENT FILING DATE: 2003-10-17

; PRIOR APPLICATION NUMBER: 60/419,268

; PRIOR FILING DATE: 2002-10-17

; NUMBER OF SEQ ID NOS: 3071

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1896

; LENGTH: 20

; TYPE: DNA

; ORGANISM: artificial

; FEATURE:

; OTHER INFORMATION: human GFAT antisense

US-10-688-706-1896

Query Match 60.0%; Score 12.6; DB 19; Length 20;

Best Local Similarity 73.7%; Pred. No. 2.1e+04;

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGCCT 20

|||:|||||
Db 19 CCCGATCCCGCAGGCCT 1

RESULT 10

US-10-688-706-2734/c

; Sequence 2734, Application US/10688706

; Publication No. US20040102412A1

; GENERAL INFORMATION:

; APPLICANT: Brochacat, Kay

; APPLICANT: Pharmacia Corp.

; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

; FILE REFERENCE: 01393/1

; CURRENT APPLICATION NUMBER: US/10/688,706

; CURRENT FILING DATE: 2003-10-17

; PRIOR APPLICATION NUMBER: 60/419,268

; PRIOR FILING DATE: 2002-10-17

; NUMBER OF SEQ ID NOS: 3071

Fri Aug 19 08:52:58 2005

us-10-774-721-38.rnpb

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2734
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GPAT antisense
US-10-688-706-2734

Query Match 60.0%; Score 12.6; DB 19; Length 20;
Best Local Similarity 73.7%; Pred. No. 2.1e+04;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUCCGACGACCT 20
Db 20 CCGATCCCGCAGCCACT 2

RESULT 11
US-10-499-544-15
; Sequence 15, Application US/10499544
; Publication No. US20050130155A1
; GENERAL INFORMATION:
; APPLICANT: Angles d'Auriac, Marc B.
; TITLE OF INVENTION: New primers for the detection and identification of bacterial
; TITLE OF INVENTION: indicator groups and virulence factors
; FILE REFERENCE: F16814USPC
; CURRENT APPLICATION NUMBER: US/10/499,544
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: PCT/NO02/00490
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: NO 20016251
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Enterobacter sp.
US-10-499-544-15

Query Match 59.0%; Score 12.4; DB 22; Length 18;
Best Local Similarity 68.8%; Pred. No. 2.6e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 UUCCGACGACCTT 21
Db 1 TTCCGCGACGCTTT 16

RESULT 12
US-10-173-240-36
; Sequence 36, Application US/10173240
; Publication No. US20030232436A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
; FILE REFERENCE: HTS-0021
; CURRENT APPLICATION NUMBER: US/10/173,240
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-240-36

Query Match 58.1%; Score 12.2; DB 17; Length 20;
Best Local Similarity 82.4%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGUCCGACGACGC 17
Db 3 GCCAGGCCCCGACGCGC 19

RESULT 13
US-10-173-240-70/C
; Sequence 70, Application US/10173240
; Publication No. US20030232436A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
; FILE REFERENCE: HTS-0021
; CURRENT APPLICATION NUMBER: US/10/173,240
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-173-240-70

Query Match 58.1%; Score 12.2; DB 17; Length 20;
Best Local Similarity 82.4%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGUCCGACGACGC 17
Db 18 GCCAGGCCCCGACGCGC 2

RESULT 14
US-10-671-395-382
; Sequence 382, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K.
; TITLE OF INVENTION: ANTISENSE EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 382
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-382

Query Match 58.1%; Score 12.2; DB 19; Length 20;
Best Local Similarity 70.6%; Pred. No. 3.3e+04;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GUUCCGACGACCTT 21
Db 1 GTTCCATCAGCCACTT 17

RESULT 15
US-10-671-395-455
; Sequence 455, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.

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; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 455
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-455

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Query Match      58.1%; Score 12.2; DB 19; Length 20;
Best Local Similarity 70.6%; Pred. NO. 3.3e+04;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy      5 GUUCCCGACAGGCACTT 21
         |||||
Db      3 GTTCCCATCAGCCACTT 19

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Search completed: August 18, 2005, 08:58:48
Job time : 1792 secs

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:17:36 ; Search time 1765 Seconds
(without alignments)
452.889 Million cell updates/sec

Title: US-10-774-721-38

Perfect score: 21
Sequence: 1 gccagucccgacagcactt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gse1:.*
9: gb_gse2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	11.2	53.3	19	8	AZ486389
C 2	10.2	48.6	19	8	AZ763411
C 3	10	47.6	20	1	AL039677
C 4	10	47.6	20	1	AL045408
C 5	10	47.6	21	8	AZ393800
C 6	9.8	46.7	17	9	AJ589126
C 7	9.8	46.7	20	8	AZ593689
C 8	9.6	45.7	16	1	AL039794
C 9	9.6	45.7	18	1	AL039892
C 10	9.6	45.7	18	1	AL043072
C 11	9.6	45.7	19	1	AL042746
C 12	9.6	45.7	19	8	AZ58446
C 13	9.6	45.7	20	1	AL043331
C 14	9.6	45.7	20	1	AL043349
C 15	9.6	45.7	20	9	AG204980
C 16	9.6	45.7	21	8	AZ794033
C 17	9.4	44.8	17	9	AJ589127
C 18	9.4	44.8	19	8	AZ466725
C 19	9.4	44.8	20	8	AZ495853
C 20	9.4	44.8	21	7	C0785256
C 21	9.4	44.8	21	8	AZ806008
C 22	9.2	43.8	15	1	AL039409
C 23	9.2	43.8	21	5	BX315383
C 24	9	42.9	20	1	AU254152

C 25	9	42.9	20	8	AZ318416
C 26	9	42.9	21	7	C0788185
C 27	8.8	41.9	20	8	AZ309156
C 28	8.8	41.9	20	8	AZ386570
C 29	8.8	41.9	20	8	AZ283352
C 30	8.8	41.9	21	1	AL043263
C 31	8.6	41.0	19	1	AI049374
C 32	8.6	41.0	20	8	AZ616822
C 33	8.6	41.0	20	8	AZ789903
C 34	8.4	40.0	19	8	AZ514533
C 35	8.4	40.0	20	8	AZ309592
C 36	8.4	40.0	20	8	AZ325340
C 37	8.4	40.0	21	5	B0593572
C 38	8.4	40.0	21	8	AZ436036
C 39	8.4	40.0	21	8	AZ609424
C 40	8.4	40.0	21	8	AZ665199
C 41	8.2	39.0	13	1	AL043127
C 42	8.2	39.0	14	1	AL039339
C 43	8.2	39.0	15	1	AL043135
C 44	8.2	39.0	15	1	AL043264
C 45	8.2	39.0	15	1	AL043298

ALIGNMENTS

RESULT 1
AZ486389/c
LOCUS
DEFINITION
AZ486389
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ486389 19 bp DNA linear GSS 05-OCT-2000
1M0314E21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0314E21 F, genomic survey sequence.

AZ486389.1 GI:10653117

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0314 row: E column: 21

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0314E21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

Fri Aug 19 08:52:59 2005

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 19;
Best Local Similarity 68.8%; Pred. No. 7.3e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 UUCCGACGACGACTT 21
 :|||||
Db 16 TTCCCATCAGGCATTT 1

RESULT 2

AZ763411/c 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
IM0558B24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0558B24 R, genomic survey sequence.

ACCESSION
AZ763411

VERSION
AZ763411.1 GI:12874413

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermaier, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0558 row: B column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0558B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.6%; Score 10.2; DB 8; Length 19;
Best Local Similarity 73.3%; Pred. No. 2.3e+06;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGUCCGACAG 15
 |||||
Db 18 GCCTGTACCCACAG 4

RESULT 3

AL039677/c 20 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION
DKFZp434H0411.r1.434 (synonym: htes3) Homo sapiens cDNA clone
EST DKFZp434H0411, mRNA sequence.

ACCESSION
AL039677

VERSION
AL039677.1 GI:49682316

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 20)

AUTHORS
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE
EST (Duesterhoeft, et al.)

JOURNAL
Unpublished (1999)

COMMENT
Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

Location/Qualifiers

1..20

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp434H0411"

/tissue_type="testis"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 47.6%; Score 10; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. No. 3e+06;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGUUCGACGACGACTT 21
 |||||
Db 20 AATTCGACCGGTACTT 3

RESULT 4

AL045408/c 20 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION
DKFZp434E105.r1.434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434E105, mRNA sequence.

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ACCESSION      AL045408
VERSION        AL045408.1  GI:49682595
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE         1 (bases 1 to 20)
JOURNAL       Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
COMMENT       Wiemann,S.
               EST (Duesterhoeft, et al.)
               Unpublished (1999)
               Contact: MIPS
               MIPS
               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES      Location/Qualifiers
               1..20
               /organism="Homo sapiens"
               /mol_type="cDNA"
               /db_xref="taxon:9606"
               /clone="DKFZp434E105"
               /tissue_type="testis"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="434 (synonym: htes3)"
               /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match      47.6%; Score 10; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. No. 3e+06;
Matches 1; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy      4 AGUUCGCGACGAGCACTT 21
       |::|::|::|::|::|
Db      20 AATTCGCGACGCGTACCT 3

RESULT 5
ACZ393800/c
LOCUS          AZ393800
DEFINITION    1M0157H04F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
               clone UUCG1M0157H04 F, genomic survey sequence.
ACCESSION     AZ393800
VERSION       AZ393800.1  GI:10508872
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0157 row: H column: 04
               Seq primer: CGTTGTAACGACGCGCAGT
               Class: plasmid ends
               High quality sequence stop: 21.
               Location/Qualifiers
               1..21
               /organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0157H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match      47.6%; Score 10; DB 8; Length 21;
Best Local Similarity 61.1%; Pred. No. 3e+06;
Matches 1; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy      4 AGUUCGCGACGAGCACTT 21
       |::|::|::|::|::|
Db      19 AGTTTTCAGCAGCACTT 2

RESULT 6
AJ589126
LOCUS          AJ589126
DEFINITION    Arabidopsis thaliana T-DNA flanking sequence, left border, clone
               545A02, genomic survey sequence.
ACCESSION     AJ589126
VERSION       AJ589126.1  GI:37938750
KEYWORDS      GSS; left border; T-DNA flanking sequence.
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
               Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
               Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
               Lepiniec,I., Caboche,M., and Lecharny,A.
TITLE         T-DNA integration into the Arabidopsis genome depends on sequences
               of pre-insertion sites
JOURNAL       EMBO Rep. 3 (12), 1152-1157 (2002)
COMMENT       2363535
               1244555
               2 (bases 1 to 17)
               Balzerque,S.
               Direct Submission
               Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
               Gaston Cremieux, 91057 Evry cedex, FRANCE
               PCR was performed on DNA from transformants of Arabidopsis thaliana
               plants from INRA (Versailles). The DNA fragment(8) resulting from
               the PCR were directly sequenced from the left or the right border
               to determine the genomic sequence flanking the insertion. T-DNA
               derived sequences were removed. Information to order the
               corresponding mutant line and a link to a database providing a
               graphical display of the insertion site are available at
               http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
               been generated in the framework of the French plant genomes

```

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program 'genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

FEATURES
source

Location/Qualifiers
1..17
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewska"
/db_xref="taxon:3702"
/clone="545A02"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature
1..17
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 46.7%; Score 9.8; DB 9; Length 17;
Best Local Similarity 69.2%; Pred. No. 3.7e+06;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 UUUCCGACAGCA 18
:|||||
Db 5 TTCCCGACCGGA 17

RESULT 7
AZ593689/c

LOCUS
DEFINITION
M0405C21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0405C21 F, genomic survey sequence.

ACCESSION
AZ593689
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0405 row: C column: 21
Seq primer: CGTGTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0405C21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number was ligated
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 20;
Best Local Similarity 69.2%; Pred. No. 3.7e+06;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CAGUUCGACAG 15
|||||
Db 17 CAGTTACCAACAG 5

RESULT 8
AL039794/c

LOCUS
DEFINITION
DKFZp434B1612_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1612, mRNA sequence.

ACCESSION
AL039794
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Wiemann, S.
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
1 (bases 1 to 16)
TITLE
JOURNAL
COMMENT
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source

Location/Qualifiers
1..16
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZp434B1612"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 45.7%; Score 9.6; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 4.6e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGUUCGACAGCAC 19
|:|||||
Db 16 AATTCCGACCGGTAC 1

RESULT 9
AL039892/c

LOCUS
DEFINITION
DKFZp434G1212_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434G1212, mRNA sequence.
ACCESSION
AL039892
VERSION
AL039892.1 GI:49682352


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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 18)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
FEATURES
source Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
1. .18
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="DKFZp434G1212"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
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Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 4 AGUUCGCCAGCGGTAC 19
| :| | | | | | |
Db 16 AATTCGGACCGGTAC 1

RESULT 10
AL043072/c
LOCUS AL043072 18 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp434B1823 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1823, mRNA sequence.
ACCESSION AL043072
VERSION AL043072.1 GI:49682480
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 18)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
FEATURES
source Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
1. .18
Location/Qualifiers
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/clone="DKFZp434B1823"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 45.7%; Score 9.6; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 4 AGUUCGCCAGCGGTAC 19
| :| | | | | | |
Db 16 AATTCGGACCGGTAC 1

RESULT 11
AL042746/c
LOCUS AL042746 19 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp434C1822 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434C1822, mRNA sequence.
ACCESSION AL042746
VERSION AL042746.1 GI:49682451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
FEATURES
source Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
1. .19
Location/Qualifiers
/organism="Homo sapiens"
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/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
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Query Match 45.7%; Score 9.6; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 4 AGUUCGCCAGCGGTAC 19
| :| | | | | | |
Db 17 AATTCGGACCGGTGC 2

RESULT 12
AZ858446/c
LOCUS AZ858446 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0163D08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0163D08 R, genomic survey sequence.
ACCESSION AZ858446
VERSION AZ858446.1 GI:13051622
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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Db 18 AATTCGGACCGGTAC 3

RESULT 11
AL042746/c
LOCUS AL042746 19 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp434C1822 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434C1822, mRNA sequence.
ACCESSION AL042746
VERSION AL042746.1 GI:49682451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
FEATURES
source Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
1. .19
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="DKFZp434C1822"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 45.7%; Score 9.6; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 4 AGUUCGCCAGCGGTAC 19
| :| | | | | | |
Db 17 AATTCGGACCGGTGC 2

RESULT 12
AZ858446/c
LOCUS AZ858446 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0163D08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0163D08 R, genomic survey sequence.
ACCESSION AZ858446
VERSION AZ858446.1 GI:13051622
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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 High quality sequence stop: 19.
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 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

ORIGIN

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 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCAGUCCGACAGG 16
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 Db 19 GCCAGGATCTACAGG 4

RESULT 13
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 LOCUS
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 DKFZp43402323 mRNA sequence.

ACCESSION AL043331
 VERSION AL043331.1 GI:49682508
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 TITLE EST (Blum, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

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 Db 18 AATTCGGACCGGCAC 3

RESULT 14

AL043349/c

LOCUS

DEFINITION DKFZp434P1923 r1 434 (synonym: htes3) Homo sapiens cDNA clone

DKFZp434P1923 mRNA sequence.

ACCESSION AL043349

VERSION AL043349.1 GI:49682510

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Blum, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Location/Qualifiers

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AG204980/c

LOCUS

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sequence.

ACCESSION AG204980

VERSION AG204980.1 GI:45237155

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

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TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@kriibb.re.kr, URL:http://pbs.grc.kriibb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcorI
R.Site 2 : EcorI.
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Qy 5 GUUCCCGACAGGCACT 20
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Db 17 GGTCCCCCAAGGCACT 2
Search completed: August 18, 2005, 07:56:24
Job time : 1767 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 05:29:57 ; Search time 842 Seconds
(without alignments)
1208.503 Million cell updates/sec

Title: US-10-774-721-38
Perfect score: 21
Sequence: 1 gccaguuccgacaggcactt 21
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: gb.in.*
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5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
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10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	6	CQ860126 Sequence
2	19	90.5	21	6	CQ860125 Sequence
3	18	85.7	20	6	CQ860119 Sequence
4	13.4	63.8	16	6	AX471987 Sequence
5	13.2	62.9	21	6	I25270 Sequence 57
6	12.8	61.0	19	6	AR163030 Sequence
7	12.8	61.0	19	6	I24629 Sequence 13
8	12.8	61.0	19	6	I25226 Sequence 13
9	12.8	61.0	20	6	AR037349 Sequence
10	12.8	61.0	20	6	AR040632 Sequence
11	12.8	61.0	20	6	I19643 Sequence 24
12	12.8	61.0	21	6	CQ848735 Sequence
13	12.4	59.0	18	6	AX797219 Sequence
14	12.4	58.1	21	6	AX614231 Sequence
15	11.8	56.2	17	6	CQ858638 Sequence
16	11.8	56.2	16	6	AR240883 Sequence
17	11.8	56.2	18	6	AX298581 Sequence
18	11.8	56.2	20	6	AR215747 Sequence
19	11.8	56.2	20	6	AX708916 Sequence

20	11.8	56.2	20	6	AX708918 Sequence
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22	11.6	55.2	18	6	AR141884 Sequence
23	11.6	55.2	18	6	E15984 Oligonucleo
24	11.6	55.2	21	8	ZAMRRN04 M82174 Zamia flori
25	11.6	55.2	21	8	ZAMRENA03 M82055 Zamia otton
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34	11.4	54.3	20	6	AR271882 Sequence
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42	11.4	54.3	21	6	I65324 Sequence 46
43	11.4	54.3	21	6	AR530445 Sequence
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45	11.2	53.3	17	6	I87791 Sequence 19

ALIGNMENTS

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LOCUS	CQ860126					
DEFINITION	CQ860126					
ACCESSION	CQ860126.1	GI:51982014				
VERSION						
KEYWORDS						
SOURCE						
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REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
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Best Local Similarity						
Matches						
Qy						
Db						
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LOCUS						
DEFINITION						
ACCESSION						

Fri Aug 19 08:52:57 2005

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VERSION AX471987.1 GI:51982013
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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DEFINITION

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VERSION AX471987.1 GI:22207038
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RESULT 5
LOCUS
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VERSION
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AUTHORS
TITLE
JOURNAL
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Best Local Similarity 72.2%; Pred. No. 1.1e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 CCAGUCCCGACAGGCAC 19
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RESULT 6
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 5270963-A 13 07-AUG-2001;
FEATURES Location/Qualifiers
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Db 4 CCAGTCCCGACAGC 19
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LOCUS Sequence 13 from patent US 5545527.
DEFINITION I24629
ACCESSION I24629
VERSION I24629.1 GI:1604499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Stevens, J.K. and Dunn, J.M.
TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 5545527-A 13 13-AUG-1996;
FEATURES Location/Qualifiers
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LOCUS Sequence 13 from patent US 5550020.
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ACCESSION I25226
VERSION I25226.1 GI:1605096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gallie, B.L., Dunn, J.M. and Stevens, J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for retinoblastoma
JOURNAL Patent: US 5550020-A 13 27-AUG-1996;
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LOCUS Sequence 24 from patent US 5801154.
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SOURCE Unknown.
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REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini, E., Bennett, C. Frank. and Dean, N.M.
TITLE Antisense oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5801154-A 24 01-SEP-1998;
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ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUUCGCGACAGG 16
||||:|||||

Db 5 GCCAGTCCCGACAGG 20
||||:|||||

RESULT 10
AR040632 AR040632 20 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 24 from patent US 5807838.
DEFINITION AR040632
ACCESSION AR040632
VERSION AR040632.1 GI:5959995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini, E., Jr. and Bennett, C. Frank.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5807838-A 24 15-SEP-1998;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUUCGCGACAGG 16
||||:|||||

Db 5 GCCAGTCCCGACAGG 20
||||:|||||

RESULT 11
I19643 I19643 20 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 24 from patent US 5510239.
DEFINITION I19643
ACCESSION I19643
VERSION I19643.1 GI:1599998
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini, E., Jr. and Bennett, C. Frank.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5510239-A 24 07-OCT-1996;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUUCGCGACAGG 16
||||:|||||

Db 5 GCCAGTCCCGACAGG 20
||||:|||||

Fri Aug 19 08:52:57 2005

```

1 (bases 1 to 20)
REFERENCE Baracchini,E. Jr. and Bennett,C.F.
AUTHORS Oligonucleotide modulation of multidrug resistance-associated
TITLE Protein
JOURNAL Patent: US 5510339-A 24 23-APR-1996;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 61.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGUCCCGACAGC 16
Db 5 GCCAGTTCACGACAGG 20
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/mol_type="unassigned DNA"

RESULT 12
CQ848735/c 21 bp DNA linear PAT 19-AUG-2004
LOCUS
DEFINITION Sequence 195 from Patent WO2004065628.
ACCESSION CQ848735
VERSION CQ848735.1 GI:51470163
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fu,G.
TITLE Quantitative multiplex detection of nucleic acids
JOURNAL Patent: WO 2004065628-A 195 05-AUG-2004;
Fu, Guoliang (GB)
FEATURES Location/Qualifiers
source 1..21
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 61.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGC 17
Db 16 CCAGTTCACGACAGC 1
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

RESULT 13
AX797219 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 15 from Patent WO03052143.
ACCESSION AX797219
VERSION AX797219.1 GI:37517872
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS angles D'Auriac,M.B. and Sirevaag,R.
TITLE New primers for the detection and identification of bacterial
indicator groups and virulence factors
JOURNAL Patent: WO 03052143-A 15 26-JUN-2003;
Angles D'Auriac, Marc B. (NO)
FEATURES Location/Qualifiers
source 1..18
/mol_type="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

1 (bases 1 to 20)
REFERENCE Baracchini,E. Jr. and Bennett,C.F.
AUTHORS Oligonucleotide modulation of multidrug resistance-associated
TITLE Protein
JOURNAL Patent: US 5510339-A 24 23-APR-1996;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 18;
Best Local Similarity 68.9%; Pred. No. 2.8e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 UUUCCGACAGGCACATT 21
Db 1 TTCCCGYCAGGCRTTT 16
||||:|||||
/mol_type="unassigned DNA"

RESULT 14
AX614231/c 21 bp DNA linear PAT 17-FEB-2003
LOCUS
DEFINITION Sequence 5256 from Patent WO02072882.
ACCESSION AX614231
VERSION AX614231.1 GI:28409660
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 5256 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES Location/Qualifiers
source 1..21
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 58.1%; Score 12.2; DB 6; Length 21;
Best Local Similarity 70.6%; Pred. No. 3.5e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGCA 18
Db 17 CCAGTTCAGAGAGGCA 1
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

RESULT 15
CQ858638 16 bp DNA linear PAT 31-AUG-2004
LOCUS
DEFINITION Sequence 100 from Patent WO2004069991.
ACCESSION CQ858638
VERSION CQ858638.1 GI:51852605
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hansen,B., Thruue,C.A., Petersen,K.D., Westergaard,M. and
Wissenbach,M.
TITLE Oligomeric compounds for the modulation of survivin expression
JOURNAL Patent: WO 2004069991-A 100 19-AUG-2004;
Santaris Pharma A/S (DK)
FEATURES Location/Qualifiers
source 1..16
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 56.2%; Score 11.8; DB 6; Length 16;
Best Local Similarity 80.0%; Pred. No. 5.7e+05;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGUCCCGACAGC 15

```


Db |||||:|||||
 2 GCCAGTCCCCACAG 16

Search completed: August 18, 2005, 06:53:23
Job time : 846 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 04:18:21 ; Search time 229 Seconds
(without alignments)
542.858 Million cell updates/sec

Title: US-10-774-721-38

Perfect score: 21

Sequence: 1 gccaguccgacggcactt 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	85.7	20	ADR27688	ADR27688 OB-RGRP a
C 2	13.4	63.8	16	ABQ78935	ABQ78935 Mouse int
C 3	13.2	62.9	19	AAQ88255	AAQ88255 Neisseria
4	13.2	62.9	21	AAT11420	AAT11420 Retinobla
C 5	12.8	61.0	18	ADP66743	ADP66743 Mouse KIA
6	12.8	61.0	19	AAT11532	AAT11532 Retinobla
7	12.8	61.0	19	AAT12851	AAT12851 PCR 5' pr
8	12.8	61.0	20	AAQ88849	AAQ88849 Antisense
9	12.8	61.0	20	AAV53600	AAV53600 Nucleotid
C 10	12.8	61.0	21	ADQ31737	ADQ31737 Multiplex
C 11	12.6	60.0	19	ABK91203	ABK91203 Human gli
12	12.6	60.0	19	ADJ56746	ADJ56746 PCR prime
13	12.6	60.0	19	ADJ64258	ADJ64258 Hepatitis
C 14	12.6	60.0	20	ADK94393	ADK94393 Primer of
C 15	12.6	60.0	20	ADP78935	ADP78935 Chimeric
C 16	12.6	60.0	20	ADP78097	ADP78097 Chimeric
17	12.4	59.0	18	ACF05415	ACF05415 Enterobac
C 18	12.4	59.0	21	ADH09468	ADH09468 Propionib
C 19	12.4	59.0	21	ADP46888	ADP46888 Human C-C
C 20	12.2	58.1	17	AAH24024	AAH24024 Yeast GAL

C 21	12.2	58.1	20	3	AAZ95350	AAZ95350 Human mtP
22	12.2	58.1	20	6	ABL52426	ABL52426 Human FLI
C 23	12.2	58.1	20	6	ABL52442	ABL52442 Human FLI
24	12.2	58.1	20	12	ADG72431	ADG72431 Human E2-
C 25	12.2	58.1	20	12	ADG72397	ADG72397 Human E2-
26	12.2	58.1	20	12	ADM14350	ADM14350 Human mPG
27	12.2	58.1	20	12	ADM14543	ADM14543 Human mPG
28	12.2	58.1	20	12	ADM14195	ADM14195 Human mPG
29	12.2	58.1	20	12	ADM14268	ADM14268 Human mPG
C 30	12	57.1	20	3	AAZ95324	AAZ95324 Human mtP
31	11.8	56.2	15	4	AAF53032	AAF53032 IGF-I oli
32	11.8	56.2	15	4	AAF53027	AAF53027 IGF-I oli
33	11.8	56.2	16	13	ADR70031	ADR70031 Human sur
C 34	11.8	56.2	18	6	AA97605	AA97605 Murine SA
C 35	11.8	56.2	18	12	ADMI5945	ADMI5945 Murine SA
C 36	11.8	56.2	20	2	AAV28296	AAV28296 Schizophy
37	11.8	56.2	20	6	ABQ74812	ABQ74812 Human TNF
38	11.8	56.2	20	10	ADG32645	ADG32645 Murine pr
C 39	11.8	56.2	20	10	ADG32643	ADG32643 PCR prime
40	11.8	56.2	20	12	ADI27267	ADI27267 Antisense
41	11.8	56.2	20	12	ADJ86220	ADJ86220 Nucleic a
42	11.8	56.2	20	12	ADJ53366	ADJ53366 Human G p
C 43	11.8	56.2	20	12	ADJ53437	ADJ53437 Human GPC
44	11.8	56.2	21	4	AAF96883	AAF96883 Human gen
C 45	11.8	56.2	21	6	ABK65513	ABK65513 Human Bin

ALIGNMENTS

RESULT 1

ADR27688

ID ADR27688 standard; DNA; 20 BP.

XX

AC ADR27688;

XX

DT 04-NOV-2004 (first entry)

XX

DE OB-RGRP antisense oligonucleotide, AS 10.

XX

KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Optional thioester"

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 20

FT /*tag= d

FT /mod_base= OTHER

FT /note= "3' triethyleneglycol spacer"

XX FR2850971-Al.

XX 13-AUG-2004.

XX

XX 10-FEB-2003; 2003FR-00001543.

XX

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XX 10-FEB-2003; 2003FR-00001543.
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders; e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 85.7%; Score 18; DB 13; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 30;
XX Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCCAGUUCGCCGACAGCA 18
XX Db 3 GCCAGTTCGCCGACAGCA 20
XX
XX RESULT 2
XX ABQ78935/c
XX ID ABQ78935 standard; DNA; 16 BP.
XX
XX AC ABQ78935;
XX
XX XX 04-NOV-2002 (first entry)
XX
XX DE Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
XX
XX KW Mouse; intermediate-conductance potassium channel; dermatological;
XX antiinflammatory; keratolytic; vulnery; antipsoriatic; atopic eczema;
XX contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratosis;
XX hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIK1;
XX PCR; primer; ss.
XX
XX OS Mus musculus.
XX
XX PN WO200253171-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 27-DEC-2001; 2001WO-EP015317.
XX

```

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PR 28-DEC-2000; 2000DE-01065475.
PR 20-MAR-2001; 2001US-0277453P.
XX
XX (SWIT-) SWITCH BIOTECH AG.
XX (UYLU-) UNIV LUDWIG MAXIMILIANS.
XX
XX Goppelt A, Alzheimer C, Koegel H;
XX
XX WPI; 2002-643295/69.
XX
XX Use of intermediate-conductance potassium channel proteins for the
XX diagnosis, prevention and treatment of disorders associated with
XX disturbed keratinocyte activity, especially psoriasis.
XX
XX Example 3; Page 119; 121pp; German.
XX
XX The invention relates to a novel use of intermediate-conductance
XX potassium channel proteins. The proteins of the invention have
XX dermatological, antiinflammatory, keratolytic, vulnery, and
XX antipsoriatic activity. The method is used especially in the field of
XX damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo, lentigo,
XX hyperkeratosis, actinic keratosis, hypertrophic scars, keloids,
XX aged skin, ulcers and especially psoriasis. The sequence represents a PCR
XX primer for the mouse potassium channel protein mIK1 of the invention
XX
XX Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 63.8%; Score 13.4; DB 6; Length 16;
XX Best Local Similarity 80.0%; Pred. No. 6.4e+03;
XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCCAGUUCGCCGACAG 15
XX Db 15 GCCAGTTCGCCGACAG 1
XX
XX RESULT 3
XX AAQ88255/c
XX ID AAQ88255 standard; DNA; 19 BP.
XX
XX AC AAQ88255;
XX
XX XX 25-MAR-2003 (revised)
XX DT 07-DEC-1995 (first entry)
XX
XX DE Neisseria pilC gene constant region probe TR60.
XX
XX KW pilC protein; pilin; pathogenic type 4 pilus bacteria; vaccine;
XX detection; bacterial adhesion; phase variation; constant region; probe;
XX Neisseria gonorrhoeae; Neisseria meningitidis; Pseudomonas aeruginosa;
XX ss.
XX
XX OS Synthetic.
XX
XX PN DE4336530-C1.
XX
XX PD 13-APR-1995.
XX
XX PF 26-OCT-1993; 93DE-04336530.
XX
XX XX 26-OCT-1993; 93DE-04336530.
XX
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX PI Meyer TFF, Rudel T, Ryf RR, Scheuerpflug IB;
XX
XX WPI; 1995-140328/19.
XX
XX Recombinant pilC-proteins derived from Neisseria gonorrhoeae - and their
XX prodn. methods; useful for immunisation against pathogen type 4 pilus
XX carrying bacteria or their detection.
XX
XX Claim 5; Page 12; 29pp; German.
XX

```

XX Sequences coding for pilin PilC proteins from *Neisseria* spp. have been
 CC isolated (see AA08239-Q8241). The pilC1 and pilC2 genes from
 CC *N. gonorrhoeae* have 84% identity. Probes were designed based on regions of
 CC shared homology (see AA08242-88261) and these constant region probes
 CC were used in Southern hybridizations to identify other pilC genes in
 CC *N. gonorrhoeae* strain MS11 and *N. meningitidis* strain A1493. Also, the same
 CC probes were used to screen a *Pseudomonas aeruginosa* strain and identified
 CC a pilC-like sequence. Gene sequences which hybridise with any of the
 CC constant region probes are claimed. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 2; Length 19;
 Best Local Similarity 72.2%; Pred. No. 8.3e+03;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCCAGUCCCGACAGGCA 18
 Db 19 GCCGTTTCCCGACGCGCA 2

RESULT 4
 AAAT11420
 ID AAAT11420 standard; DNA; 21 BP.
 XX
 AC AAAT11420;
 XX
 DT 09-SEP-1996 (first entry)
 XX
 DE Retinoblastoma gene, RB1, exon 1 PCR 5' primer.
 XX
 KW Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;
 KW mutation; polymerase chain reaction; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601908-A1.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US008604.
 XX
 PR 08-JUL-1994; 94US-00271942.
 XX
 PA (VSI-) VISIBLE GENETICS INC.
 PA (HSCR-) HSC RES & DEV LP.
 XX
 PI Gallie BL, Dunn JM, Stevens JK, Hui M;
 XX WPI; 1996-097637/10.
 XX
 PT Identifying mutation(s) in RB1 exons by quantitative amplification - and
 PT by comparing length of amplification products and sequencing, for
 PT diagnosis and genetic screening of retinoblastoma.
 XX
 PS Claim 12; Page 22; 48pp; English.
 XX
 CC AAAT11420-T11473 are PCR amplification primers used for the amplification
 CC of exons 1 to 27 and the promoter of the human retinoblastoma RB1 gene,
 CC used to amplify RB1 exons for use in a method of diagnosing mutations in
 CC the RB1 gene. By comparing the lengths of amplification products of RB
 CC exons from a suspected RB patient with those of RB wild-type DNA,
 CC patients can be diagnosed early which may avoid the need for
 CC radiotherapy. Any difference in length of exons between a suspected RB
 CC patient and those from wild-type RB1 indicates either a deletion or
 CC insertion mutation. Further sequencing of suspect exons can pinpoint the
 CC mutation. The method is directed to the diagnosis of and targeted genetic
 CC screening for retinoblastoma in family members of a retinoblastoma
 CC patient
 XX
 SQ Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 2; Length 21;
 Best Local Similarity 72.2%; Pred. No. 8.4e+03;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCAGUCCCGACAGGCA 19
 Db 4 CCAAGTTCCCGACAGGCA 21

RESULT 5
 ADP66743/c
 ID ADP66743 standard; cDNA; 18 BP.
 XX
 AC ADP66743;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Mouse KIAA0377 forward primer.
 XX
 KW ss; acid phosphatase; BT42-I; BT42; histidine acid phosphatase;
 KW hydrolysis; phosphate ester; BT42-II; deletion; fasting;
 KW genetically induced; obesity; isoform; metabolic disease; dysfunction;
 KW metabolic syndrome; obesity; diabetes; eating disorder; cachexia;
 KW hypertension; coronary heart disease; hypercholesterolaemia;
 KW dyslipidemia; osteoarthritis; gallstone; liver fibrosis; primer.
 XX
 OS Mus sp.
 XX
 PN WO2004050007-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 01-DEC-2003; 2003WO-EP013521.
 XX
 PR 29-NOV-2002; 2002EP-00026693.
 XX
 PA (DEVE-) DEVELOGEN AG.
 XX
 PI Schreiter K;
 XX
 PD WPI; 2004-460971/43.
 XX
 PT New pharmaceutical composition comprising a BT-42 homologous protein or
 PT nucleic acid, and carriers, diluents or/and additives, useful for
 PT treating obesity, hyperlipidemia, osteoarthritis, cell masses.
 XX
 PS Example 4; Page 39; 79pp; English.
 XX
 CC This sequence is a primer which was used in the amplification of the
 CC mouse KIAA0377 coding sequence. KIAA0377 is homologous to human BT42.
 CC BT42 contains the central signature of a histidine acid phosphatase,
 CC which are known to hydrolyze phosphate ester at low pH and are able to
 CC use a wide spectrum of substrates. The two BT42 isoforms of the
 CC invention, BT42-I hypercholesterolaemia of 40 amino acids compared to
 CC mouse BT42. Also BT42-II contains an additional exon of 40 amino acids.
 CC BT42 is regulated by fasting and by genetically induced obesity. BT42,
 CC and the disclosed isoforms, may be used for the manufacture of an agent
 CC for detecting or/and verifying, for the treatment, alleviation and/or
 CC prevention of metabolic diseases or dysfunctions, including metabolic
 CC syndrome, obesity or/and diabetes, as well as related disorders such as
 CC eating disorder, cachexia, hypertension, coronary heart disease,
 CC hypercholesterolaemia, dyslipidemia, osteoarthritis, gallstones, or liver
 CC fibrosis, in cells, cell masses, organs and/or subjects in vivo or in
 CC vitro. The BT42 nucleic acid molecule and polypeptide are useful for the
 CC manufacture of a medicament for the treatment of obesity, diabetes,
 CC or/and metabolic syndrome for controlling the function of a gene or/and a
 CC gene product, which is influenced or/and modified by a BT42 homologous
 CC polypeptide, for identifying substances capable of interacting with a
 CC BT42 homologous polypeptide, and for the production of a non-human
 CC transgenic animal which over- or under-expresses the BT42.
 XX
 SQ Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

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us-10-774-721-38.rng

```

XX AC AAT12851;
XX XX
XX DT 22-OCT-1996 (first entry)
XX DE
XX DE PCR 5' primer for exon 1 of human RB1 (retinoblastoma-1) gene.
XX XX
XX XX PCR; polymerase chain reaction; retinoblastoma; tumour suppressor;
XX KW cancer; mutation; identification; diagnosis; cystic fibrosis;
XX KW hierarchy assay; method; specificity; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO9607761-A2.
XX XX
XX PD 14-MAR-1996.
XX XX
XX PF 07-JUL-1995; 95WO-US008606.
XX XX
XX PR 08-JUL-1994; 94US-00271946.
XX XX
XX PA (VISI-) VISIBLE GENETICS INC.
XX XX
XX PI Dunn JM, Stevens JK, Capatos D, Matthews DE;
XX XX WPI; 1996-171632/17.
XX XX
XX XX Testing for a disease-associated mutation in a gene - using a hierarchy
XX PT of tests selected to optimise performance while minimising cost.
XX XX
XX PS Example 1; Page 32; 63pp; English.
XX XX
XX CC AAT12839-T12899 (excluding AAT12878) are PCR primers used to amplify
XX CC various regions of the RB-1 genome, including exons 1-27, the promoter
XX CC region and a control sequence unrelated to RB-1 from chromosome 15. The
XX CC primers are used in an example of a method for testing a disease-
XX CC associated mutation in a gene, the gene may not necessarily be a tumour
XX CC suppressor gene like the retinoblastoma gene another example is the
XX CC cystic fibrosis transmembrane conductance regulator (CFTR) gene which may
XX CC be analysed using the same method. The primers are used in various
XX CC groupings to produce a hierarchical assay useful to test a group of
XX CC patients suspected to have a genetic mutation. The method allows the
XX CC optimum (or near optimum) diagnostic algorithm by considering the cost
XX CC and the sensitivity and specificity of each test
XX XX
XX SQ Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCGCCACAGGC 17
Db 4 CCAGTTCCCCACAGAC 19

RESULT 8
AAQ86849
ID AAQ86849 standard; DNA; 20 BP.
XX XX
XX AC AAQ86849;
XX XX
XX DT 13-DEC-1995 (first entry)
XX XX
XX DE Antisense oligonucleotide ISIS 8363 hybridises to MRP gene.
XX XX
XX KW Untranslated region; coding sequence; chemotherapeutic drug treatment;
XX KW antisense; modulation; multidrug resistance protein; drug; cancer; ss.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX misc_feature 1. .20
FT
```

```

Query Match 61.0%; Score 12.8; DB 12; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGUUCGCCACAGG 16
Db 16 GCCAGTTCCCCACAGG 1

RESULT 6
AAT11532
ID AAT11532 standard; DNA; 19 BP.
XX XX
XX AC AAT11532;
XX XX
XX DT 10-SEP-1996 (first entry)
XX XX
XX DE Retinoblastoma gene, RB1, exon 1 PCR 5' primer.
XX XX
XX KW Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;
XX KW mutation; polymerase chain reaction; PCR; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO9601908-A1.
XX XX
XX PD 25-JAN-1996.
XX XX
XX PF 07-JUL-1995; 95WO-US008604.
XX XX
XX PR 08-JUL-1994; 94US-00271942.
XX XX
XX PA (VISI-) VISIBLE GENETICS INC.
XX PA (HSCR-) HSC RES & DEV LP.
XX XX
XX PI Gallie BL, Dunn JM, Stevens JK, Hui M;
XX XX WPI; 1996-097637/10.
XX XX
XX XX Identifying mutation(s) in RB1 exons by quantitative amplification - and
XX PT by comparing length of amplification products and sequencing, for
XX PT diagnosis and genetic screening of retinoblastoma.
XX XX
XX PS Claim 12; Page 14; 48pp; English.
XX XX
XX CC AAT11532 is a PCR amplification primer used for the amplification of exon
XX CC 1 of the human retinoblastoma RB1 gene. This primer and many other
XX CC primers (see AAT11420-T11473) are used to amplify RB1 exons for use in a
XX CC method of diagnosing mutations in the RB1 gene. By comparing the lengths
XX CC of amplification products of RB exons from a suspected RB patient with
XX CC those of RB wild-type DNA, patients can be diagnosed early which may
XX CC avoid the need for radiotherapy. Any difference in length of exons
XX CC between a suspected RB patient and those from wild-type RB1 indicates
XX CC either a deletion or insertion mutation. Further sequencing of suspect
XX CC exons can pinpoint the mutation. The method is directed to the diagnosis
XX CC of and targeted genetic screening for retinoblastoma in family members of
XX CC a retinoblastoma patient
XX XX
XX SQ Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCGCCACAGGC 17
Db 4 CCAGTTCCCCACAGAC 19

RESULT 7
AAT12851
ID AAT12851 standard; DNA; 19 BP.
```

```

FT      /*tag= a
FT      /note= "contains phosphorothioate internucleotide
FT      linkages"
XX
XX
XX      WO9510938-A1.
XX
XX      27-APR-1995.
XX
XX      23-SEP-1994; 94WO-US010827.
XX
XX      18-OCT-1993; 93US-00136811.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Baracchini E, Bennett CF;
XX
XX      WPI; 1995-169974/22.
XX
XX      New oligo:nucleotide cpds., esp. for cancer therapy - which are
XX      specifically hybridisable with nucleic acid encoding multi:drug
XX      resistance-associated protein.
XX
XX      Claim 7; Page 11; 36pp; English.
XX
XX      Oligonucleotides AAQ86826-50 are antisense oligonucleotides used to
XX      modulate the expression of the multidrug resistance protein (MRP) by
XX      hybridising with the multidrug resistance (MDR) gene or its RNA message.
XX      This sequence is targeted to the 3' untranslated region (3'UTR) of the
XX      MDR gene. The oligonucleotides can be used to improve the efficacy of
XX      chemotherapeutic drug treatment of a disease such as cancer or to prevent
XX      multidrug resistance developing during drug treatment of a disease
XX
XX      Query Match      61.0%; Score 12.8; DB 2; Length 20;
XX      Best Local Similarity 75.0%; Pred. No. 1.3e+04;
XX      Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      1 GCCAGUCCCGCAGG 16
XX      |||||:|:| | |||
XX      5 GCCAGTTCGCGCAGG 20
XX
XX      Db
XX
XX      RESULT 9
XX      AAV53600
XX      ID      AAV53600 standard; DNA; 20 BP.
XX
XX      AC      AAV53600;
XX
XX      DT      25-MAR-2003 (revised)
XX      DT      20-NOV-1998 (first entry)
XX
XX      DE      Nucleotide sequence of a phosphorothioate oligonucleotide 24.
XX
XX      KW      Phosphorothioate oligonucleotide; antisense; inhibition; cancer;
XX      KW      multidrug resistance; multidrug resistant protein; MRP; chemotherapy; human;
XX      KW      leukotriene; inflammatory condition; ss.
XX
XX      OS      Synthetic.
XX      OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..20
XX      FT      /*tag= a
XX      FT      /note= "phosphorothioate backbone"
XX
XX      PN      US5801154-A.
XX
XX      PD      01-SEP-1998.
XX
XX      PF      08-APR-1997; 97US-00835770.
XX
XX      PR      18-OCT-1993; 93US-00136811.

```

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PR      16-APR-1996; 96US-00628731.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      PI      Bennett CF, Dean NM, Baracchini E;
XX
XX      WPI; 1998-494825/42.
XX
XX      Anti:sense oligo:nucleotide(s) inhibiting multi:drug resistance protein
XX      expression - useful for increasing the efficacy of drugs that certain
XX      conditions have become resistant to e.g. small cell lung cancer.
XX
XX      Claim 11; Col 12; 29pp; English.
XX
XX      This is the nucleotide sequence of the phosphorothioate oligonucleotide
XX      used in the method of the invention, involving the use of antisense
XX      oligonucleotides to inhibit multidrug resistance. The oligonucleotides
XX      are used for the antisense inhibition of multidrug resistance proteins (MRPs).
XX      These proteins are commonly found in some cancers which initially respond
XX      to chemotherapy, but overexpression of the protein leads to chemotherapy
XX      drug resistance. They are administered with the drugs to attempt to
XX      enhance efficacy of the drugs. MRPs are also expressed in other ailments,
XX      and as such, the oligonucleotides can be used to treat these conditions
XX      as well. The sequences are based on the human MRP and are used to treat
XX      conditions such as cancers, especially small-cell lung cancer, prevention
XX      of development of multidrug resistance during chemotherapy, and treatment
XX      of conditions characterised by leukotriene production, especially
XX      inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX      SQ      Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      61.0%; Score 12.8; DB 2; Length 20;
XX      Best Local Similarity 75.0%; Pred. No. 1.3e+04;
XX      Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      1 GCCAGUCCCGCAGG 16
XX      |||||:|:| | |||
XX      5 GCCAGTTCGCGCAGG 20
XX
XX      Db
XX
XX      RESULT 10
XX      ADQ31737/c
XX      ID      ADQ31737 standard; DNA; 21 BP.
XX
XX      AC      ADQ31737;
XX
XX      DT      21-OCT-2004 (first entry)
XX
XX      DE      Multiplex amplification of human SNP fragments, primer #153.
XX
XX      KW      Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP;
XX      KW      single nucleotide polymorphism.
XX
XX      OS      Homo sapiens.
XX      OS      Synthetic.
XX
XX      PN      US2004146866-A1.
XX
XX      PD      29-JUL-2004.
XX
XX      PF      24-JAN-2003; 2003US-00349780.
XX
XX      PR      24-JAN-2003; 2003US-00349780.
XX
XX      PA      (FUGG/) FU G.
XX
XX      PI      Fu G;
XX
XX      WPI; 2004-552653/53.
XX
XX      Analyzing multiple targets in polynucleotide, by providing multiple
XX      primers with target nucleic acids, digesting nucleic acid products with
XX      cognate restriction enzymes, amplifying digested products, and detecting

```

Fri Aug 19 08:52:58 2005

PA (AGUE/) AGUERA M.
PA (BELI/) BELIN M.
PA (CHAR/) CHARRIER E.
PA (HONO/) HONORAT J.
PA (RICA/) RICARD D.
PA (ROGE/) ROGEMOND V.
XX
XX Aguera M, Belin M, Charrier E, Honorat J, Ricard D, Rogemond V;
PI WPI; 2002-627172/67.
XX
XX Prevention or treatment of myelin disorders, such as multiple sclerosis,
PT by administering an agent selected from a Ulp/CRMP protein, a nucleic
PT acid coding for the protein, or an antibody directed against protein.
XX
XX Example; Page 8; 44pp; English.
XX
XX The invention relates to a new method for prevention or treatment of
CC myelin disorders, comprises administering to a patient an effective
CC amount of an agent selected from a Ulp (Unc-33-like protein/CRMP
CC (collapsin response mediator protein) protein, a nucleic acid coding for
CC Ulp/CRMP, an antisense sequence capable of specifically hybridizing with
CC the nucleic acid, an antibody directed against Ulp/CRMP, or an aptamer
CC capable of binding Ulp/CRMP, and a pharmacologically acceptable carrier.
CC Also included are methods of diagnosing a myelin disorder in a subject,
CC identifying agents useful for the prevention or treatment of myelin
CC disorders, using the Ulp/CRMP proteins/nucleic acids, agents capable of
CC modulating the function or expression of the proteins (increasing or
CC decreasing), and a method for identifying an endogenous agent as a
CC therapeutic target for the prevention or the treatment of myelin
CC disorders. The agents are useful for preventing or treating a myelin
CC disorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus
CC 1) associated myelopathy and neurodegenerative diseases (PND), autoimmune
CC disease, paraneoplastic neurodegenerative diseases (PND), autoimmune
CC neurodegenerative disorder. Ulp/CRMP proteins are involved in
CC the processes of myelination, demyelination and remyelination. The
CC to a Ulp/CRMP protein are useful for diagnosing a myelin disorder. The
CC present sequence is a reverse transcriptase (RT)-PCR primer for glial
CC fibrillary associated protein (GFAP, an astrocytic marker protein) used
CC as a control in an experiment to detect mRNA encoding Ulp proteins
XX
XX Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 12.6; DB 6; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.7e+04;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 CCAGUUCGCCGACGAGC 20
Db 19 CCAGTTACCGAGGAGC 1
RESULT 12
ADJ56746
ID ADJ56746 standard; DNA; 19 BP.
XX
XX ADJ56746;
XX
XX 06-MAY-2004 (first entry)
XX
XX PCR primer used to amplify the GBV-B NS5A gene SeqID 16.
XX ss; GB virus B; GBV-B; HCV; flavivirus; hepatitis C virus; antiviral;
XX vaccine; virucidal; antiinflammatory; PCR; primer; NSSA.
XX Hepatitis GB virus B.
XX
XX WO2004005498-A1.
XX
XX 15-JAN-2004.
XX
XX 02-JUL-2003; 2003WO-US021002.
XX
XX

PA amplified products.
PA Example 2; SEQ ID NO 195; 65pp; English.
XX
XX The invention relates analysing multiple targets in polynucleotide,
CC involves providing a set or sets of multiple primers with target nucleic
CC acids in separate reactions of primer extension or amplification, where
CC the reactions produce nucleic acid products in that each nucleic acid
CC fragments comprise at least one restriction site, digesting nucleic acid
CC products of the separate reactions on the restriction sites with cognate
CC restriction enzymes, joining digested products derived from the separate
CC reactions together, where randomly joining nucleic acid fragments, and
CC the separated reactions are created, amplifying the joined products, and
CC detecting the amplified products. Also included are an oligonucleotide
CC primer for detecting target nucleic acid sequence (comprising a 3',
CC complementary portion and 5' non-complementary portion, where the 5' non-
CC complementary portion comprises a restriction enzyme site, where the
CC restriction site acts as detection marker in the process of detecting
CC target nucleic acid sequence, where the detection signal generated from
CC enzymatic manipulation on restriction site of reaction product is
CC indicative of the presence of target nucleic acid sequence) and a kit for
CC use in analysis and detection of multiple targets in a polynucleotide
CC (comprising a set of multiple primers, universal primers,
CC restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all
CC enzymes, and dNTPs). The method is useful for analysing multiple targets
CC in a polynucleotide and for genotyping mutations, preferably single
CC nucleotide polymorphisms (SNPs), and for analysing differential gene
CC expression profiles, genomic methylation patterns and any specific
CC nucleic acids from any source. The method enables analysis of multiple
CC targets quantitatively. An experiment was performed, using the method of
CC the invention, where SNPs were detected in 70 human genomic DNA
CC fragments, simultaneously. The present sequence is a primer used in the
XX
XX above experiment.
XX
XX Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 61.0%; Score 12.8; DB 13; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCAGUUCGCCGACGAGC 17
Db 16 CCAGTTACCGAGGAGC 1
RESULT 11
ABK91203/c
ID ABK91203 standard; DNA; 19 BP.
XX
XX
XX
XX 05-NOV-2002 (first entry)
XX
XX Human glial fibrillary associated protein, GFAP, RT-PCR primer #2.
XX
XX Human; ss; Ulp; CRMP; collapsin response mediator protein; PCR;
XX Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;
XX paraneoplastic neurodegenerative disease; PND; myelination;
XX demyelination; remyelination; myelin disorder; multiple sclerosis;
XX autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;
XX human T lymphocyte virus 1; reverse transcriptase PCR; primer;
XX glial fibrillary associated protein; GFAP.
XX
XX Homo sapiens.
XX
XX US2002119944-A1.
XX
XX 29-AUG-2002.
XX
XX 09-NOV-2001; 2001US-00986632.
XX
XX 09-NOV-2000; 2000US-0246751P.
XX
XX

Fri Aug 19 08:52:58 2005

QY 2 CCAGUUCGACAGGCACT 20
Db 20 CCCGATCCCGCAGGCACT 2

Search completed: August 18, 2005, 06:25:08
Job time : 231 secs

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUUCGACAGGCACT 20
Db 20 CGAGGTCCAGACAGCACT 2

RESULT 15
ADP78935/c
ID ADP78935 standard; DNA; 20 BP.
XX AC ADP78935;
XX DT 12-AUG-2004 (first entry)
XX Chimeric phosphorothioate oligonucleotide #2734.
XX GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..4
FT /*tag= a
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT modified_base 17..20
FT /*tag= b
FT /mod_base= other
FT /note= "2-methoxyethyl wing"

XX WO2004035763-A2.
XX 29-APR-2004.
XX 02-OCT-2003; 2003WO-US033332.
XX 17-OCT-2002; 2002US-0419268P.
XX (PHAA) PHARMACIA CORP.
XX Broschat KO, Crosby SD;
XX WPI; 2004-348453/32.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
XX (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
XX ischemia/reperfusion injury.
XX Claim 4; SEQ ID NO 2734; 175pp; English.
XX The present invention relates to a compound which specifically hybridizes
XX with a nucleic acid molecule encoding GFAT, and inhibits the expression
XX of GFAT. Specifically claimed are antisense oligonucleotides capable of
XX modulating the expression of GFAT, and which comprise any of the 3063
XX sequences of 20 base pairs, given in the specification. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with GFAT, such as a disease or condition, e.g. diabetes, a
XX cardiovascular or neurological disorder, ischemia/reperfusion injury.
XX They are also useful in research and diagnostics for modulating the
XX expression of GFAT. The present sequence represents a chimeric
XX phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
XX oligonucleotides inhibit human GFAT expression.
XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 12; Length 20;
Best Local Similarity 73.7%; Pred. No. 1.7e+04;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:25:21 ; Search time 72.5 Seconds
(without alignments)
473.956 Million cell updates/sec

Title: US-10-774-721-38

Perfect score: 21

Sequence: 1 gccagucccgacaggcaactt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	13.2	62.9	19	3	US-08-637-732A-26
2	13.2	62.9	21	1	US-08-271-942A-57
3	13.2	62.9	21	3	US-08-779-916A-57
4	13.2	62.9	21	5	PCT-US95-08604-57
5	12.8	61.0	19	1	US-08-271-946A-13
6	12.8	61.0	19	1	US-08-271-942A-13
7	12.8	61.0	19	3	US-08-779-916A-13
8	12.8	61.0	19	3	US-08-750-232-13
9	12.8	61.0	19	5	PCT-US95-08604-13
10	12.8	61.0	20	1	US-08-136-811-24
11	12.8	61.0	20	1	US-08-835-770-24
12	12.8	61.0	20	1	US-08-628-731-24
13	12.8	61.0	20	3	US-09-275-680-7
C 14	12.2	58.1	17	3	US-09-366-257-38
C 15	12.2	58.1	20	3	US-09-366-257-38
C 16	12	57.1	20	3	US-09-366-257-12
C 17	11.8	56.2	17	3	US-09-375-318-50
18	11.8	56.2	20	3	US-09-844-634-62
19	11.8	56.2	20	4	US-10-177-573-15
20	11.6	55.2	18	2	US-08-897-340-26
21	11.6	55.2	18	3	US-09-252-329-26
22	11.6	55.2	20	3	US-09-418-641-23
23	11.6	55.2	21	4	US-09-693-205A-34
24	11.4	54.3	15	3	US-09-054-832-27
25	11.4	54.3	15	4	US-09-640-953-27
26	11.4	54.3	18	3	US-09-054-830-17
C 27	11.4	54.3	18	3	US-09-658-679A-5

28 11.4 54.3 18 4 US-09-431-385-17 Sequence 17, Appl
29 11.4 54.3 20 2 US-08-229-528-42 Sequence 42, Appl
30 11.4 54.3 20 4 US-09-657-346A-126 Sequence 126, Appl
c 31 11.4 54.3 21 1 US-08-116-389-4 Sequence 4, Appl
32 11.4 54.3 21 1 US-08-066-325-46 Sequence 46, Appl
33 11.4 54.3 21 1 US-08-708-431-4 Sequence 4, Appl
c 34 11.4 54.3 21 1 US-08-912-976-3 Sequence 3, Appl
c 35 11.4 54.3 21 2 US-08-880-830-4 Sequence 4, Appl
c 36 11.4 54.3 21 4 US-09-657-472-1648 Sequence 1648, Ap
c 37 11.4 54.3 21 5 PCT-US94-13895-4 Sequence 4, Appl
38 11.2 53.3 17 1 US-08-369-796-19 Sequence 19, Appl
39 11.2 53.3 17 2 US-08-852-091-19 Sequence 19, Appl
40 11.2 53.3 17 5 PCT-US95-17025-19 Sequence 19, Appl
41 11.2 53.3 18 1 US-08-484-816-23 Sequence 23, Appl
42 11.2 53.3 18 1 US-08-476-625-23 Sequence 23, Appl
43 11.2 53.3 18 2 US-08-949-076-23 Sequence 23, Appl
44 11.2 53.3 18 2 US-08-484-519-23 Sequence 23, Appl
45 11.2 53.3 20 2 US-08-651-692-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-637-732A-26/c
; Sequence 26, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant Pilc Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/637,732A
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer T60"
US-08-637-732A-26

Query Match 62.9%; Score 13.2; DB 3; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCCAGUCCCCACAGGCA 18

us-10-774-721-38.rni

Fri Aug 19 08:52:58 2005

19 GCCGTTCCCGACTGGCA 2

Db

RESULT 2

US-08-271-942A-57
; Sequence 57, Application US/08271942A

; Patent No. 5550020

; GENERAL INFORMATION:

; APPLICANT: Gallie, Brenda L.

; APPLICANT: Dunn, James M.

; APPLICANT: Stevens, John K.

; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma

; NUMBER OF SEQUENCES: 123

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: 1992 Commerce Street, Suite 309

; CITY: Yorktown Heights

; STATE: NY

; COUNTRY: USA

; ZIP: 10598-4412

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS 5.0

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/271,942A

; FILING DATE: 08-JUL-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Marina T. Larson

; REGISTRATION NUMBER: 32,038

; REFERENCE/DOCKET NUMBER: VGEN.P-003-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 245-3252

; TELEFAX: (914) 962-4330

; TELEX:

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; HYPOTHETICAL: no

; ANTI-SENSE: no

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: human

; FEATURE:

; NAME/KEY: primer for exon 1 of human RB1 gene

; US-08-271-942A-57

Query Match

Best Local Similarity 62.9%; Score 13.2; DB 1; Length 21;

Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY

2 CCAGUUCGCGACGAGC 19

4 CCAGTTCGCCACAGC 21

Db

RESULT 3

US-08-779-916A-57

; Sequence 57, Application US/08779916A

; Patent No. 6063567

; GENERAL INFORMATION:

; APPLICANT: Gallie, Brenda L.

; APPLICANT: Dunn, James M.

; APPLICANT: Stevens, John K.

; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma

; NUMBER OF SEQUENCES: 123

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: 1992 Commerce Street, Suite 309

; CITY: Yorktown Heights

; STATE: NY

; COUNTRY: USA

; ZIP: 10598-4412

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS 5.0

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,916A

; FILING DATE: 07-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/271,942

; FILING DATE: 08-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Marina T. Larson

; REGISTRATION NUMBER: 32,038

; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 245-3252

; TELEFAX: (914) 962-4330

; TELEX:

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; HYPOTHETICAL: no

; ANTI-SENSE: no

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: human

; FEATURE:

; NAME/KEY: primer for exon 1 of human RB1 gene

; US-08-779-916A-57

Query Match

Best Local Similarity 72.2%; Score 13.2; DB 3; Length 21;

Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY

2 CCAGUUCGCGACGAGC 19

4 CCAGTTCGCCACAGC 21

Db

RESULT 4

PCT-US95-08604-57

; Sequence 57, Application PC/TUS9508604

; GENERAL INFORMATION:

; APPLICANT: Visible Genetics Inc.

; APPLICANT: HSC Research and Development Limited Partnership

; APPLICANT: Gallie, Brenda L.

; APPLICANT: Dunn, James M.

; APPLICANT: Stevens, John K.

; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma

; NUMBER OF SEQUENCES: 125

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: 1992 Commerce Street, Suite 309

CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,942
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
FEATURE:
NAME/KEY: primer for exon 1 of human RB1 gene
PCT-US95-08604-57
Query Match 62.9%; Score 13.2; DB 5; Length 21;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CCAGUCCCCGACAGGC 19
Db 4 CCAGTCCCCCAGCAGC 21
RESULT 5
US-08-271-946A-13
Sequence 13, Application US/08271946A
Patent No. 5545527
GENERAL INFORMATION:
APPLICANT: Stevens, John K.
APPLICANT: Dunn, James M.
TITLE OF INVENTION: Method for Testing for Mutations in DNA
TITLE OF INVENTION: from a Patient Sample
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271.946A

FILING DATE: 08-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-002-US
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
FEATURE:
NAME/KEY: primer for exon 1 of human RB1 gene
US-08-271-946A-13
Query Match 61.0%; Score 12.8; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CCAGUCCCCGACAGGC 17
Db 4 CCAGTCCCCCAGCAGC 19
RESULT 6
US-08-271-942A-13
Sequence 13, Application US/08271942A
Patent No. 5550020
GENERAL INFORMATION:
APPLICANT: Gallie, Brenda L.
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271.942A
FILING DATE: 08-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US
TELECOMMUNICATION INFORMATION:

us-10-774-721-38.rni

Fri Aug 19 08:52:58 2005

```
;
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
;
US-08-271-942A-13
Query Match 61.0%; Score 12.8; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUCCCCGACGAGC 17
| | | | | | | | | |
Db 4 CCAGTTCCTCCACAGAC 19

RESULT 7
US-08-779-916A-13
; Sequence 13, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; APPLICANT: Hui, May
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Opedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
;
US-08-779-916A-13
Query Match 61.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUCCCCGACGAGC 17
| | | | | | | | | |
Db 4 CCAGTTCCTCCACAGAC 19

RESULT 8
US-08-750-232-13
; Sequence 13, Application US/08750232
; Patent No. 6270963
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Opedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,946
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
;
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
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US-08-750-232-13

Query Match 61.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCAGUCCCGACAGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 4 CCAGTCCCGACAGC 19

RESULT 9

PCT-US95-08604-13
; Sequence 13, Application PC/TUS9508604
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: HSC Research and Development Limited Partnership
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08604
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
PCT-US95-08604-13

Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCAGUCCCGACAGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 4 CCAGTCCCGACAGC 19

RESULT 10
PCT-US95-08606-13
; Sequence 13, Application PC/TUS9508606
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,946
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
PCT-US95-08606-13

Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCAGUCCCGACAGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 4 CCAGTCCCGACAGC 19

RESULT 11
US-08-136-811-24
; Sequence 24, Application US/08136811
; Patent No. 5510239
; GENERAL INFORMATION:
; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
; APPLICANT: Clarence Frank

us-10-774-721-38.rni

Fri Aug 19 08:52:58 2005

```

;
; TITLE OF INVENTION: Oligonucleotide Interference with
; TITLE OF INVENTION: Multidrug Resistance
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,811
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-136-811-24

Query Match 61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUCCGACAGG 16
Db 5 GCCAGTTCGACGAGG 20
|||||:|||||

RESULT 12
US-08-835-770-24
; Sequence 24, Application US/08835770
; Patent No. 5801154
; GENERAL INFORMATION:
; APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett
; APPLICANT: and Nicholas M. Dean
; TITLE OF INVENTION: Oligonucleotide Modulation of Multidrug
; TITLE OF INVENTION: Resistance-Associated Protein
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,770
; FILING DATE: Herewith
; CLASSIFICATION: 514

```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,811
; FILING DATE: 10/18/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/628,731
; FILING DATE: 04/16/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-835-770-24

Query Match 61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUCCGACAGG 16
Db 5 GCCAGTTCGACGAGG 20
|||||:|||||

RESULT 13
US-08-628-731-24
; Sequence 24, Application US/08628731
; Patent No. 5807838
; GENERAL INFORMATION:
; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
; APPLICANT: Clarence Frank
; TITLE OF INVENTION: Oligonucleotide Interference with
; TITLE OF INVENTION: Multidrug Resistance
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,731
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,811
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear

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; ANTI-SENSE: Yes
US-08-628-731-24

Query Match      61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUCCCGACAGG 16
Db 5 GCCAGTTCCAGGCAGG 20
      |||||:| | |||
      |||||:| | |||

RESULT 14
US-09-275-680-7/c
; Sequence 7, Application US/09275680
; Patent No. 6221630
; GENERAL INFORMATION:
; APPLICANT: Hopper, James E
; TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
; TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
; FILE REFERENCE: 98428
; CURRENT APPLICATION NUMBER: US/09/275,680
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7

Query Match      58.1%; Score 12.2; DB 3; Length 17;
Best Local Similarity 70.6%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCCAGUCCCGACAGGC 17
Db 17 GCCAGTTGTCAACAGGC 1
      |||||:| | |||
      |||||:| | |||

RESULT 15
US-09-366-257-38/c
; Sequence 38, Application US/09366257
; Patent No. 6030837
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-MITOCHONDRIAL EXPRESSION
; FILE REFERENCE: RTS-0073
; CURRENT APPLICATION NUMBER: US/09/366,257
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-366-257-38

Query Match      58.1%; Score 12.2; DB 3; Length 20;
Best Local Similarity 76.5%; Pred. No. 5.6e+03;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CAGUCCCGACAGGCAC 19
Db 20 CAGTGCCCGAGAGACAC 4
      |||:| | | | |
      |||:| | | | |
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Search completed: August 18, 2005, 07:58:56
Job time : 74.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 00:02:48 ; Search time 852 Seconds
(without alignments)
8494.798 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gctcgttggcaggctgc.....gttacctgcattgttta 1114

Scoring table: IDENTITY NUC
Gap 10.0, Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1114	100.0	1114	21	US-10-774-721-21
2	1114	100.0	1114	21	Sequence 21, Appl
3	1111.6	99.8	2732	9	US-10-956-157-2162
4	1111.6	99.8	2732	9	Sequence 2162, Ap
5	1077	96.7	1156	17	US-09-925-302-178
6	869.6	78.1	874	10	US-09-925-302-178
7	768.4	69.0	207542	22	US-10-893-315-148
					Sequence 178, App
					Sequence 161, App
					Sequence 2, Appl
					Sequence 148, App

8	768.4	69.0	207557	22	US-10-893-315-134	Sequence 134, App
9	648	58.2	648	21	US-10-774-721-1	Sequence 1, Appl
10	600	53.9	600	21	US-10-956-157-7397	Sequence 7397, Ap
11	599.6	53.8	601	22	US-10-893-315-733	Sequence 733, App
12	577.4	51.8	647	19	US-10-283-975A-466	Sequence 466, App
13	396	35.5	396	14	US-10-038-010-23	Sequence 23, Appl
14	396	35.5	396	21	US-10-774-721-3	Sequence 3, Appl
15	393	35.3	1128	21	US-10-774-721-5	Sequence 7, Appl
16	393	35.3	1359	21	US-10-774-721-5	Sequence 5, Appl
17	349.6	31.4	384	17	US-10-242-535A-41292	Sequence 41292, A
18	349.6	31.4	384	18	US-10-085-783A-41292	Sequence 41292, A
19	174.6	15.7	664	20	US-10-842-740-56	Sequence 56, Appl
20	174.6	15.7	770	9	US-09-984-245-82	Sequence 82, Appl
21	174.6	15.7	770	10	US-09-986-262-82	Sequence 82, Appl
22	174.6	15.7	770	10	US-09-983-966-82	Sequence 82, Appl
23	174.6	15.7	770	14	US-10-059-395-82	Sequence 82, Appl
24	174.6	15.7	770	14	US-10-143-090-82	Sequence 82, Appl
25	174.6	15.7	770	17	US-10-264-237-552	Sequence 552, App
26	174.6	15.7	770	21	US-10-960-251-82	Sequence 82, Appl
27	174.6	15.7	2694	9	US-09-989-722-275	Sequence 275, App
28	174.6	15.7	2694	9	US-09-989-723-275	Sequence 275, App
29	174.6	15.7	2694	9	US-09-989-279-275	Sequence 275, App
30	174.6	15.7	2694	9	US-09-989-727-275	Sequence 275, App
31	174.6	15.7	2694	9	US-09-989-731-275	Sequence 275, App
32	174.6	15.7	2694	9	US-09-989-732-275	Sequence 275, App
33	174.6	15.7	2694	9	US-09-991-073-275	Sequence 275, App
34	174.6	15.7	2694	9	US-09-990-442-275	Sequence 275, App
35	174.6	15.7	2694	9	US-09-991-163-275	Sequence 275, App
36	174.6	15.7	2694	9	US-09-993-604-275	Sequence 275, App
37	174.6	15.7	2694	9	US-09-990-456-275	Sequence 275, App
38	174.6	15.7	2694	9	US-09-989-721-275	Sequence 275, App
39	174.6	15.7	2694	9	US-09-992-598-275	Sequence 275, App
40	174.6	15.7	2694	9	US-09-989-293A-275	Sequence 275, App
41	174.6	15.7	2694	9	US-09-989-735-275	Sequence 275, App
42	174.6	15.7	2694	9	US-09-990-444-275	Sequence 275, App
43	174.6	15.7	2694	9	US-09-991-181-275	Sequence 275, App
44	174.6	15.7	2694	9	US-09-990-730-275	Sequence 275, App
45	174.6	15.7	2694	9	US-09-990-436-275	Sequence 275, App

ALIGNMENTS

RESULT 1

US-10-774-721-21
; Sequence 21, Application US/10774721
; Publication No: US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774, 721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461, 005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-774-721-21

Query Match 100.0%; Score 1114; DB 21; Length 1114;

Best Local Similarity 100.0%; Pred. No. 2.6e-309; Indels 0; Gaps 0;
Matches 1114; Conservative 0; Mismatches 0;

QY 1 GTCTGGCTTGGCAGGCTGCCGGGCGGTGCGCAGGAAGCGGAAAGAGCGCGGCCCGCCAG 60
Db 1 GTCTGGCTTGGCAGGCTGCCGGGCGGTGCGCAGGAAGCGGAAAGAGCGCGGCCCGCCAG 60
QY 61 TTCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 61 TTCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGCTTACTGGCCCTTATT 180
Db 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGCTTACTGGCCCTTATT 180
QY 181 CGTCTGATTTTCACGCGCATCTCCCGCATCCCGCATTCATTCGCCAAAGAGTCACCTA 240
Db 181 CGTCTGATTTTTCACGCGCATCTCCCGCATTCATTCGCCAAAGAGTCACCTA 240
QY 241 TGACCTCAGATGAACAGTAGTGCCTGTCGGAACTGGCATATTTCTTCACTACTGGAAT 300
Db 241 TGACCTCAGATGAACAGTAGTGCCTGTCGGAACTGGCATATTTCTTCACTACTGGAAT 300
QY 301 TGTGTGTTCTGCTTGGGATTTCTGTATTCTTGTCTGTGGCTGTGATCAAAATGGG 360
Db 301 TGTGTGTTCTGCTTGGGATTTCTGTATTCTTGTCTGTGGCTGTGATCAAAATGGG 360
QY 361 AGCTCGGGCTTGTGTTGGCAGCAATGAGTCATTTTCCCTTACAAATTCAGGGTTTTT 420
Db 361 AGCTCGGGCTTGTGTTGGCAGCAATGAGTCATTTTCCCTTACAAATTCAGGGTTTTT 420
QY 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480
Db 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480
QY 481 TACAGTGCAATGAAATTTTTCAGTCTGATATCTGATACATGTCGACATGCGGCATT 540
Db 481 TACAGTGCAATGAAATTTTTCAGTCTGATATCTGATACATGTCGACATGCGGCATT 540
QY 541 TTACTATGAATTTTAAATGCTGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600
Db 541 TTACTATGAATTTTAAATGCTGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600
QY 601 GAAAGACTTCATTAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAAATTAG 660
Db 601 GAAAGACTTCATTAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAAATTAG 660
QY 661 ATTATGTTACTCAAAATTAATGTTTACTTGTGCTGTTTGTGCTGTTTGTGCTGCTCAGAG 720
Db 661 ATTATGTTACTCAAAATTAATGTTTACTTGTGCTGTTTGTGCTGTTTGTGCTGCTCAGAG 720
QY 721 AAATATATTAACGCACTCTTGTAGGCACTGCCACCTTATGCAATGCAATCGAAACCTTTT 780
Db 721 AAATATATTAACGCACTCTTGTAGGCACTGCCACCTTATGCAATGCAATCGAAACCTTTT 780
QY 781 GCTTGGGATGTCTTGAGAGGCGAGATAAGCTGAGCAGGCTCTCATGACCCAGGAA 840
Db 781 GCTTGGGATGTCTTGAGAGGCGAGATAAGCTGAGCAGGCTCTCATGACCCAGGAA 840
QY 841 GSCCGGGTGGATCCCTCTTGTGTGTGTAGTCCATGCTTATTAAGTGTGSCCCACAGAC 900
Db 841 GSCCGGGTGGATCCCTCTTGTGTGTGTAGTCCATGCTTATTAAGTGTGSCCCACAGAC 900
QY 901 CAAGAGCCTCAACATTTCTAGAGCCTTATAGAAATGCAATCTGAGGCCCTCTG 960
Db 901 CAAGAGCCTCAACATTTCTAGAGCCTTATAGAAATGCAATCTGAGGCCCTCTG 960
QY 961 GACCCAGGATTTTGTAGATCCAAAGGAGTCTGATGCAATGAAAGTTTGAAGACA 1020
Db 961 GACCCAGGATTTTGTAGATCCAAAGGAGTCTGATGCAATGAAAGTTTGAAGACA 1020
QY 1021 TCATCATAGAGAAGTAAACATCACACCCAACTTCCTTATCTTTCAGTGGCTTAAACCACT 1080
Db 1021 TCATCATAGAGAAGTAAACATCACACCCAACTTCCTTATCTTTCAGTGGCTTAAACCACT 1080
QY 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114

Db 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114
RESULT 2
US-10-956-157-2162
; Sequence 2162, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounse, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH.
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2162
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-2162
Query Match 100.0%; Score 1114; DB 21; Length 1114;
Best Local Similarity 100.0%; Pred. No. 2.6e-309; Indels 0; Gaps 0;
Matches 1114; Conservative 0; Mismatches 0;
QY 1 GTCGTGCTTGGCAGGCTGCCGGGCGGTGCGCAGGAAGCGGAAAGAGCGCGGCCCGCCAG 60
Db 1 GTCGTGCTTGGCAGGCTGCCGGGCGGTGCGCAGGAAGCGGAAAGAGCGCGGCCCGCCAG 60
QY 61 TTCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 61 TTCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGCTTACTGGCCCTTATT 180
Db 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGCTTACTGGCCCTTATT 180
QY 181 CGTCTGATTTTTCACGCGCATCTCCCGCATTCCTTACAAAGAGTCACCTA 240
Db 181 CGTCTGATTTTTCACGCGCATCTCCCGCATTCCTTACAAAGAGTCACCTA 240
QY 241 TGACCTCAGATGAACAGTAGTGCCTGTCGGAACTGGCATATTTCTTCACTACTGGAAT 300
Db 241 TGACCTCAGATGAACAGTAGTGCCTGTCGGAACTGGCATATTTCTTCACTACTGGAAT 300
QY 301 TGTGTGTTCTGCTTGGGATTTCTGTATTCTTGTCTGTGGCTGTGATCAAAATGGG 360
Db 301 TGTGTGTTCTGCTTGGGATTTCTGTATTCTTGTCTGTGGCTGTGATCAAAATGGG 360
QY 361 AGCTCGGGCTTGTGTTGGCAGCAATGAGTCATTTTCCCTTACAAATTCAGGGTTTTT 420
Db 361 AGCTCGGGCTTGTGTTGGCAGCAATGAGTCATTTTCCCTTACAAATTCAGGGTTTTT 420
QY 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480
Db 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480
QY 481 TACAGTGCAATGAAATTTTTCAGTCTGATATCTGATACATGTCGACATGCGGCATT 540
Db 481 TACAGTGCAATGAAATTTTTCAGTCTGATATCTGATACATGTCGACATGCGGCATT 540
QY 541 TTACTATGAATTTTAAATGCTGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600
Db 541 TTACTATGAATTTTAAATGCTGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600
QY 601 GAAAGACTTCATTAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAAATTAG 660
Db 601 GAAAGACTTCATTAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAAATTAG 660
QY 661 ATTATGTTACTCAAAATTAATGTTTACTTGTGCTGTTTGTGCTGTTTGTGCTGCTCAGAG 720

661	Db		ATTATGTTACTCAAATTTATGTTACTGTTTGGCTGTTTCATGTAGTCAAGGTGCTCTCAGA	720
721	Qy		AAATATATTAAACGAGTCTTGTCGAGAGTCGCCACCTTATGSCAGTGCATCGAAACCTTTT	780
721	Db		AAATATATTAAACGAGTCTTGTCGAGAGTCGCCACCTTATGSCAGTGCATCGAAACCTTTT	780
781	Qy		GCTTGGGGATGTGCTTGAGAGGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA	840
781	Db		GCTTGGGGATGTGCTTGAGAGGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA	840
841	Qy		GGCCGGGGTGATCCCTCTTTGTGTGTGTCAGTGTATTTAAAGTGTGGCCCCACAGAC	900
841	Db		GGCCGGGGTGATCCCTCTTTGTGTGTGTCAGTGTATTTAAAGTGTGGCCCCACAGAC	900
901	Qy		CAAGAGCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGATCTGAAGCCCCACTCTG	960
901	Db		CAAGAGCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGATCTGAAGCCCCACTCTG	960
961	Qy		GACCCAGACATTTTGTATGAGATCCAAGGAGTTGTATGCACATGAAGTTTGAAGAACA	1020
961	Db		GACCCAGACATTTTGTATGAGATCCAAGGAGTTGTATGCACATGAAGTTTGAAGAACA	1020
1021	Qy		TCATCATAGAGAAGTAACATCACACCCAACCTCTCTTATCTTTCCAGTGGCTAAACCACT	1080
1021	Db		TCATCATAGAGAAGTAACATCACACCCAACCTCTCTTATCTTTCCAGTGGCTAAACCACT	1080
1081	Qy		TAACTCTCTGGGTGTACCTGCTCATTTGTTTA	1144
1081	Db		TAACTCTCTGGGTGTACCTGCTCATTTGTTTA	1144

RESULT 3

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US-09-925-302-178
; Sequence 178, Application US/09925302
; Patent NO. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1653)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2664)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2699)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-302-178

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Query Match	99.8%	Score 1111.6;	DB 9;	Length 2732;
Best Local Similarity	99.7%	Pred. No. 2.2e-308;		
Matches 1111;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	GTCTGGCTTGGCGAGGTGCTCCCGGGCCGTCGACAGAACCCGGAAGACGCGCGCCCCCAG	60	
Db	18	GTCTGGCTTGGCGAGGTGTCMCGGGCCGTCGACAGAACCCGGAAGACGCGCGCCCCCAG	77	
Oy	61	TTCCGGGAGACATGCGGGCGGCTTAAAGTCTCTGGGCATTATCTTTCAGTGGGGCTATTGG	120	

RESULT 4

Db	78	 CTCGGAGACATGCGCGGCGTTAAAGCTCTCGTGGCAATTATCCCTTCAGTGGGCGCTATTGG	137
Qy	121	 ACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATTAATGGCTTTTACTTGGGCCCTTATT	180
Db	138	 ACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATTAATGGCTTTTACTTGGGCCCTTATT	197
Qy	181	 CGTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTCAATGCGCAAAAGAGTCAACCTA	240
Db	198	 CGTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTCAATGCGCAAAAGAGTCAACCTA	257
Qy	241	 TGACTCAGATGCAACAGTAGTGCCTGTGCGGNACTGGCATATTTCTTCACTACTGGAAT	300
Db	258	 TGACTCAGATGCAACAGTAGTGCCTGTGCGGNACTGGCATATTTCTTCACTACTGGAAT	317
Qy	301	 TGTGTGTTTCTGCGCTTTGGGATTTCTCGTATATCTTGTCTGTGTGCTGTGATCAAAATGGGG	360
Db	318	 TGTGTGTTTCTGCGCTTTGGGATTTCTCGTATATCTTGTCTGTGTGCTGTGATCAAAATGGGG	377
Qy	361	 AGCCTCGGCGCTTGTGTGGCAGGCAATGCAGTCAATTTCTCTTCAAAATCAAGGGTTTTT	420
Db	378	 AGCCTCGGCGCTTGTGTGGCAGGCAATGCAGTCAATTTCTCTTCAAAATCAAGGGTTTTT	437
Qy	421	 CCATTATTTTGGAGAGGAGATCAATTTAGCTGGGAGCAGTGGTAGCATCTTTATCTCTGAT	480
Db	438	 CCATTATTTTGGAGAGGAGATCAATTTAGCTGGGAGCAGTGGTAGCATCTTTATCTCTGAT	497
Qy	481	 TACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATTT	540
Db	498	 TACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATTT	557
Qy	541	 TTACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACCTTTAA	600
Db	558	 TTACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTTATATATCATGTTCACCTTTAA	617
Qy	601	 GAAGACTTCATAGTAGGAGATGAGTTTTTCTCAGCAAAATAGACCTGTCAAAATTTAG	660
Db	618	 GAAGACTTCATAGTAGGAGATGAGTTTTTCTCAGCAAAATAGACCTGTCAAAATTTAG	677
Qy	661	 ATTATGTTACTCAAAATTTATGTTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTCTCAGA	720
Db	678	 ATTATGTTACTCAAAATTTATGTTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTCTCAGA	737
Qy	721	 AAATATATTAACCGAGTCTTTGTAGGACGTGCCACTTATGCAAGTGCATCGAAACCTTTT	780
Db	738	 AAATATATTAACCGAGTCTTTGTAGGACGTGCCACTTATGCAAGTGCATCGAAACCTTTT	797
Qy	781	 GCTTTGGGATGCTTTGGAGGACGATACCGCTGAAGCAGCGCTCTCATGACCCAGGAA	840
Db	798	 GCTTTGGGATGCTTTGGAGGACGATACCGCTGAAGCAGCGCTCTCATGACCCAGGAA	857
Qy	841	 GGCGGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTTAAAGTGTGGCCCAACAGAC	900
Db	858	 GGCGGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTTAAAGTGTGGCCCAACAGAC	917
Qy	901	 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAAGATCTGAAGCCCACTCTG	960
Db	918	 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAAGATCTGAAGCCCACTCTG	977
Qy	961	 GACCCAGGACATTTTGCATGAGATCCAAAGGAGTTGTATGCACATGAAGATTTTGAGAAGCA	1020
Db	978	 GACCCAGGACATTTTGCATGAGATCCAAAGGAGTTGTATGCACATGAAGATTTTGAGAAGCA	1037
Qy	1021	 TCATCATAGAGAAGTAAACATCACACCCAACTTCTCTTATCTTTTCCAGTGGCTAAACCCT	1080
Db	1038	 TCATCATAGAGAAGTAAACATCACACCCAACTTCTCTTATCTTTTCCAGTGGCTAAACCCT	1097
Qy	1081	 TAACCTCTCTGGGTGTTTACTGCTCATTTGTGTTTA	1114
Db	1098	 TAACCTCTCTGGGTGTTTACTGCTCATTTGTGTTTA	1131

RESULT 4

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US-09-925-302-178
; Sequence 178, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 178
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1653)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2664)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2699)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-178

Query Match          99.8%; Score 1111.6; DB 10; Length 2732;
Best Local Similarity 99.7%; Pred. No. 2.2e-308;
Matches 1111; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  GTCTGCTGGCAGCGCTCCCGGCGCTGGCAGAGCCCGAAGCAGCCGCGCCCGCCAG 60
DB      18  GTCTGCTGGCAGCGCTGCMCGGCGCGTGGGAGAGCCCGAAGCAGCCGCGCGCCCGCCAG 77

QY      61  TTCGGGAGACATGGCGGGCGTTAAAGACTCTCGTGGCAATTATCCTTCAGTGGGGCTATTGG 120
DB      78  CTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCAATTATCCTTCAGTGGGGCTATTGG 137

QY      121  ACTGACTTTCTTATGCTGGGATGTGCCTTAGAGGATTTATGGCGTTTACTGGCCCTTATT 180
DB      138  ACTGACTTTCTTATGCTGGGATGTGCCTTAGAGGATTTATGGCGTTTACTGGCCCTTATT 197

QY      181  GCTGCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTCAATGTCACAAAGAGTCACCTA 240
DB      198  CGTCCCTGATTTTCCAGGCCATCTCCCCCATCCCCCATTTCAATGTCACAAAGAGTCACCTA 257

QY      241  TGACTCAGATGCACACAGTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACCTACTGGAAT 300
DB      258  TGACTCAGATGCACCACTAGTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACCTACTGGAAT 317

QY      301  TGTGTTTCTGCCTTTGGATTTCTGTATTTCTTGCTCGTGTGGCTGTGATCAAAATGGGG 360
DB      318  TGTGTTTCTGCCTTTGGATTTCTGTATTTCTTGCTCGTGTGGCTGTGATCAAAATGGGG 377

QY      361  AGCCTGGCGCCTTGTTTGGCAGCAATGCAGTCAATTTCCCTTACAATTCAGAGGTTT 420
DB      378  AGCCTGGCGCCTTGTTTGGCAGCAATGCAGTCAATTTCCCTTACAATTCAGAGGTTT 437

QY      421  CCTTATATTTGGAGAGAGGATGATTTTAGCTGGGACGAGTGTAGCACTTTATTCTGAT 480
DB      438  CCTTATATTTGGAGAGAGGATGATTTTAGCTGGGACGAGTGTAGCACTTTATTCTGAT 497

QY      481  TACAGTGCAATTGAATTTCTTAGAACTCATATACTATCTATATCATGTCACATCGGCGATT 540
DB      498  TACAGTGCAATTGAATTTCTTAGAACTCATATACTATCTATATCATGTCACATCGGCGATT 557

QY      541  TTACTATGAAATTTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGTCACATTAA 600

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Qy 10 GGGCAGGCTGCCGGGCGTGGCAGAGCGGAGCAGCGCGGCCCGCCAGTTCGGGAGA 69
Db 34 GGGCAGGCTGCCGGGCGTGGCAGAGCGGAGCAGCGCGGCCCGCCAGTTCGGGAGA 93
Qy 70 CATGCGGGCGTTAAAGCTCTCGTGGCAATATCTTCAGTGGGGCTATTGGACTGACTTT 129
Db 94 CATGCGGGCGTTAAAGCTCTCGTGGCAATATCTTCAGTGGGGCTATTGGACTGACTTT 153
Qy 130 TCTTATGCTGGGATGTGCTTAGAGGATTATG-----CGCTTTACTG 171
Db 154 TCTTATGCTGGGATGTGCTTAGAGGATTATGCGCTGGTCCAACTGACAGCGTTTACTG 213
Qy 172 GCCCTTATTCCTGCTGATTTTCCAGCCCATCTCCCATCCCATCTTCATTTCACAAAG 231
Db 214 GCCCTTATTCCTGCTGATTTTCCAGCCCATCTCCCATCCCATCTTCATTTCACAAAG 273
Qy 232 AGTCACCTATGACTCAGATGCAACAGTAGTGCCTGTGCGGAATGCGCATATTTCTTCAC 291
Db 274 AGTCACCTATGACTCAGATGCAACAGTAGTGCCTGTGCGGAATGCGCATATTTCTTCAC 333
Qy 292 TACTGGAATTTGTTTCTGCTTTCCTTTGGATTTCTGTTATTTCTGCTGTTGGCTGTGAT 351
Db 334 TACTGGAATTTGTTTCTGCTTTCCTGATTTCTGTTATTTCTGCTGTTGGCTGTGAT 393
Qy 352 CAATGGGAGCCTGCGGCTTGTGTTGGCAGGCAATGCACTCATTTTCTTCAATTCAC 411
Db 394 CAATGGGAGCCTGCGGCTTGTGTTGGCAGGCAATGCACTCATTTTCTTCAATTCAC 453
Qy 412 AGGCTTTTCTTATATTTGAAGAGGAGATGATTTTAGCTGGGAGAGTGGTAGCACTT 471
Db 454 AGGCTTTTCTTATATTTGGAGAGGAGATGATTTTAGCTGGGAGAGTGGTAGCACTT 513
Qy 472 TATTCTGATTAACAGTGCAATGAAATTTCTTAGAATCTCATCTATCTGTATACATGTGCACA 531
Db 514 TATTCTGATTAACAGTGCAATGAAATTTCTTAGAATCTCATCTATCTGTATACATGTGCACA 573
Qy 532 TGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGT 591
Db 574 TGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGT 633
Qy 592 TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGATTTTATCTCAGCAAAATAGACCTGT 651
Db 634 TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGATTTTATCTCAGCAAAATAGACCTGT 693
Qy 652 CAATTTAGATTATGTTACTCAAAATATGTTACTTGTGTTGGCTGTTCAATGAGTCAAGGT 711
Db 694 CAATTTAGATTATGTTACTCAAAATATGTTACTTGTGTTGGCTGTTCAATGAGTCAAGGT 753
Qy 712 GCTCTCAGAAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTATGCAATGCAATCG 771
Db 754 GCTCTCAGAAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTATGCAATGCAATCG 813
Qy 772 AAACCTTTTGTCTGGGATGTGTTGGAGAGCAGATAACGCTGAAGCAGGCTCTCATG 831
Db 814 AAACCTTTTGTCTGGGATGTGTTGGAGAGCAGATAACGCTGAAGCAGGCTCTCATG 873
Qy 832 ACCCAGGAAGCGCGGGTGGATCCCTCTTTGTTGTAGTCCATGCTATTAAGAGTGTGG 891
Db 874 ACCCAGGAAGCGCGGGTGGATCCCTCTTTGTTGTAGTCCATGCTATTAAGAGTGTGG 933
Qy 892 CCCACAGACCAAGAGCCTCAACATTTCTAGAGCTTATTAGAAATGAGAAATCTGAAGC 951
Db 934 CCCACAGACCAAGAGCCTCAACATTTCTAGAGCTTATTAGAAATGAGAAATCTGAAGC 993
Qy 952 CCCACTCTGGACCCAGGACATTTTATGATGAGATCCAAAGGAGTGTGATGCAATGAAAGTT 1011
Db 994 CCCACTCTGGACCCAGGACATTTTATGATGAGATCCAAAGGAGTGTGATGCAATGAAAGTT 1053
Qy 1012 TGAGAAGCATCATCATAGAGAAGTAAACATCACACCCCACTTCTTATCTTTCCAGTGGC 1071
Db 1054 TGAGAAGCATCATCATAGAGAAGTAAACATCACACCCCACTTCTTATCTTTCCAGTGGC 1113
Qy 1072 TAAACCACTTAACCTCTCTGGGTTTACCTGCTCATTTGTTTGA 1114
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Db 1114 TAAACCACTTAACCTCTCTGGGTTTACCTGCTCATTTGTTTGA 1156
RESULT 6
US-09-993-756A-2
; Sequence 2, Application US/09993756A
; Publication No. US20030166847A1
; GENERAL INFORMATION:
; APPLICANT: Akermblom, Ingrid E.
; TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR
; GENE-RELATED PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993.756A
; FILING DATE: 05-No. US20030166847A1-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/212.153
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/843.370
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/691.071
; FILING DATE: August 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0111-1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 874 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: HNT2NOT01
; CLONE: 492703
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-993-756A-2
Query Match 78.1%; Score 869.6; DB 10; Length 874;
Best Local Similarity 99.4%; Pred. No. 4.6e-239;
Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCTGGCTTGGCAGGCTGCCCCGGCGGTGGCAGGAAGCCGCGGCGCCCGCCAG 60
Db 1 GTCTGGCTTGGCAGGCTGCCCCGGCGGTGGCAGGAAGCCGCGGCGCCCGCCAG 60
Qy 61 TTCGGGAGACATGCGGGCGGTAAAGCTCTCGTGGCATTATCTTCAGTGGGGCTATTGG 120
Db 61 TTCGGGAGACATGCGGGCGGTAAAGCTCTCGTGGCATTATCTTCAGTGGGGCTATTGG 120
Qy 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTTAGCGCTTTACTGCGCCCTTATT 180
Db 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTTAGCGCTTTACTGCGCCCTTATT 180
Qy 181 CGTCTGATTTTCACGCCATCTCCCCCATCTCCCATTTTCATTCGCAAAAGATCACCTA 240
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Db 191 CGTCTGATTTTCCAGCGCATCTCCCCATCCCCATTTTCATTTGCCAAAAGAGCTCACCTA 240
Qy 241 TGACTCAGATGCAACAGTAGTGCTGTGGAACTGGCATATTTCTTCACTACTGGAAT 300
Db 241 TGACTCAGATGCAACAGTAGTGCTGTGGAACTGGCATATTTCTTCACTACTGGAAT 300
Qy 301 TGTGTTCTGCTTTTGGATTTCTGTATTTCTTGTCTGTGTGGCTGTGATCAAAATGGG 360
Db 301 TGTGTTCTGCTTTTGGATTTCTGTATTTCTTGTCTGTGTGGCTGTGATCAAAATGGG 360
Qy 361 AGCTGCGGCTGTGTGGAGGCAATGCGAGTCAATTTCTTCAATTCAGGGTTTTT 420
Db 361 AGCTGCGGCTGTGTGGAGGCAATGCGAGTCAATTTCTTCAATTCAGGGTTTTT 420
Qy 421 CTTTATATTTGGAAGGAGAGATGATTTAGCTGGGAGCAGTGGTAGCACTTTATCTGAT 480
Db 421 CTTTATATTTGGAAGGAGAGATGATTTAGCTGGGAGCAGTGGTAGCACTTTATCTGAT 480
Qy 481 TACAGTGCAATGAAATTTCTTAGAATCTATCTATCTATATCATGTGCACATGGGCAT 540
Db 481 TACAGTGCAATGAAATTTCTTAGAATCTATCTATCTATATCATGTGCACATGGGCAT 540
Qy 541 TTAATATGAAATTTAATATGCTGGGTTTTTAACTTATATATCATGTGCTCACTTTAA 600
Db 541 TTAATATGAAATTTAATATGCTGGGTTTTTAACTTATATATCATGTGCTCACTTTAA 600
Qy 601 GAAAGACTTCATAGTAGAGATGAGTTTTTATTTCTCAGCAAAATAGACCTGTCAAAATTTAG 660
Db 601 GAAAGACTTCATAGTAGAGATGAGTTTTTATTTCTCAGCAAAATAGACCTGTCAAAATTTAG 660
Qy 661 ATTATGTTACTCAAAATATGTTACTTTGTTGGCTGTGATGCAAGCTGCTCTCAGA 720
Db 661 ATTATGTTACTCAAAATATGTTACTTTGTTGGCTGTGATGCAAGCTGCTCTCAGA 720
Qy 721 AAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTATGCAAGTGCATCGAAACCTTTT 780
Db 721 AAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTATGCAAGTGCATCGAAACCTTTT 780
Qy 781 GTTTGGGGATGTCTTGGAGGCGAGATAACGCTGAAGAGGCTCTCATGACCCAGGAA 840
Db 781 GTTTGGGGATGTCTTGGAGGCGAGATAACGCTGAAGAGGCTCTCATGACCCAGGAA 840
Qy 841 GCGCGGGTGCATCCCTTTTGTGTGTGATGCCA 874
Db 841 GCGCGGGTGGTCCCTTTTGTGTGTGATGCCA 874

RESULT 7
; Sequence 148, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 207542
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(207542)
; OTHER INFORMATION: n = A,T,C or G
US-10-893-315-148

Query Match 69.0%; Score 768.4; DB 22; Length 207542;
Best Local Similarity 99.2%; Pred. No. 1.5e-208;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 337 TCGTGTGCTGTGATCAAAATGGGAGCTGGGCTGTGTGGCAGCAATGCACTCAT 396
Db 13025 TCTTGTCTTTTCAGATCAAAATGGGAGCTGGGCTGTGTGGCAGCAATGCACTCAT 13084
Qy 397 TTTCTCTTCAAAATCAAGGGTTTTTCTTATATATTTTGGAAAGAGAGATGATTTAGCTGGGA 456
Db 13085 TTTCTCTTCAAAATCAAGGGTTTTTCTTATATATTTTGGAAAGAGAGATGATTTAGCTGGGA 13144
Qy 457 GCAGTGTGTAGCACTTTATTTCTGATTCAGTGCATTTGAATTTCTTGAAGCTCATCTATCT 516
Db 13145 GCAGTGTGTAGCACTTTATTTCTGATTCAGTGCATTTGAATTTCTTGAAGCTCATCTATCT 13204
Qy 517 GTATACATGTGCACATGGGCAATTTTACTATCAAAATTTAATATGCTGGTTTTTAAATAC 576
Db 13205 GTATACATGTGCACATGGGCAATTTTACTATCAAAATTTAATATGCTGGTTTTTAAATAC 13264
Qy 577 CTTTATATATCATGTTTCACTTTAAGAAAGACTTTTAAAGAGATGATGATTTTATCTC 636
Db 13265 CTTTATATATCATGTTTCACTTTAAGAAAGACTTTTAAAGAGATGATGATTTTATCTC 13324
Qy 637 AGCAATATGACCTGTCAAAATTTAGATTTTACTTCAAAATTTATGTTTGTGCTGT 696
Db 13325 AGCAATATGACCTGTCAAAATTTAGATTTTACTTCAAAATTTATGTTTGTGCTGT 13384
Qy 697 TCATGTAGTCACGCTGTCTCAGAAAAATATATTAACGAGCTTTGTAGGAGCTGCCACC 756
Db 13385 TCATGTAGTCACGCTGTCTCAGAAAAATATATTAACGAGCTTTGTAGGAGCTGCCACC 13444
Qy 757 TTATGCAAGTGCATCGAAACCTTTTGTGGGATGCTTTGGAGAGCAGATAACGCTGA 816
Db 13445 TTATGCAAGTGCATCGAAACCTTTTGTGGGATGCTTTGGAGAGCAGATAACGCTGA 13504
Qy 817 AGCAGGCTCTCATGACCCAGGAGCGGGGTGGATCCCTCTTTGTGTGTAGTCCATG 876
Db 13505 AGCAGGCTCTCATGACCCAGGAGCGGGGTGGATCCCTCTTTGTGTGTAGTCCATG 13564
Qy 877 CTATTAAGTGTGGCCACAGACCAAGAGCTCAACATTTCTTAGAGCTTTATTAGAA 936
Db 13565 CTATTAAGTGTGGCCACAGACCAAGAGCTCAACATTTCTTAGAGCTTTATTAGAA 13624
Qy 937 TGCAGATCTGAAGCCCACTCTGACCCAGGACATTTTGTATGATGATCCAAAGAGTTGT 996
Db 13625 TGCAGATCTGAAGCCCACTCTGACCCAGGACATTTTGTATGATGATCCAAAGAGTTGT 13684
Qy 997 ATGCACATGAAAGTTTGAAGAGCATCATATAGAGATTAACATCACACCCAACTTCT 1056
Db 13685 ATGCACATGAAAGTTTGAAGAGCATCATATAGAGATTAACATCACACCCAACTTCT 13744
Qy 1057 TATCTTTCAAGTGGCTTAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTA 1114
Db 13745 TATCTTTCAAGTGGCTTAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTA 13802

RESULT 8
; Sequence 134, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
US-10-893-315-134

; SEQ ID NO 134
; LENGTH: 207557
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(207557)
; OTHER INFORMATION: n = A,T,C or G
US-10-893-315-134

Query Match 69.0%; Score 768.4; DB 22; Length 207557;
Best Local Similarity 99.2%; Pred. No. 1.5e-208;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 337 TCGTGTGGCTGTGATCAAAATGGGAGCGCTGGCGCTGTGTGGCAGCAATGAGTCAAT 396
Db 13025 TCTTGCTTTTCAGATCAAAATGGGAGCGCTGGCGCTGTGTGGCAGCAATGAGTCAAT 13084

Qy 397 TTTCCCTTACAAATCAAGGGTTTTCCCTATATTTTGGAGAGAGATGATTTAGCTGGGA 456
Db 13085 TTTCCCTTACAAATCAAGGGTTTTCCCTATATTTTGGAGAGAGATGATTTAGCTGGGA 13144

Qy 457 GCAGTGGTAGCACCTTATCTTGATTTACAGTGCATTTGAATTTCTTAGAACTCATATCTATCT 516
Db 13145 GCAGTGGTAGCACCTTATCTTGATTTACAGTGCATTTGAATTTCTTAGAACTCATATCTATCT 13204

Qy 517 GTATACATGTGCATGCGGCATTTTACTAGAAATTTAATATATGCTGGTTTTTTAATAC 576
Db 13205 GTATACATGTGCATGCGGCATTTTACTATGAAATTTAATATGCTGGTTTTTTAATAC 13264

Qy 577 CTTTATATATCATGTTTCACTTTAAGAAAGACTTCAATAGTAGGAGATGAGTTTTATTTCTC 636
Db 13265 CTTTATATATCATGTTTCACTTTAAGAAAGACTTCAATAGTAGGAGATGAGTTTTATTTCTC 13324

Qy 637 AGCAAAATAGACCTGTCAAAATTTAGATTTATGTTACTCAAAATTTATCTTCTTTGGCTGT 696
Db 13325 AGCAAAATAGACCTGTCAAAATTTAGATTTATGTTACTCAAAATTTATCTTCTTTGGCTGT 13384

Qy 697 TCATGTAGTACAGGTGTCTCAGAAAATATATTAACGAGTCTTTGTAGGAGCTGCCACC 756
Db 13385 TCATGTAGTACAGGTGTCTCAGAAAATATATTAACGAGTCTTTGTAGGAGCTGCCACC 13444

Qy 757 TTATGCAGTGCATCGAAACCTTTTGTGGGGATGTGCTTGGAGAGGAGATTAACGCTGA 816
Db 13445 TTATGCAGTGCATCGAAACCTTTTGTGGGGATGTGCTTGGAGAGGAGATTAACGCTGA 13504

Qy 817 AGCAGGCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTGTGTGTAGTCCATG 876
Db 13505 AGCAGGCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTGTGTGTAGTCCATG 13564

Qy 877 CTATTTAAAGTGTGGCCACAGACCAAGAGCTCAACATTTCTTAGAGCCTTTATTAGAAA 936
Db 13565 CTATTTAAAGTGTGGCCACAGACCAAGAGCTCAACATTTCTTAGAGCCTTTATTAGAAA 13624

Qy 937 TGCAGAAATCTGAAGCCCACTCTCGAACCCAGGACATTTTGATGATGATCCAAAGAGTTGT 996
Db 13625 TGCAGAAATCTGAAGCCCACTCTCGAACCCAGGACATTTTGATGATGATCCAAAGAGTTGT 13684

Qy 997 ATGCACATGAAGTTTGAGAGCATCATCATAGAGAGTAAACATCACACCAACTTCCCT 1056
Db 13685 ATGCACATGAAGTTTGAGAGCATCATCATAGAGAGTAAACATCACACCAACTTCCCT 13744

Qy 1057 TATCTTTCCAGTGGCTAAACCACTTAACTCTCTGCGGTGTTCCTGTCTCATTTCTTTTA 1114
Db 13745 TATCTTTCCAGTGGCTAAACCACTTAACTCTCTGCGGTGTTCCTGTCTCATTTCTTTTA 13802

RESULT 9

US-10-774-721-1
; Sequence 1, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf

RESULT 10

US-10-956-157-7397
; Sequence 7397, Application US/10956157
; Publication No. US20050118625A1

; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-774-721-1

Query Match 58.2%; Score 648; DB 21; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 CACTTTATCTGATTACAGTGCATTTGAATTTCTTAGAACTCATATCTATCTGTATACATGT 526
Db 1 CACTTTATCTGATTACAGTGCATTTGAATTTCTTAGAACTCATATCTATCTGTATACATGT 60

Qy 527 GCACATCGGCATTTTACTATGAAATTTAATATCTCGGTTTTTAACTCTGGTTTTTAACTCTTATATAT 586
Db 61 GCACATCGGCATTTTACTATGAAATTTAATATCTCGGTTTTTAACTCTGGTTTTTAACTCTTATATAT 120

Qy 587 CATGTTCACTTTTAAAGAGCTTCATAAGTAGGAGATGAGTTTTTATTCTCAGCAAAATAGA 646
Db 121 CATGTTCACTTTTAAAGAGCTTCATAAGTAGGAGATGAGTTTTTATTCTCAGCAAAATAGA 180

Qy 647 CTTGTCAAAATTTAGATTTATGTTACTCAAAATATGTTTACTTGTGGTGTGTTTCAATGATGC 706
Db 181 CTTGTCAAAATTTAGATTTATGTTTACTCAAAATATGTTTACTTGTGGTGTGTTTCAATGATGC 240

Qy 707 ACGTGTCTCTCAGAAAATATATTAAACGAGTCTTTGTAGGAGCTGCCACCTTATGCACTG 766
Db 241 ACGTGTCTCTCAGAAAATATATTAAACGAGTCTTTGTAGGAGCTGCCACCTTATGCACTG 300

Qy 767 CATCGAAACCTTTTGTCTTGGGGATGTGCTTGGAGAGGAGATTAACGCTGAAAGCAGGCCTC 826
Db 301 CATCGAAACCTTTTGTCTTGGGGATGTGCTTGGAGAGGAGATTAACGCTGAAAGCAGGCCTC 360

Qy 827 TCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTGTAGTCCATGCTATTAAAG 886
Db 361 TCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTGTAGTCCATGCTATTAAAG 420

Qy 887 TGTGGCCCAAGAGAGCGCTCAACATTTCTTAGAGCCTTATTAGAAATGCAAGATCT 946
Db 421 TGTGGCCCAAGAGAGCGCTCAACATTTCTTAGAGCCTTATTAGAAATGCAAGATCT 480

Qy 947 GAAGCCCACTCTCTGAGCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGA 1006
Db 481 GAAGCCCACTCTCTGAGCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGA 540

Qy 1007 AAGTTTGAGAGCATCATCATAGAGAGTAAACATCAACCCAACTTCCTTCTTTTCCA 1066
Db 541 AAGTTTGAGAGCATCATCATAGAGAGTAAACATCAACCCAACTTCCTTCTTTTCCA 600

Qy 1067 GTGCTAAACCACTTAACTCTCTGGGTGTTCCTGTCTCATTTCTTTTA 1114
Db 601 GTGCTAAACCACTTAACTCTCTGGGTGTTCCTGTCTCATTTCTTTTA 648

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; PRIORITY FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7397
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-7397

Query Match 53.9%; Score 600; DB 21; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	515	CTGTATACATGTCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAT	574
DB	1	CTGTATACATGTCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAT	60
QY	575	ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTCATAAGTAGAGATGAGTTTATTC	634
DB	61	ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTCATAAGTAGAGATGAGTTTATTC	120
QY	635	TCAGCAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTTGGCT	694
DB	121	TCAGCAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTTGGCT	180
QY	695	GTTTCATGATGTCACCGTGTCTCAGAAATATATTAACGCAGTCTTTAGGCGAGTGC	754
DB	181	GTTTCATGATGTCACCGTGTCTCAGAAATATATTAACGCAGTCTTTAGGCGAGTGC	240
QY	755	CCTTATGCAATGTCATCGAAACCTTTTGTCTGGGGATGTCTTGGAGGCGAGATAACGCT	814
DB	241	CCTTATGCAATGTCATCGAAACCTTTTGTCTGGGGATGTCTTGGAGGCGAGATAACGCT	300
QY	815	GAAGCAGGCTCTCATGACCCAGGAGCGCGGGTGGATCCCTCTTGTGTGTAGTCCA	874
DB	301	GAAGCAGGCTCTCATGACCCAGGAGCGCGGGTGGATCCCTCTTGTGTGTAGTCCA	360
QY	875	TGCTATTAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA	934
DB	361	TGCTATTAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA	420
QY	935	AATGAGAAATCTGAAGCCCTCTCTGACCCAGGACATTTTGTATGAGATCCAAAGGATT	994
DB	421	AATGAGAAATCTGAAGCCCTCTCTGACCCAGGACATTTTGTATGAGATCCAAAGGATT	480
QY	995	GTATGCATGAAAGTTTGAAGAGCATCATATAGAGAGTAAACATCACCCCACTTC	1054
DB	481	GTATGCATGAAAGTTTGAAGAGCATCATATAGAGAGTAAACATCACCCCACTTC	540
QY	1055	CTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCACTTTGTTA	1114
DB	541	CTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCACTTTGTTA	600

RESULT 11
US-10-893-315-733
; Sequence 733, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; PRIORITY FILING DATE: 2004-07-19

; PRIOR APPLICATION NUMBER: 60/231,397
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 733
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-733

Query Match 53.8%; Score 599.6; DB 22; Length 601;
Best Local Similarity 99.8%; Pred. No. 1.7e-161;
Matches 599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	515	CTGTATACATGTCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAT	574
DB	1	CTGTATACATGTCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAT	60
QY	575	ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTCATAAGTAGAGATGAGTTTATTC	634
DB	61	ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTCATAAGTAGAGATGAGTTTATTC	120
QY	635	TCAGCAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTTGGCT	694
DB	121	TCAGCAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTTGGCT	180
QY	695	GTTTCATGATGTCACCGTGTCTCAGAAATATATTAACGCAGTCTTTAGGCGAGTGC	754
DB	181	GTTTCATGATGTCACCGTGTCTCAGAAATATATTAACGCAGTCTTTAGGCGAGTGC	240
QY	755	CCTTATGCAATGTCATCGAAACCTTTTGTCTGGGGATGTCTTGGAGGCGAGATAACGCT	814
DB	241	CCTTATGCAATGTCATCGAAACCTTTTGTCTGGGGATGTCTTGGAGGCGAGATAACGCT	300
QY	815	GAAGCAGGCTCTCATGACCCAGGAGCGCGGGTGGATCCCTCTTGTGTGTAGTCCA	874
DB	301	GAAGCAGGCTCTCATGACCCAGGAGCGCGGGTGGATCCCTCTTGTGTGTAGTCCA	360
QY	875	TGCTATTAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA	934
DB	361	TGCTATTAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA	420
QY	935	AATGAGAAATCTGAAGCCCTCTCTGACCCAGGACATTTTGTATGAGATCCAAAGGATT	994
DB	421	AATGAGAAATCTGAAGCCCTCTCTGACCCAGGACATTTTGTATGAGATCCAAAGGATT	480
QY	995	GTATGCATGAAAGTTTGAAGAGCATCATATAGAGAGTAAACATCACCCCACTTC	1054
DB	481	GTATGCATGAAAGTTTGAAGAGCATCATATAGAGAGTAAACATCACCCCACTTC	540
QY	1055	CTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCACTTTGTTA	1114
DB	541	CTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCACTTTGTTA	600

RESULT 12
US-10-283-975A-466
; Sequence 466, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; PRIORITY FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIORITY FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIORITY FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIORITY FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIORITY FILING DATE: 2001-10-30

; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 466
; LENGTH: 647
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(647)
; OTHER INFORMATION: N=any base
US-10-283-975A-466

Query Match 51.8%; Score 577.4; DB 19; Length 647;

Best Local Similarity 98.6%; Pred. No. 4.4e-155;
Matches 644; Conservative 0; Mismatches 3; Indels 6; Gaps 6;

Qy	352	CMAATGGGGAGCCCTGGTGGCAGGCAATGCAATGCAATTTTCCCTTCAAAATTC	411
Db	1	CMAATGGGGAGCCCTGGTGGCAGGCAATGCAATGCAATTTTCCCTTCAAAATTC	59
Qy	412	AGGTTTTTCTTATATTTTGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTT	471
Db	60	AGGTTTTTCTTATATTTTGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTT	119
Qy	472	TATTCGATACAGTGCATTTCTTAGAATCTCATATCTCTGTATACATGTCAC	531
Db	120	TATTCGATACAGTGCATTTCTTAGAATCTCATATCTCTGTATACATGTCAC	179
Qy	532	TGGGCAATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGT	591
Db	180	TGGGCAATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGT	239
Qy	592	TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGATTTTATTTCTCAGCAATAGACCTGT	651
Db	240	TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGATTTTATTTCTCAGCAATAGACCTGT	299
Qy	652	CAAAATTTAGATTATGTTACTCAAAATATGTTACTTTGCTGCTGTTATGAGTACAGGT	711
Db	300	CAAAATTTAGATTATGTTACTCAAAATATGTTACTTTGCTGCTGTTATGAGTACAGGT	359
Qy	712	GCTCTCAGAAATATATTAAAGCAGCTTTGAGCAGCTGCGACCTTATGAGTGCATCG	771
Db	360	GCTCTCAGAAATATATTAAACAGCTTTGAGCAGCTGCGACCTTATGAGTGCATCG	419
Qy	772	AAACCTTTTGGTGGGATGCTTTGGAGAGCAGATAACGCTGAAGCAGGCTCTCATG	831
Db	420	AAACCTTTTGGTGGGATGCTTTGGAGAGCAGATAACGCTGAAGCAGGCTCTCATG	479
Qy	832	ACCAGGAAGCCGGGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTTAAAGTGTGG	891
Db	480	ACCAGGAAGCCGGGGTGGATCCCT-TTTTGTTGTTAGTCCATGCT-ATTTAAAGTGTGG	537
Qy	892	CCCAAGACCAAGAGCCCTCAACATTTCTAGAGCTTTATAGAAATGAGAAATCTGAAGC	951
Db	538	CCCAAGACCAAGAGCCCTCAACATTTCTAGAGCTTTATAGAAATGAGAAATCTGAAG-	596
Qy	952	CCCACTCTGGACCCAGGACATTTTATGAGATCCAAAGAGTGTGTATGACAT 1004	
Db	597	CCCACTCTGGACCCAGGACATTTTATGAGATCC-ATTTATGAGATCC-ATTTATGATGTCNCAT 647	

RESULT 13

US-10-038-010-23
; Sequence 23, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377

; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(396)
; OTHER INFORMATION: Human OBRGRP
US-10-038-010-23

Query Match 35.5%; Score 396; DB 14; Length 396;

Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	71	ATGCGGGCGCTTAAAGCTCTCGTGGCAATATCCCTTCACTAGTGGGGCTATTGGACTGACTTTT	130
Db	1	ATGCGGGCGCTTAAAGCTCTCGTGGCAATATCCCTTCACTAGTGGGGCTATTGGACTGACTTTT	60
Qy	131	CTTATGCTGGGATGTGCTTTAGAGGATTTATGGCGTTTACTGGCCCTTATTCGTCCTGATT	190
Db	61	CTTATGCTGGGATGTGCTTTAGAGGATTTATGGCGTTTACTGGCCCTTATTCGTCCTGATT	120
Qy	191	TTCCACGCCATCTCCCCCATCCCCCATTTCAATGTCGCAAAAGAGTCACCTATGACTCAGAT	250
Db	121	TTCCACGCCATCTCCCCCATCCCCCATTTCAATGTCGCAAAAGAGTCACCTATGACTCAGAT	180
Qy	251	GCACACAGTAGTGCCTGCTCGGGAATGSCATATTTCTTCACTACTGGAATTTGTTGTTCT	310
Db	181	GCACACAGTAGTGCCTGCTCGGGAATGSCATATTTCTTCACTACTGGAATTTGTTGTTCT	240
Qy	311	GCCTTTGGATTTCTGTTTATTTCTTCTGCTGCTGCTGATCAAAATGGGAGCCTGCGGC	370
Db	241	GCCTTTGGATTTCTGTTTATTTCTTCTGCTGCTGCTGATCAAAATGGGAGCCTGCGGC	300
Qy	371	CTTGTGTTGGCAGCAATGAGTCATTTTCTTCAAAATTTCAAGGGTTTTCCTTATATTT	430
Db	301	CTTGTGTTGGCAGCAATGAGTCATTTTCTTCAAAATTTCAAGGGTTTTCCTTATATTT	360
Qy	431	GGAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAG 466	
Db	361	GGAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAG 396	

RESULT 14

US-10-774-721-3
; Sequence 3, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(396)

OTHER INFORMATION:
US-10-774-721-3

Query Match 35.5%; Score 396; DB 21; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 ATGGCGGGGTTAAAGCTCTCGTGGCATATCCCTTCAGTGGGGCTATTGGACTGACTTTT 130
Db 1 ATGGCGGGGTTAAAGCTCTCGTGGCATATCCCTTCAGTGGGGCTATTGGACTGACTTTT 60
Qy 131 CTTATGCTGGGATGTGCTTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATT 190
Db 61 CTTATGCTGGGATGTGCTTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATT 120
Qy 191 TTCCACGCCATCTCCCCCATCCCCCATTTTCAATGCCCCAAAGAGTCACCTATGACTCAGAT 250
Db 121 TTCCACGCCATCTCCCCCATCCCCCATTTTCAATGCCCCAAAGAGTCACCTATGACTCAGAT 180
Qy 251 GCAACCCAGTAGTGTCTGTGGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 310
Db 181 GCAACCCAGTAGTGTCTGTGGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 240
Qy 311 GCCTTTGGATTTCCTGTATTCTTGTCTGTGGTGTGATCAAAATGGGGAGCCTGCGGC 370
Db 241 GCCTTTGGATTTCCTGTATTCTTGTCTGTGGTGTGATCAAAATGGGGAGCCTGCGGC 300
Qy 371 CTTGTGTTGGAGGCAATCGAGTCATTTTCCCTTACAAATCAAGGGTTTTCCTTATATT 430
Db 301 CTTGTGTTGGAGGCAATCGAGTCATTTTCCCTTACAAATCAAGGGTTTTCCTTATATT 360
Qy 431 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGG 466
Db 361 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGG 396

RESULT 15

US-10-774-721-7
Sequence 7, Application US/10774721
Publication No. US2005009042A1
GENERAL INFORMATION:
APPLICANT: JOCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: UHLMANN, Eugen
TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
FILE REFERENCE: FRAV2003/0005 US NP
CURRENT APPLICATION NUMBER: US/10/774, 721
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/461,005
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 1128
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: OB RGRP YFP
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: OB RGRP YFP
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1128)
OTHER INFORMATION:
US-10-774-721-7

Query Match 35.3%; Score 393; DB 21; Length 1128;
Best Local Similarity 100.0%; Pred. No. 6.8e-102;

Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 ATGGCGGGGTTAAAGCTCTCGTGGCATATCCCTTCAGTGGGGCTATTGGACTGACTTTT 130
Db 1 ATGGCGGGGTTAAAGCTCTCGTGGCATATCCCTTCAGTGGGGCTATTGGACTGACTTTT 60
Qy 131 CTTATGCTGGGATGTGCTTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATT 190
Db 61 CTTATGCTGGGATGTGCTTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATT 120
Qy 191 TTCCACGCCATCTCCCCCATCCCCCATTTTCAATGCCCCAAAGAGTCACCTATGACTCAGAT 250
Db 121 TTCCACGCCATCTCCCCCATCCCCCATTTTCAATGCCCCAAAGAGTCACCTATGACTCAGAT 180
Qy 251 GCAACCCAGTAGTGTCTGTGGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 310
Db 181 GCAACCCAGTAGTGTCTGTGGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 240
Qy 311 GCCTTTGGATTTCCTGTATTCTTGTCTGTGGTGTGATCAAAATGGGGAGCCTGCGGC 370
Db 241 GCCTTTGGATTTCCTGTATTCTTGTCTGTGGTGTGATCAAAATGGGGAGCCTGCGGC 300
Qy 371 CTTGTGTTGGAGGCAATCGAGTCATTTTCCCTTACAAATCAAGGGTTTTCCTTATATT 430
Db 301 CTTGTGTTGGAGGCAATCGAGTCATTTTCCCTTACAAATCAAGGGTTTTCCTTATATT 360
Qy 431 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGG 463
Db 361 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGG 393

Search completed: August 18, 2005, 03:10:07
Job time : 860 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 17:45:53 ; Search time 5148 Seconds
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Title: US-10-774-721-21
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

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11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1114	100.0	1114	6	CQ716942 Sequence
2	1114	100.0	1114	6	CQ860109 Sequence
3	1114	100.0	1114	6	CQ878351 Sequence
4	1114	100.0	1114	9	HSOBRGRP
5	1069	96.0	1080	6	CQ783702 Sequence
6	1069	96.0	1080	6	BD127789 Primer fo
7	1069	96.0	1080	9	AK074841
8	1067	95.8	2388	6	AX779959 Sequence
9	1057.6	94.9	1092	9	BC056250 Homo sapi
10	1023.4	91.9	1056	9	BC011027
11	869.6	78.1	874	6	AR020775 Sequence
12	869.6	78.1	874	6	BD132522 A novel h
13	768.4	69.0	16112	9	AC119800 Homo sapi
14	765.8	68.7	1614	9	AK130096
15	648	58.2	648	6	CQ860089 Sequence
16	588.4	52.8	629	6	CQ780218 Sequence
17	588.4	52.8	629	6	CQ781626 Sequence
18	588.4	52.8	629	6	BD124927 Primer fo
19	588.4	52.8	629	6	BD126335

20	577.4	51.8	647	6	AX775150
21	533.2	47.9	647	11	BV208716
c 22	498.4	44.7	546	6	CQ780977 Sequence
c 23	498.4	44.7	546	6	BD125686 Primer fo
24	399.8	35.9	1966	10	BC062003
25	396	35.5	396	6	CQ860091 Sequence
26	396	35.5	396	9	CR541737 Homo sapi
27	393	35.3	393	9	CR541647 Homo sapi
28	393	35.3	1128	6	CQ860095 Sequence
29	393	35.3	1359	6	CQ860093 Sequence
30	387.6	34.8	1859	10	BC004744 Mus muscu
31	365.2	32.8	635	10	MMAJ11565
32	357.4	32.1	447	10	AF139209 Rattus no
33	349.6	31.4	384	6	CQ696366 Sequence
c 34	330.4	29.7	153350	2	AC108402 Mus muscu
c 35	330.4	29.7	187184	10	AC121826
36	275.6	24.7	3641	5	AJ720495 Gallus ga
37	246.6	22.1	1815	10	BC010289 Mus muscu
38	246	22.1	246	6	AX677228 Sequence
39	245	22.0	1012	5	CR761280 Xenopus t
40	241.8	21.7	1019	5	BC053822 Xenopus 1
41	238.6	21.4	1032	5	BC078594 Xenopus 1
42	190.8	17.1	505	11	G26889 human STS S
43	185.8	16.7	2609	10	BC004677 Mus muscu
44	184.2	16.5	3327	5	BC043984 Xenopus 1
45	179.8	16.1	1167	5	CR385373 Gallus ga

ALIGNMENTS

RESULT 1
LOCUS CQ716942 1114 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 2876 from Patent WO02068579.
ACCESSION CQ716942
VERSION CQ716942.1 GI:42277799
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

JOURNAL Patent: WO 02068579-A 2876 06-SEP-2002;

FEATURES PB Corporation (NY) (US)

source

1. .1114
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1114; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 2.4e-290;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GTCTGGCTTGGCAGGCTGCCCGGCGCTGGCAGGAGCCGCGGCCGAGCCGCGGCCAG	60
Db	1	GTCTGGCTTGGCAGGCTGCCCGGCGCTGGCAGGAGCCGCGGCCGAGCCGCGGCCAG	60
Qy	61	TTCCGGGACATGCGGGCGCTTAAAGCTCTCGTGGCATTCCTTCAGTGGGGCTATTGG	120
Db	61	TTCCGGGACATGCGGGCGCTTAAAGCTCTCGTGGCATTCCTTCAGTGGGGCTATTGG	120
Qy	121	ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGATTATGCGCTTTACTGGCCCTTATT	180
Db	121	ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGATTATGCGCTTTACTGGCCCTTATT	180
Qy	181	CGTCTGATTTTCCACGCCATCTCCCCCATCCCATTTTCATTGCCAAAGATCACCTA	240

Fri Aug 19 08:52:53 2005

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
1	Jockers,R., Couturier,C. and Uhlmann,E.
Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor	
Patent: WO 2004/72293-A 21 26-AUG-2004;	
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)	
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source	1..1114
/organism="Homo sapiens"	
/mol_type="unassigned DNA"	
/db_xref="taxon:9606"	
ORIGIN	
Query Match 100.0%; Score 1114; DB 6; Length 1114;	
Best Local Similarity 100.0%; Pred. No. 2.4e-290;	
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GTCTGGCTTGGCGAGCTGCCGGCGCTGGCAGGAAGCCGGAAGCAGCGCGGCCCGAG 60
Db	1 GTCTGGCTTGGCGAGCTGCCGGCGCTGGCAGGAAGCCGGAAGCAGCGCGGCCCGAG 60
Qy	61 TTCTGGGAGACATCGCGGGCTTAAAGCTCTCTGCGGATTAATCTTCTAGTGGGCTATTGG 120
Db	61 TTCTGGGAGACATCGCGGGCTTAAAGCTCTCTGCGGATTAATCTTCTAGTGGGCTATTGG 120
Qy	121 ACTGACTTTCTTATGCTGGGATGTCCTTAGAGGATTAATGGGCTTACTTGGCCCTTATT 180
Db	121 ACTGACTTTCTTATGCTGGGATGTCCTTAGAGGATTAATGGGCTTACTTGGCCCTTATT 180
Qy	181 CGTCTGATTTTCCAGCCCATCTCCCCATCCCCCATCTCCCCATCTCCCCATCTCCCTA 240
Db	181 CGTCTGATTTTCCAGCCCATCTCCCCATCTCCCCATCTCCCCATCTCCCTA 240
Qy	241 TGACTCAGATGCAACAGTAGTGGCTGCGGAGTGGCATATTTCTTCACTACTGGAAT 300
Db	241 TGACTCAGATGCAACAGTAGTGGCTGCGGAGTGGCATATTTCTTCACTACTGGAAT 300
Qy	301 TGTGTTTCTGCTTTGGATTTCTGTTATTTCTGCTCGTGGCTGTGATCAATGGGG 360
Db	301 TGTGTTTCTGCTTTGGATTTCTGTTATTTCTGCTCGTGGCTGTGATCAATGGGG 360
Qy	361 AGCCTGCGGCTTGTGTTGGCAGGCAATGCAATTTCCCTTACAAATCAAGGGTTTTT 420
Db	361 AGCCTGCGGCTTGTGTTGGCAGGCAATGCAATTTCCCTTACAAATCAAGGGTTTTT 420
Qy	421 CCTTATATTTGGAAGAGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATCTGAT 480
Db	421 CCTTATATTTGGAAGAGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATCTGAT 480
Qy	481 TACAGTGCAATGCAATTTCTTAGAATCTATATCTGTATCATGTCACATCGGCAAT 540
Db	481 TACAGTGCAATGCAATTTCTTAGAATCTATCTGTATCATGTCACATCGGCAAT 540
Qy	541 TTACTATGAATTTTAATATGCTGGGTTTTTAATACCTTTTAAATATATATCATGTTAA 600
Db	541 TTACTATGAATTTTAATATGCTGGGTTTTTAATACCTTTTAAATATATATCATGTTAA 600
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Qy	901 CAAGAGCTCAACATTTCTTAGAGCTTTATAGAAATGCAATCTGAAAGCTGCAAGCTCTG 960
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CQ860109	
LOCUS	
DEFINITION	
SEQUENCE	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
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Sequence 21 from Patent WO2004/72293.	
CQ860109	
GI:51981997	
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Homo sapiens	
PAT 10-SEP-2004	
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Db 841 GGCGGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAGTGTGGCCACAGAC 900
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Qy 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114
Db 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114

RESULT 3
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LOCUS CQ878351 1114 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 4 from Patent WO2004080272.
ACCESSION CQ878351
VERSION CQ878351.1 GI:53790910
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baillieu, B., Rouille, Y., Seron, K. and Belouard, S.
TITLE Use of the genes leptok1 and ob-rgr for the screening of active compounds for weight gain or loss or diabetes in human or animal subjects
JOURNAL Patent: WO 2004080272-A 4 23-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
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71..466
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ORIGIN
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Best local Similarity 100.0%; Pred. No. 2.4e-290;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTTATCTTCACTAGTGGGCTATTGG 120
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RESULT 4
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DEFINITION Sequence 3842 from Patent EP1396543.
ACCESSION CQ783702.1 GI:45503609
VERSION CQ783702.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primers for synthesizing full length cDNA clones and their use
JOURNAL Patent: EP 1396543-A 3842 10-MAR-2004;
RESEARCH Association for Biotechnology (JP)
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ORIGIN
Query Match 96.0%; Score 1069; DB 6; Length 1080;
Best Local Similarity 99.9%; Pred. No. 3.6e-278;
Matches 1080; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy 153 AGGATTATGGGCTTACTGGCCCTATTTCGCTCTGATTTCCAGCCATCTCCCCATCC 212
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Db 241 AACTGGCATATTTCTTCACTACTGGAATTGTTGTTCTGCTTGGATTTCTGTTATTC 300
Qy 333 TTGCTCGTGTGGCTGTGATCAAAATGGGAGCCTCGGCGCTTGTGTTGGAGGCAATGCG 392
Db 301 TTGCTCGTGTGGCTGTGATCAAAATGGGAGCCTCGGCGCTTGTGTTGGAGGCAATGCG 360
Qy 393 TCATTTTCTTACAAATCAAGGGTTTTCCTTATATTGGAGGAGATGATTTTAGCT 452
Db 361 TCATTTTCTTACAAATCAAGGGTTTTCCTTATATTGGAGGAGATGATTTTAGCT 420
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Db 421 GGGAGCAGTGTAGCAGCTTTATCTGATTTACAGTGCATTTGAATTTCTTAGAATCTACT 480
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Qy 1113 T 1113
Db 1080 T 1080
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RESULT 6
BD127789 1080 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127789
VERSION BD127789.1 GI:23222734
KEYWORDS JP 2002017375-A/3220.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3220 22-JAN-2002;
HELIIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3220
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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(39)..(431).
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Best Local Similarity		99.9%; Pred. No. 3.6e-278;
Matches 1080; Conservative		0; Mismatches 0; Indels 1; Gaps 1;
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Db	1	AGGAAGCCGGAAGCAGCCGCGCCAGTTTCGGGAGACATGCGCGGCGTTAAAGCTCTCG 60
QY	93	TGGCATTATCTTCAGTGGGGCTATTGGACTGACTTTCTTATGCTGGGATGTGCCTTAG 152
Db	61	TGGCATTATCTTCAGTGGGGCTATTGGACTGACTTTCTTATGCTGGGATGTGCCTTAG 120
QY	153	AGGATTATGGCGTTTACTGGCCCTTATTGCTCCTGAATTTCCAGCCCATCTCCCCATCC 212
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QY	633	TCTCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTATGTTTGTGG 692
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QY	693	CNTGTTTCATGTAGTCAGCGTGCTCTCAGAAAATATATTAAACGAGCTTTGTAGGAGCTGC 752
Db	660	CTGTTTCATGTAGTCAGCGTGCTCTCAGAAAATATATTAAACGAGCTTTGTAGGAGCTGC 719
QY	753	CACCTTTATCGATGCATAACCTTTTCTTGGGGATGTGTTGGAGAGGACAGATAACG 812
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Db	1020	TCCTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTACTGCTCATTTGTT 1079
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Db	1080	T 1080

RESULT 7

AK074841

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

1080 bp mRNA linear PRI 03-SEP-2002

Homo sapiens cDNA FLJ90360 fis, clone NT2RP2003664, highly similar to Homo sapiens mRNA for leptin receptor gene.

AK074841

AK074841.1 GI:22760546

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 1080)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- and 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

Location/Qualifiers

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/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

Query Match 96.0%; Score 1069; DB 9; Length 1080;

Best Local Similarity 99.9%; Pred. No. 3.6e-278;

Matches 1080; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 33 AGGAAGCCGGAAGCAGCCGCGCCAGTTTCGGGAGACATGCGCGGCGTTAAAGCTCTCG 92

Db 1 AGGAAGCCGGAAGCAGCCGCGCCAGTTTCGGGAGACATGCGCGGCGTTAAAGCTCTCG 60

QY 93 TGGCATTATCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCCTTAG 152

Db 61 TGGCATTATCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCCTTAG 120

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Db |||
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Db |||
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Db |||
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LOCUS

2388 bp DNA linear PAT 14-JUL-2003

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DEFINITION Sequence 2116 from Patent WO03039443.
ACCESSION AX779959.1 GI:32696953
VERSION AX779959.1
KEYWORDS
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Haerlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 2116 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE);
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
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NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
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Series: IRAL Plate: 48 Row: c Column: 17
This clone was selected for full length sequencing because it
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1. 1092

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23. 418

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ORIGIN

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Best Local Similarity 99.6%; Pred No. 4.4e-275;
Matches 1060; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 9
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DEFINITION Homo sapiens leptin receptor gene-related protein, mRNA (cDNA clone
MGC:61988 IMAGE:4328021), complete cds.
ACCESSION BC056250
VERSION BC056250.1 GI:33990029
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1092)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toohiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Smalios, D.E.,
Butterfield, Y.S., Krzyzanski, M.I., Skalek, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1092)
Strausberg, R.

Direct Submission
Submitted (11-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

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DEFINITION IMAGE:4296363), partial cds.
ACCESSION BC011027
VERSION BC011027.2 GI:34783168
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1056)
Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Narusins, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Young, A.C., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, G.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1056)
Straussberg, R.
Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:15029639.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 19 Row: 0 Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4504978.
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DEFINITION	Sequence 2 from patent US 5789198.		
ACCESSION	AR020775		
VERSION	AR020775.1	GI:3975390	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 874)		
AUTHORS	Akerblom, I. E.		
TITLE	Human leptin receptor-related protein		
JOURNAL	Patent: US 5789198-A 2 04-AUG-1998;		
FEATURES	Location/Qualifiers		
source	1..874		
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Best Local Similarity	99.4%; Pred. No. 3.5e-224;		
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Db	1	GTCTGGCTTGGGCAAGGCTGCCCGGCGTGGCAGGAGCGGAGCAGCGGCCCCAG	60
QY	61	TTCCGGGAGACATGCGCGGCGTTAAAGCTCTCGTGGCATATCTCTAGTGGGCTATTGG	120
Db	61	TTCCGGGAGACATGCGCGGCGTTAAAGCTCTCGTGGCATATCTCTAGTGGGCTATTGG	120
QY	121	ACTGACTTTTCTTATGCTGGGATGTGCTTAGAGGATATGGCGTTTACTGGCCCTTATT	180
Db	121	ACTGACTTTTCTTATGCTGGGATGTGCTTAGAGGATATGGCGTTTACTGGCCCTTATT	180
QY	181	CGTCTGATTTTCCACGCGCATCTCCCCCATCCCCCATTTTCAATGCCAAAAGAGTCACTTA	240
Db	181	CGTCTGATTTTCCACGCGCATCTCCCCCATCCCCCATTTTCAATGCCAAAAGAGTCACTTA	240
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Db	241	TGACTCAGATGCAACCCAGTAGTGCCTGTCGGGAACCTGGCATATTTCTTCACTACTGGAAT	300
QY	301	TGTTGTTTCTGCTTTGGATTTCTGTTTATTTCTTGTGCTGTGATCAAAATGGGG	360
Db	301	TGTTGTTTCTGCTTTGGATTTCTGTTTATTTCTTGTGCTGTGATCAAAATGGGG	360
QY	361	AGCTCGGGCTTGTGTTGGCAGGCAATGCAATTTTCTTCAATTTCAAGGGTTTTT	420
Db	361	AGCTCGGGCTTGTGTTGGCAGGCAATGCAATTTTCTTCAATTTCAAGGGTTTTT	420
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Db	421	CTTTATATTTGGAAGAGGAGATGATTTTAGCTGGAGCAGTGTAGTACCTTTATCTGAT	480
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Db	481	TACAGTGCATTTGAATTTCTTAGAACTCATATCTGTATACATGTGCAATGCGGCATT	540
QY	541	TTACTATGAAATTTAATATGCTGGTTTTTAACTCTTTATATATCATGTTCACTTTAA	600
Db	541	TTACTATGAAATTTAATATGCTGGTTTTTAACTCTTTATATATCATGTTCACTTTAA	600
QY	601	GAAAGACTTCATAAGTAGGAGATGAGTTTTTATTTCTCAGCAATAGACCTGTCAAATTTAG	660

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LOCUS      BD132522
DEFINITION A novel human leptin receptor gene-related protein..
ACCESSION BD132522
VERSION    BD132522.1 GI:23227467
KEYWORDS  JP 2002509427-A/1.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 874)
AUTHORS  Akerblom,I.E.
TITLE     A novel human leptin receptor gene-related protein
JOURNAL  Patient: JP 2002509427-A 1 26-MAR-2002;
COMMENT  INCYTE PHARMACEUTICALS INC
        PN JP 2002509427-A/1
        PD 26-MAR-2002
        PF 25-JUL-1997 JP 1998508261
        PR 01-AUG-1996 US 08/691071,15-APR-1997 US 08/843370 PI
        PC C12P7/40,C12M1/00
        CC
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ORIGIN
Query Match 78.1%; Score 869.6; DB 6; Length 874;
Best Local Similarity 99.4%; Pred. No. 3.5e-224;
Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy      1 GTCTGGCTTGGGAGGCTGCCCGGCGTGCAGGAGCCGGAAGCAGCCGCGGCCCGAG 60
Db      1 GTCTGGCTTGGGAGGCTGCCCGGCGTGCAGGAGCCGGAAGCAGCCGCGGCCCGAG 60
Qy      61 TTCGGGAGACATGCGGCGGTAAAGCTCTCGTGGCATTATCTTCAGTGGGCTATTGG 120
Db      61 TTCGGGAGACATGCGGCGGTAAAGCTCTCGTGGCATTATCTTCAGTGGGCTATTGG 120
Qy      121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGAGATTATGGCGTTTACTGGCCCTATT 180
Db      121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGAGATTATGGCGTTTACTGGCCCTATT 180
Qy      181 CGTCTGATTTTCAACGCGCATCTCCCGCATCCCGCATTTTCATTTGCGAAAGAGTCACTTA 240
Db      181 CGTCTGATTTTCAACGCGCATCTCCCGCATCCCGCATTTTCATTTGCGAAAGAGTCACTTA 240
Qy      241 TGACTCAGATCGAACCGAGTAGTGGCTGTCGGGAAGTGGCATATTTCTTCACTACTGGAAT 300
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Db      301 TGTGTTTCTGCCCTTTGGATTTCTCTGTTATTTCTTCTGCTGCTGCTGCTGATCAAAATGGGG 360
Qy      361 AGCTCGGGCTTGTGTTGGCAGGCAATGCAAGTCAATTTTCTTCAAAATCAAGGGTTTTT 420
Db      361 AGCTCGGGCTTGTGTTGGCAGGCAATGCAAGTCAATTTTCTTCAAAATCAAGGGTTTTT 420
Qy      421 CCTTATATTTGGAAAGAGAGATGATTTTGTAGCTGGGAGCAGTGGTAGCACTTTTATTTCTGAT 480
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Db      541 TTACTATGAAATTTAAATATGCTGGGTTTTTAAATACCTTTATATATATATATCATGTTCACTTTAA 600
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Db      781 GCTTGGGGATGCTGTTGGAGAGGAGATAAAGCTGTAAGCAGGCTCTCATGACCCAGGAA 840
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Db      841 GGCCGGGGTGGATCCCTCTTTKTTTGTAGTCCA 874

RESULT 13
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LOCUS      AC119800
DEFINITION Homo sapiens chromosome 1 clone RP4-630A11, complete sequence.
ACCESSION AC119800 ALJ157946
VERSION    AC119800.2 GI:25815349
KEYWORDS  HTG.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 161112)
AUTHORS  Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE     Direct Submission
JOURNAL  Unpublished
REFERENCE 2 (bases 1 to 161112)
AUTHORS  Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE     Direct Submission
JOURNAL  Submitted (02-MAY-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 161112)
AUTHORS  Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE     Direct Submission
JOURNAL  Submitted (28-NOV-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
COMMENT   On Nov 28, 2002 this sequence version replaced gi:20389314.
          ----- Genome Center

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Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgchgs@u.washington.edu
 Drafting Center: SC

----- Project Information

Center project name: chr-1
 Center clone name: RP4-630A11 (sc0810)
 ----- Summary Statistics
 Sequencing vector: plasmid; 68% of reads
 Chemistry: Dye-terminator ET; 25% of reads
 Chemistry: Dye-terminator Big Dye; 75% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 160526 bases at least Q40
 Consensus quality: 161073 bases at least Q30
 Consensus quality: 161107 bases at least Q20
 Insert size: 161112; sum-of-contigs
 Quality coverage: 8.8x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': Mapping in progress
 3': RP11-430H12 (UWGC:sc0702) AC097063, 50135-bp overlap

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI				BglII				HindIII			
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2184	2158	5671	5808	449	<800						
8065	8117	3403	3485	512	<800						
486	<800	10596	10659	2814	2807						
106	<800	5998	5808	1247	1212						
3938	3930	5361	5256	4695	4701						
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454	<800	677	<800	2017	2035
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4116	4117	4018	3959	6353	6156
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12984	12767	792	800	3180	3218
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130	<800	2529	2477	6622	6531
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2498	2561	3173	3194	451	<800
7241	7277	267	<800	5443	5392
3987	3930	799	800	10983	10933
2101	2063	884	899	655	<800
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3624	3611	1616	1588	1339	1318
1719	1676	186	<800	3903	3862
225	<800	9748	9982	1055	1081
23802	23955	5416	5448	7669	7660
9969	9806	5849	5808	7048	7002
6234	6179	7584	7591	4279	4362
760	796	2653	2682	653	<800
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3628	3611	2996	3022	7722	7660
4092	4117	3925	3959	6160	6156
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2577	2561	2408	2477	1120	1081
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----- 2651 ----- 2682 ----- 9332 ----- 9221
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----- 15 ----- 800 -----
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----- 4449 ----- 4362 -----
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----- 685 ----- 800 -----
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----- 2363 ----- 2389 -----
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----- 1715 ----- 1696 -----
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----- 5171 ----- 5082 -----
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----- 1030 ----- 1081 -----
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Qy 577 CTTTATATATCATGTTCATTTTGAAGAAGCTTCATAGTAGGAGATGAGTTTATTTCTC 636
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Qy 877 CTTATTAAGTGTGGCCCAACAGAGCCCTCAACATTTTCTTAGAGCCCTTATTAGAAA 936
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DEFINITION Homo sapiens cDNA FLJ26586 fis, clone LNF07412.
ACCESSION AKI30096
VERSION AKI30096.1 GI:34526837
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,
Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,
Onogawa, S., Kaeriyama, S., Satoh, N., Matsuura, H., Takahashi, E.,
Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
Terashima, Y., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K.,
Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B.,
Nagai, K., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1614)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
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Db 838 TCTTGTCTTTTCAGATCAAAATGGGAGCCTGGGCCCTTGTGTGGCAGCAATGCAGTCAT 897

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Db 121 CATGTTCATCTTTAAGAAAGACTTCAATAGTAGAGATGAGTTTATTTCTCAGCAATAGA 180

QY 647 CCTGTCAAAATTTAGATTATTTACTCAAAATTTATTTCTTTGTTGGCTGTTTCAATGATC 706

Db 181 CCTGTCAAAATTTAGATTATTTACTCAAAATTTATTTCTTTGTTGGCTGTTTCAATGATC 240

QY 707 ACGTGTCTCTCAGAAATATATTAACGCAGTCTTTGAGGAGGCTGCCACCTTATGCAATG 766

Db 241 ACGTGTCTCTCAGAAATATATTAACGCAGTCTTTGAGGAGGCTGCCACCTTATGCAATG 300

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QY 1067 GTGCGTAAACCACTTAACTCTCTGGGTGTTACCTGCTCATTTGTTTA 1114

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Search completed: August 18, 2005, 01:39:47
Job time : 5157 secs

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QY 577 CTTTATATATCATGTTTCACTTTAAGAAAGACTTCAATAGTAGAGATGAGTTTATTTCTC 636

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Db 1138 AGCAATAGACCTGTCAAAATTTAGATTATTTACTCAAAATTTATTTCTTGTGGCTGT 1197

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Db 1198 TCATGTAGTACGCGTCTCTCAGAAATATATTAACGCAGTCTTTGAGGAGGCTGCCACC 1257

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Db 1498 ATGCACATGAAGTTTTCAGAGAGCATCATATAGAGAGTAAACATCACCCCACTTCT 1557

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Db 1558 TATCTTCCAGTGGCTAAACACTTAACTCTCTGGGTGTTACTGCTCATTTGTTT 1614

RESULT 15
Q0860089
LOCUS Q0860089 648 bp DNA linear PAT 11-SEP-2004
DEFINITION Sequence 1 from Patent WO2004072293.
ACCESSION Q0860089
VERSION Q0860089.1 GI:51981977

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Jockers, R., Couturier, C. and Uhlmann, E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 1 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source Location/Qualifiers
1..648
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 58.2%; Score 648; DB 6; Length 648;

Result No.	Score	Query Match	Length	DB	ID	Description	
1	869.6	78.1	874	1	US-08-691-071-2	Sequence 2, Appli	
2	869.6	78.1	874	2	US-08-843-370-2	Sequence 2, Appli	
3	174.6	15.7	2701	4	US-09-839-709-1	Sequence 1, Appli	
4	162	14.5	3800	4	US-09-023-655-885	Sequence 885, App	
5	162	14.5	3871	2	US-08-599-4558-3	Sequence 3, Appli	
6	162	14.5	3871	3	US-09-069-781B-3	Sequence 3, Appli	
7	162	14.5	3871	3	US-09-137-132-3	Sequence 3, Appli	
8	162	14.5	3871	3	US-08-864-564A-3	Sequence 3, Appli	
9	162	14.5	3871	3	US-09-094-410-3	Sequence 3, Appli	
10	162	14.5	3871	4	US-08-708-123D-3	Sequence 3, Appli	
11	162	14.5	3871	4	US-08-583-153A-3	Sequence 3, Appli	
12	162	14.5	3871	4	US-08-570-142D-3	Sequence 3, Appli	
13	162	14.5	3871	4	US-08-638-524B-3	Sequence 3, Appli	
14	109.4	9.8	3909	3	US-09-043-816E-12	Sequence 12, Appli	
15	90.4	8.1	3102	4	US-08-780-563-6	Sequence 6, Appli	
16	90.4	8.1	4102	4	US-08-780-562-1	Sequence 1, Appli	
17	84.4	7.6	3004	4	US-08-780-562-5	Sequence 5, Appli	
18	55.4	5.0	63982	4	US-09-949-016-16769	Sequence 16769, A	
c	19	53.2	4.8	247293	4	US-09-949-016-17590	Sequence 17590, A
	20	52.4	4.7	176373	3	US-09-128-155-17	Sequence 17, Appli
21	52.2	4.7	23456	4	US-09-949-016-12989	Sequence 12989, A	
22	52.2	4.7	23458	4	US-09-949-016-12605	Sequence 12605, A	
23	51.6	4.6	205163	4	US-09-949-016-17009	Sequence 17009, A	
24	50.4	4.5	189	4	US-09-573-080A-194	Sequence 194, App	
25	50.4	4.5	69642	4	US-09-949-016-15339	Sequence 15339, A	
c	26	50.2	4.5	285986	4	US-09-949-016-12287	Sequence 12287, A
	27	50.2	4.5	288031	4	US-09-949-016-14864	Sequence 14864, A

61	QY	TTTCGGGAGACATGGCGGGGTTAAAGCTCTCGTGGCATTTATCCTTCAGTGGGCTATTGG	120
61	Db		
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121	Db		
121	QY	ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTAAGCGTTTACTTGCCCTTATT	180
121	Db		
181	QY	CGTCTGTATTTTCCAGGCCATCTCCCCCATCCCCCATTTCAATTGCCAAAGAGTCACCTTA	240
181	Db		
181	QY	CGTCTGTATTTTCCAGGCCATCTCCCCCATCCCCCATTTCAATTGCCAAAGAGTCACCTTA	240
181	Db		
241	QY	TGACTCAGATGCAACAGTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACCTACTGGAT	300
241	Db		
241	QY	TGACTCAGATGCAACAGTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACCTACTGGAT	300
241	Db		
301	QY	TGTTGTTTCTGCTTTGGATTTCTGTTATTTCTGCTCGTGTGGCTGTGATCAAAATGGGG	360
301	Db		
301	QY	TGTTGTTTCTGCTTTGGATTTCTGTTATTTCTGCTCGTGTGGCTGTGATCAAAATGGGG	360
301	Db		
361	QY	AGCTCGGGCTTGTGTTGGCAGCAATGAGTCATTTCTTCAATTTCAAGGTTTTTT	420
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361	QY	AGCTCGGGCTTGTGTTGGCAGCAATGAGTCATTTCTTCAATTTCAAGGTTTTTT	420
361	Db		
421	QY	CCATTATTTTGGAGAGGAGATGATTTAGCTGGGACAGTGGTAGCACATTTATCTGAT	480
421	Db		
421	QY	CCATTATTTTGGAGAGGAGATGATTTAGCTGGGACAGTGGTAGCACATTTATCTGAT	480
421	Db		
481	QY	TACAGTGCATGGAATTTCTTAGAATCATATCTATCTATACATGTGCACATCGGCATT	540
481	Db		
481	QY	TACAGTGCATGGAATTTCTTAGAATCATATCTATCTATACATGTGCACATCGGCATT	540
481	Db		
541	QY	TTACTATGAATTTTAAATATGCTGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA	600
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541	QY	TTACTATGAATTTTAAATATGCTGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA	600
541	Db		
601	QY	GAAGAATTTCATAGTAGGAGATGAGTTTATTTCTCAGCAATAGACTGTCAAAATTTAG	660
601	Db		
601	QY	GAAGAATTTCATAGTAGGAGATGAGTTTATTTCTCAGCAATAGACTGTCAAAATTTAG	660
601	Db		
661	QY	ATTATGTTACTCAAAATATGTTACTTGTGCTGTGTTCAATGATGACGGTGCTCTAGA	720
661	Db		
661	QY	ATTATGTTACTCAAAATATGTTACTTGTGCTGTGTTCAATGATGACGGTGCTCTAGA	720
661	Db		
721	QY	AAATATATTAACGCAGTCTGTAGGCAGCTGCACCTTATGCAGTGATCGAAACCTTTT	780
721	Db		
721	QY	AAATATATTAACGCAGTCTGTAGGCAGCTGCACCTTATGCAGTGATCGAAACCTTTT	780
721	Db		
781	QY	GCTTCGGGATGTGCTTGGAGAGCGAGATAACGCTGAAGCAGGCTCTCATGACCCAGGA	840
781	Db		
781	QY	GCTTCGGGATGTGCTTGGAGAGCGAGATAACGCTGAAGCAGGCTCTCATGACCCAGGA	840
781	Db		
841	QY	GGCCGGGTGGATCCCTCTTCTGTTGTAGTCCA	874
841	Db		
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841	Db		

RESULT 2	
US-08-843-370-2	
Sequence 2, Application US/08843370	
Patent No. 5874535	
GENERAL INFORMATION:	
APPLICANT: Akerblom, Ingrid E.	
TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR	
TITLE OF INVENTION: GENE-RELATED PROTEIN	
NUMBER OF SEQUENCES: 4	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Incyte Pharmaceuticals, Inc.	
STREET: 3174 Porter Drive	
CITY: Palo Alto	
STATE: CA	
COUNTRY: U.S.	

Db 541 TTACTATGAATTAATATGCTGGGTTTTTAATACCTTTATATATCATGTTCACTTAA 600
Qy 601 GAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACTGTCAAATTTAG 660
Db 601 GAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACTGTCAAATTTAG 660
Qy 661 ATTATGTTACTCAAAATATGTTTACTTTTGGCTGTTTCATGATGACGGTGTCTCAGA 720
Db 661 ATTATGTTACTCAAAATATGTTTACTTTTGGCTGTTTCATGATGACGGTGTCTCAGA 720
Qy 721 AAATATATTAACGAGCTCTTGTAGGACGCTGCCACCTTATGTCAGTGCATCGAAACCTTTT 780
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Qy 781 GCTTGGGATGTGCTTGGAGAGGAGATAACGCTGGAAGCAGGCTCTCATGACCCAGAA 840
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Qy 841 GCGCGGGGTGATCCCTCTTGTGTTGTAGTCCA 874
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RESULT 3
US-09-839-709-1
; Sequence 1, Application US/09839709
; Patent No. 6517489
; GENERAL INFORMATION:
; APPLICANT: Mao, Yumin
; APPLICANT: Xie, Yi
; APPLICANT: Huang, Yan
; TITLE OF INVENTION: NEW PROTEIN ASSOCIATED WITH LEPTIN RECEPTOR FOR OBESITY AND THE
; TITLE OF INVENTION: ENCODING SEQUENCE THEREOF AND THE METHODS FOR PRODUCING SAME AND
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 9548.60USWO
; CURRENT APPLICATION NUMBER: US/09/839,709
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/CN99/00167
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: CN 98121474.6
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-839-709-1

Query Match 15.7%; Score 174.6; DB 4; Length 2701;
Best Local Similarity 65.0%; Pred. No. 3.1e-45;
Matches 258; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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Qy 128 TTCTCTATGCTGGAGTGTGCTTAGAGGATATGCGGTTTACTGCGCCCTTATTCGTCCTG 187
Db 142 TTTTGTAGCTTGAGATGTGCGCTTCCATATATACAAATATCTGCGCCCTTGTGTTCTA 201
Qy 188 ATTTTCCAGCGCATCTCCCCCATCCCCCATTTTCATGCGCAAAAGAGTCACTATGACTCA 247
Db 202 TTTTTTTACATCTTTTACCTATTTCCATCTGTCATAGCAAGAGATTAGTGATGATACA 261
Qy 248 GATGCAACAGTAGTGTGCTGCGGAAGTGCATATTTCTTCACTACTGGAATTTGTTT 307
Db 262 GATGCTATGATAAGCTGTGTAAGAACTTGCCATCTTTCTTACAAACGGGCAATTTGCTG 321
Qy 308 TCTGCTTTGATTTCTGTTTATTTCTGCTGCTGCTGCTGATCAAAATGGGAGCTGCG 367
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Qy 368 GGCCTTGTGTGGCAGCATGAGTCTTCTTACATTTCAAGGGTTTTTCTTTATA 427
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Qy 428 TTTGGAGAGGAGATGATTTTGTAGCTGGGAGCAGTGGT 464
Db 442 TTTGGAGAGGAGGACGACTTCAGCTGGCAGCAGTGGT 478

RESULT 4
US-09-023-655-885
; Sequence 885, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 885:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1139594
US-09-023-655-885

Query Match 14.5%; Score 162; DB 4; Length 3800;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTGGCTTGGCAGGCTGCCCGGCGCTGGCAGGAAGCCGAGAGCGCGCCCGCAG 60
Db 12 GTCTGGCTTGGCAGGCTGCCCGGCGCTGGCAGGAAGCCGAGAGCGCGCCCGCAG 71
Qy 61 TTGGGAGACATGGCGGCGCTTAAAGCTCTCGTGGCAATTATCTTTCAGTGGGGCTATTGG 120
Db 72 TTGGGAGACATGGCGGCGCTTAAAGCTCTCGTGGCAATTATCTTTCAGTGGGGCTATTGG 131
Qy 121 ACTGACTTTTCTTATGCTGGGATGCTGCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGCTGCTTAGAGGATTATGG 173

Fri Aug 19 08:52:54 2005

us-10-774-721-21.rni

Db 132 ACTGACTTTCTTATGCTGGATGTGCCTTAGAGGATTATGG 173

RESULT 5
US-08-599-455B-3
; Sequence 3, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194....3688

US-08-599-455B-3
Query Match 14.5%; Score 162; DB 2; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTGGCTTGGCAGCTGCCGGCCGTGGCAGGAAGCCGGAAGCAGCGCCGCCCGCCAG 60
DB 12 GTCCTGGCTTGGCAGCTGCCGGCCGTGGCAGGAAGCCGGAAGCAGCGCCGCCCGCCAG 71

QY 61 TTCGGGAGACATGGCCGGCGTTAAAGCTCTCGTGCAATTATCCTTCAGTGGGGCTATTGG 120
DB 72 TTCGGGAGACATGGCCGGCGTTAAAGCTCTCGTGCAATTATCCTTCAGTGGGGCTATTGG 131

QY 121 ACTGACTTTCTTATGCTGGATGTGCCTTAGAGGATTATGG 162
|||||

RESULT 6
US-09-069-781B-3
; Sequence 3, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,781B
; FILING DATE: 29-APRIL-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194....3688

US-09-069-781B-3
Query Match 14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-069-781B-3

Qy 1 GTCTGGCTTGGCAGGCTGCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 60
Db |||||
12 GTCTGGCTTGGCAGGCTGCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 71
Qy 61 TTCGGGAGACATGCGGCGGTTAAAGCTCTCTGGCATTATCTTTCAGTGGGCTATTGG 120
Db 72 TTCGGGAGACATGCGGCGGTTAAAGCTCTCTGGCATTATCTTTCAGTGGGCTATTGG 131
Qy 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 7

US-09-137-132-3
; Sequence 3, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
US-09-137-132-3

Query Match 14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTGGCTTGGCAGGCTGCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 60
Db 12 GTCTGGCTTGGCAGGCTGCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 71
Qy 61 TTCGGGAGACATGCGGCGGCGTTAAAGCTCTCTGGCATTATCTTTCAGTGGGCTATTGG 120
Db 72 TTCGGGAGACATGCGGCGGCGTTAAAGCTCTCTGGCATTATCTTTCAGTGGGCTATTGG 131
Qy 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 8

US-08-864-564A-3
; Sequence 3, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,564A
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283

—

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
; US-08-708-123D-3

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Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTGGCTTGGCGAGGCTGCCCGGCGCTGCGCAGGAGCCGGAAGCAGCCGCGGCCCCAG 60
Db 12 GTCTGGCTTGGCGAGGCTGCCCGGCGCTGCGCAGGAGCCGGAAGCAGCCGCGGCCCCAG 71

Qy 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131

Qy 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 11
US-08-583-153A-3
; Sequence 3, Application US/08583153A
; Patent No. 6506877
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153A
; FILING DATE: 28-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
; US-08-583-153A-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTGGCTTGGCGAGGCTGCCCGGCGCTGCGCAGGAGCCGGAAGCAGCCGCGGCCCCAG 60
Db 12 GTCTGGCTTGGCGAGGCTGCCCGGCGCTGCGCAGGAGCCGGAAGCAGCCGCGGCCCCAG 71

Qy 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131

Qy 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 12
US-08-570-142D-3
; Sequence 3, Application US/08570142D
; Patent No. 6509189
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570.142D
; FILING DATE: 11-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/014001
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
;
US-08-570-142D-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGAGCTGCGCGCGCTGGCAGGAGCGGAGCAGCGCGCGCCAG 60
Db 12 GTCTGGCTTGGCAGAGCTGCGCGCGCTGGCAGGAGCGGAGCAGCGCGCGCCAG 71

QY 61 TTCGGGAGACATGCGCGCGCGTTAAAGCTCTCGTGGCATATCTTCAGTGGGGCTATTGG 120
Db 72 TTCGGGAGACATGCGCGCGCGTTAAAGCTCTCGTGGCATATCTTCAGTGGGGCTATTGG 131

QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 13
US-08-638-524B-3
; Sequence 3, Application US/08638524B
; Patent No. 6548269
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB
; TITLE OF INVENTION: CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,524B
; FILING DATE: 28-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/018001
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
;
US-08-638-524B-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGAGCTGCGCGCGCTGGCAGGAGCGGAGCAGCGCGCGCCAG 60
Db 12 GTCTGGCTTGGCAGAGCTGCGCGCGCTGGCAGGAGCGGAGCAGCGCGCGCCAG 71

QY 61 TTCGGGAGACATGCGCGCGCGTTAAAGCTCTCGTGGCATATCTTCAGTGGGGCTATTGG 120
Db 72 TTCGGGAGACATGCGCGCGCGTTAAAGCTCTCGTGGCATATCTTCAGTGGGGCTATTGG 131

QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 14
US-09-043-816E-12
; Sequence 12, Application US/09043816E
; Patent No. 6414128
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Willson, Tracy
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Gainsford, Timothy
; APPLICANT: Alexander, Warren S.
; APPLICANT: Metcalf, Donald
; APPLICANT: NG, Ashley
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; TITLE OF INVENTION: ENCODING SAME
; FILE REFERENCE: 11268
; CURRENT APPLICATION NUMBER: US/09/043,816E
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (27)..(68)
; OTHER INFORMATION: N is a or g or c or t
; NAME/KEY: unsure
; LOCATION: (923)
; OTHER INFORMATION: R is g or a
; NAME/KEY: unsure
; LOCATION: (2315)
; OTHER INFORMATION: S is g or c
US-09-043-816E-12

Query Match          9.8%; Score 109.4; DB 3; Length 3909;
Best Local Similarity 91.9%; Pred. No. 4.6e-24;
Matches 113; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 49 CCGGGCCCCCAGTTCCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAG 108
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Db 21 CCGGCGCCAGCTCGGAGACATGGGGGCGTTAAAGCTCTCGTGGNATTATCCTTCAG 80
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Qy 109 TGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATTATGGCGTTA 168
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Db 81 TGGGGTATTGGACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATTATGGATTGG 140
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Qy 169 CTG 171
Db 141 CAG 143
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RESULT 15
US-08-780-562-6
; Sequence 6, Application US/08780562
; Patent No. 6541604
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780.562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/
; FILING DATE: 01/08/97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3102 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-780-562-6

Query Match          8.1%; Score 90.4; DB 4; Length 3102;
Best Local Similarity 98.9%; Pred. No. 5.4e-18;
Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 71 ATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 130
      |||||
Db 15 ACGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 74
      |||||

Qy 131 CTTATGCTGGGATGCTGCTTAGAGGATTATGG 162
      |||||
Db 75 CTTATGCTGGGATGCTGCTTAGAGGATTATGG 106
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
9974.970 Million cell updates/sec

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Perfect score: 1114
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: gb_est2:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gsl1:*
9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	903.4	81.1	1050	1	AL550884
3	881	79.1	1026	1	AL552981
4	805.8	72.3	952	5	BX417049
5	790.6	71.0	1004	5	BX417586
6	784.4	70.4	786	1	AL571122
7	776.8	69.7	805	1	AL709947
8	775	69.6	811	5	BX378815
9	771.6	69.3	996	5	BQ959135
10	767.2	68.9	914	5	BUI189726
11	766.4	68.8	899	5	BQ424209
12	763.4	68.5	835	7	CF594097
13	747.2	67.1	786	6	CA311840
14	741.8	65.7	765	6	CA311840
15	729.6	65.5	739	1	AL699934
16	728.6	65.5	739	1	AL700785
17	718.4	64.5	810	2	B8615001
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19	709.4	63.7	711	7	CN427830
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22	706.8	63.4	746	5	BU620279
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	35	656	58.9	696	6	CB529317
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	37	651.8	58.5	880	6	CB984985
	38	645.6	58.0	720	6	CA439961
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	41	640.6	57.5	690	1	AV763446
	42	639	57.4	653	5	BU580876
	43	632.8	56.8	752	4	BI833417
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ALIGNMENTS

RESULT 1
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LOCUS BX462364 1040 bp mRNA linear EST 06-MAY-2004
DEFINITION BX462364 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
Clone CS0DG007YG08 5-PRIME, mRNA sequence.
ACCESSION BX462364
VERSION BX462364.2 GI:47065982
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1040)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31029418.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 384.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS0DG007BD04QPI&c=384.f.
Location/Qualifiers
1. .1040
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG007YG08"
/tissue type="B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of the
pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

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Best Local Similarity 96.0%; Pred. No. 7.6e-242;


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QY 530 CATGGCGCATTTTACTATGAATTTAAATATGCTGGGTTTTTAAATACCTTTATATATCAT 589
Db 481 CATGGCGCATTTTACTATGAATTTAAATATGCTGGGTTTTTAAATACCTTTATATATCAT 540
QY 590 GTTCACTTTAAGAAAGACTTTCATAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCT 649
Db 541 GTTCACTTTAAGAAAGACTTTCATAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCT 600
QY 650 GTCAAAATTTAGATTTAGTACTCAAAATATGTTACTGTTGGCTGTTCACTAGTAGTCAG 709
Db 601 GTCAAAATTTAGATTTAGTACTCAAAATATGTTACTGTTGGCTGTTCACTAGTAGTCAG 660
QY 710 GTGCTCTCAGAAAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTTATGCAAGTGCAT 769
Db 661 GTGCTCTCAGAAAATATATTAACGCA-TCTTGTAGGAGCTG-CACCTTATGCAAGTGCAT 718
QY 770 CGAAACCTTTTGTCTGGGATGTGCTTGGAGAGGAGATAAACGCTGAAGCAGGCTCTCA 829
Db 719 CGAAACCTTTTGTCTGGGATGTGCTTGGAGAGGAGATAAACGCTGAAGCAGGCTCTCA 778
QY 830 TGACCCAGAGAGCGGGGTGATCCCTCTTGTGTAGTCCATGCTATTAAGTGT 889
Db 779 TGACCCAGAGAGCGGGGTGATCCCTCTTGTGTAGTCCATGCTATTAAGTGT 838
QY 890 GGCCACAGACCAAGAGCTCAACATTTCTTAGAGCTTTATAGAAATGCAGAACTCGAA 949
Db 839 GGCCACAGACCAAGAGCTCAACATTTCTTAGAGCTTTATAGAAATGCAGAACTCGAA 898
QY 950 GCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAG 1009
Db 899 G-CCCACTCTGGACCCAGGACATTTTGATGAGAT-CAAGGAGTTGTATGCAATGAAGT 956
QY 1010 TTGAGAGAGATCATATAGAGAGTAAACATCACACCAACTTC 1054
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RESULT 3

AL552981
LOCUS
DEFINITION
AL552981 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1072YL04 5-PRIME, mRNA sequence.

AL552981
ACCESSION
AL552981.3 GI:45857751

EST.
KEYWORDS

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1026)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31274795.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of invitrogen. This sequence belongs to sequence cluster
384.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?e=CS0D1072DF02QPI&c=384.f.

Location/Qualifiers

1..1026

/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YL04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 79.1%; Score 881; DB 1; Length 1026;
Best Local Similarity 96.7%; Pred. No. 7.6e-232;
Matches 939; Conservative 11; Mismatches 16; Indels 5; Gaps 5;
QY 49 CCGCGGCCCGGCTCGGGAGACATCGGGGGCGTTAAAGCTCTCGTGGCATTTATCTTCAG 108
Db 10 CCGGATCCCGAGCTCGGGAGACATCGGGGGCTTAAAGCTCTCGTGGCATTTATCTTCAG 69
QY 109 TGGGGCTATTGGAAGTGAATTTTCTTATGCTGGGATGTCCTTAGAGGATTAAGCGTTTA 168
Db 70 TGGGGCTATTGGAAGTGAATTTTCTTATGCTGGGATGTCCTTAGAGGATTAAGCGTTTA 129
QY 169 CTGGCCCTTATTGCTGCTGATTTTCCACGCCATCTCCCCCATCCGCCATTTTCATTGCCAA 228
Db 130 CTGGCCCTTATTGCTGCTGATTTTCCACGCCATCTCCCCCATCCGCCATTTTCATTGCCAA 189
QY 229 AAGAGTCACTTATGACTCAGATGCAACAGTAGTGCCTGTGCGGAACCTGGGCATATTTCTT 288
Db 190 AAGAGTCACTTATGACTCAGATGCAACAGTAGTGCCTGTGCGGAACCTGGGCATATTTCTT 249
QY 289 CACTACTGGAATTTGTTTCTGCTTTGGAATTTCTGTTAATCTTGTCTGTGGCTGT 348
Db 250 CACTACTGGAATTTGTTTCTGCTTTGGAATTTCTGTTAATCTTGTCTGTGGCTGT 309
QY 349 GATCAAAATGGGAGCCTCGGCGCTTGTGTTGGCAGGCAATGCAGTCAATTTTCTTACAA 408
Db 310 GATCAAAATGGGAGCCTCGGCGCTTGTGTTGGCAGGCAATGCAGTCAATTTTCTTACAA 369
QY 409 TCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGTAGCA 468
Db 370 TCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGTAGCA 429
QY 469 CTTTATTTCTGATTAACAGTGCAATGAAATTTCTTAGAACTCATATCTATCTGTATACATG 528
Db 430 CTTTATTTCTGATTAACAGTGCAATGAAATTTCTTAGAACTCATATCTATCTGTATACATG 489
QY 529 ACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCA 588
Db 490 ACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCA 549
QY 589 TGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACC 648
Db 550 TGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACC 609
QY 649 TGTCAAAATTTAGATTAATGTTTACTCAAAATATGTTTACTTTGTTGGCTGTTTCAATGATC 708
Db 610 TGTCAAAATTTAGATTAATGTTTACTCAAAATATGTTTACTTTGTTGGCTGTTTCAATGATC 669
QY 709 GGTGCTCTCAGAAATATATTTAACGCAATTTGTTAGGAGCTGCCACCTTATGCAATGCA 768
Db 670 GGTGCTCTCAGAAATATATTTAACGCAATTTGTTAGGAGCTGCCACCTTATGCAATGCA 729
QY 769 TCGAAACCTTTTGTCTGGGATGTTCTTGGAGAGGAGATAACCTGAAGCAGGCTCTC 828
Db 730 TCGAAACCTTTTGTCTGGGATGTTCTTGGAGAGGAGATAACCTGAAGCAGGCTCTC 789
QY 829 ATGACCCAGGAAGGCC-GGGGTGGATCCCTCTTT-TGTGTTAGTCCATGCTATTAAGAAG 886
Db 790 ATGACCCAGGAAGGCCGGGGTGGATCCCTCTTTGGTGTGKAGTCCATGCTATTAAGAAG 849
QY 887 TGTGGCCCAAGCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAAGATCT 946

Fri Aug 19 08:52:55 2005

us-10-774-721-21.rst

Db	850	TGTGCCCCACAGAACAGAGCCTCCACATTTCTTAGAGCTTATTWGAATGCAKATCT	909	Db	190	AGAGTCACTATGACTCAGATGCAACACAGTAGTGCCTGCGGAACTGGCATATTTCTT	249
Qy	947	GAAGCCCACTCTGGACCCAGACATTTTGTATGATGATCCAAAGAGTGTATGACATGA	1006	Qy	289	CACACTGGAATTTGTTTCTGCTTTTGGATTTCTGTATTTCTTGTCTGCTGCTGT	348
Db	910	GARG-CCCACTCTGGA-CCMGACATTTTGTATGATCCAAAGGAG-TGTATGCMAGAA	966	Db	250	CACACTGGAATTTGTTTCTGCTTTTGGATTTCTGTATTTCTTGTCTGCTGCTGT	309
Qy	1007	AGTTTGTAGAA 1017		Qy	349	GATCAAAATGGGAGCCTGCGGCTTGTGTGGCAGCAATGAGTCAATTTTCTTCAAT	408
Db	967	AGTTKRGARSA 977		Db	310	GATCAAAATGGGAGCCTGCGGCTTGTGTGGCAGCAATGAGTCAATTTTCTTCAAT	369
RESULT 4				Qy	409	TCAGGGTTTTTCTTATATTTTGAAGAGAGATGATTTTAGCTGGAGCAGTGGTAGCA	468
LOCUS	BX417049	952 bp mRNA linear EST 01-MAY-2004		Db	370	TCAGGGTTTTTCTTATATTTTGAAGAGAGATGATTTTAGCTGGAGCAGTGGTAGCA	429
DEFINITION	BX417049 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YJ23	5-PRIME, mRNA sequence.		Qy	469	CTTTATTTCTGATTACAGTGCATTTCTTGAAGAACTCATACTATCTATCTATATATCA	528
ACCESSION	BX417049.2	GI:46933188		Db	430	CTTTATTTCTGATTACAGTGCATTTCTTGAAGAACTCATACTATCTATATATCA	489
VERSION	EST.			Qy	529	ACATGCGGCATTTTACTATGAAATTTAAATGCTGGGTTTTTAAATACCTTTATATCA	588
KEYWORDS	Homo sapiens (human)			Db	490	ACATGCGGCATTTTACTATGAAATTTAAATGCTGGGTTTTTAAATACCTTTATATCA	549
SOURCE	Homo sapiens			Qy	589	TGTTCACTTTAAGAAAGACTTTCAAGTAGGAGATGAGTTTTTATCTCAGCAATAGACC	648
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	550	TGTTCACTTTAAGAAAGACTTTCAAGTAGGAGATGAGTTTTTATCTCAGCAATAGACC	609
REFERENCE	1 (bases 1 to 952)			Qy	649	TGTCAAATTTAGATTATGTTACTCAAAATTTATGTTACTTGTGGCTTTTATGTTAGTCAC	708
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			Db	610	TGTCAAATTTAGATTATGTTACTCAAAATTTATGTTACTTGTGGCTTTTATGTTAGTCAC	669
TITLE	Full-length cDNA libraries and normalization			Qy	709	GGTCTCTCAGAAATATATTTAAGCAGTCTTTAGGAGCTGCGCACCCTTATGAGTGA	768
JOURNAL	Unpublished (2001)			Db	670	GGTCTCTCAGAAATATATTTAAGCAGCTTTAGGAGCTGCGCACCCTTATGAGTGA	728
COMMENT	On May 13, 2003 this sequence version replaced gi:30654341.			Qy	769	TCGAAACCTTTTGTCTTGGGATGTGCTTGGAGAGGAGATAACGCTGAAGCAGGCTCTC	828
	Contact: Genoscope			Db	729	TCGAAACCTTTTGTCTTGGGATGTGCTTGGAGAGGAGATAACGCTGAAGCAGGCTCTC	788
	Genoscope - Centre National de Sequencage			Qy	829	ATGACCCAGGAGGCGGGGTGGATCCCTCTTCTGTGTAGTCCATCTATTTAAAGTG	888
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			Db	789	ATGACCCAGGAGGCGGGGTGGAT-CCCTCTTGTGTGTAGTCCATCTATTTAAAGTG	847
	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr			Qy	889	TGGCCACACA 897	
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			Db	848	GCCACACA 856	
	end enriched, double-strand cDNA was digested with Not I and cloned			RESULT 5			
	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			BX417586			
	was not normalized. Library was constructed by Life Technologies, a			LOCUS			
	division of Invitrogen.			DEFINITION			
FEATURES	Location/Qualifiers			5-PRIME, mRNA sequence.			
source	1. .952			ACCESSION			
	/organism="Homo sapiens"			VERSION			
	/mol_type="mRNA"			KEYWORDS			
	/db_xref="taxon:9606"			SOURCE			
	/clone="CS0DE003YJ23"			ORGANISM			
	/tissue_type="PLACENTA"			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	/clone_lib="Homo sapiens PLACENTA"			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed			1 (bases 1 to 1004)			
	with a NotI-oligo(dT) primer. Five prime end enriched,			Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
	double-strand cDNA was digested with Not I and cloned into			Full-length cDNA libraries and normalization			
	the Not I and EcoRV sites of the pCMVSPORT 6 vector.			Unpublished (2001)			
	Library was not normalized."			On May 13, 2003 this sequence version replaced gi:30642089.			
ORIGIN				Contact: Genoscope			
Query Match	72.3%; Score 805.8; DB 5; Length 952;			Genoscope - Centre National de Sequencage			
Best Local Similarity	98.4%; Pred. No. 4.4e-211;			2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Matches	835; Conservative 0; Mismatches 12; Indels 2; Gaps 2;			Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
Qy	49	CCGGGCCCCAGTTGCGGAGACATGGCGGGGTTAAAGCTCTCGTGGCATTCCTTCAG	108	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
Db	10	CCGGGATCCAGCTCGGAGACATGGCGGGGTTAAAGCTCTCGTGGCATTCCTTCAG	69	end enriched, double-strand cDNA was digested with Not I and cloned			
Qy	109	TGGGGCTATTGACATGCTTTCTTATGCTGGATGTGCCCTTAGAGATTATGCGTTTA	168	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
Db	70	TGGGGCTATTGACATGCTTTCTTATGCTGGATGTGCCCTTAGAGATTATGCGTTTA	129	was not normalized. Library was constructed by Life Technologies, a			
Qy	169	CTGGCCCTATTGCTCTGATTTTCCAGCCATCTCCGCCATCCCGCATTCATGCGAA	228	division of Invitrogen.			
Db	130	CTGGCCCTATTGCTCTGATTTTCCAGCCATCTCCGCCATCCCGCATTCATGCGAA	189	This sequence belongs to sequence cluster 384.f			
Qy	229	AGAGTCACTATGATCAGATGCAACCAAGTAGTGCCTGTCGGAACTGGCATATTTCTT	288	For more information about this cluster, see			
				http://www.genoscope.cns.fr/cdna?s=CS0DE003CE12QP1&c=384.f.			

This sequence belongs to sequence cluster 384.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?8=CS0D010CF02QP1&c=384.f>.
 Location/Qualifiers
 1. 1004
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D010YL03"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 71.0%; Score 790.6; DB 5; Length 1004;
 Best Local Similarity 97.1%; Pred. No. 7.1e-207;
 Matches 848; Conservative 0; Mismatches 19; Indels 6; Gaps 4;
 Qy 85 AGCTCTCGTGGCATTATCTTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATG 144
 Db 1 AGCTCTCGTGGCATTATCTTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATG 60
 Qy 145 TGCCTTAGAGATTATGCGGTTACTGGCCCTTATTCCTGATTTTCCACGCATCTC 204
 Db 61 TGCCTTAGAGATTATGCGGTTACTGGCCCTTATTCCTGATTTTCCACGCATCTC 120
 Qy 205 CCCATCCCCATTTCATGTCACAAAGAGTACCTATGACTCAGATGCAACAGTAGTGC 264
 Db 121 CCCATCCCCATTTCATGTCACAAAGAGTACCTATGACTCAGATGCAACAGTAGTGC 180
 Qy 265 CTGTGGGAACCTGGCATATTTCTTCACTACTGGAATGCTGCTTCTGCTTTGGATTTC 324
 Db 181 CTGTGGGAACCTGGCATATTTCTTCACTACTGGAATGCTGCTTCTGCTTTGGATTTC 240
 Qy 325 TGTTATCTTCTGCTGTGGCTGTGATCAAAATGGGAGCCTGCGGCCCTTGTGTGGCAGG 384
 Db 241 TGTTATCTTCTGCTGTGGCTGTGATCAAAATGGGAGCCTGCGGCCCTTGTGTGGCAGG 300
 Qy 385 CAATGCAGTCAATTTCTTACAAATTCAGGGTTTTTCTTATATTTTGAAGAGAGATGA 444
 Db 301 CAATGCAGTCAATTTCTTACAAATTCAGGGTTTTTCTTATATTTGAAGAGAGATGA 360
 Qy 445 TTTTACGTGGGAGAGTGTAGCACTTTTCTGATTACAGTGCATGAATTTCTTAGAA 504
 Db 361 TTTTACGTGGGAGAGTGTAGCACTTTTCTGATTACAGTGCATGAATTTCTTAGAA 420
 Qy 505 CTCATCTATCTGTATACATGTGCACATGCGGCATTTTCTATGAAATTTAATATGCTGG 564
 Db 421 CTCATCTATCTGTATACATGTGCACATGCGGCATTTTCTATGAAATTTAATATGCTGG 480
 Qy 565 GTTTTAAATACCTTTATATATATGTTCACTTTTAAAGAAAGACTTCATAGTAGAGATG 624
 Db 481 GTTTTAAATACCTTTATATATATGTTCACTTTTAAAGAAAGACTTCATAGTAGAGATG 540
 Qy 625 AGTTTATTTCTCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTATTTAC 684
 Db 541 AGTTTATTTCTCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTATTTAC 600
 Qy 685 TTGTTTGGCTGTTCATGTAGTCACGGTCTCTCAGAAAATATATTAACGAGTCTTTGTAG 744
 Db 601 TTGTTTGGCTGTTCATGTAGTCACGGTCTCTCAGAAAATATATTAACGCA-TCTTTAG 659
 Qy 745 GCAGTGCACCTTATGCAATGCAATCGAAACCTTTTGTCTTGGGAGATGCTTGGAGAGGC 804
 Db 660 GCAGTGCACCTTATGCAATGCAATCGAAACCTTTTGTCTTGGGAGATGCTTGGAGAGGC 719
 Qy 805 AGATAACCTGACGAGCCCTCTCATGACCCAGGAGCCGGGTGGATCCCTCTTTGTG 864
 Db 720 AGATAACCTGACGAGCCCTCTCATGACCCAGGAGCCGGGTGGAT-CCTCTTTGTG 778

Qy 865 TTGTAGTCCATGCTATTAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAG 924
 Db 779 TTGTAGTCCATGCTATTAAAGTGTGG-CCACAGCAAGAGCTCAACATTTCTTAGAG-- 835
 Qy 925 CCTTATTAGAAATGCAGAACTCTGAAGCCCACT 957
 Db 836 -CTTATTAGAAATGCAGATCTGAAGCCCACTCT 867
 RESULT 6
 AL571122 786 bp mRNA linear EST 05-APR-2004
 LOCUS AL571122 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 DEFINITION clone CSODI027YK17 5-PRIME, mRNA sequence.
 ACCESSION AL571122
 VERSION AL571122.3 GI:46237227
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 786)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31292526.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 384.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?8=CS0D1027AF09QP1&c=384.f>.
 Location/Qualifiers
 1. 786
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="CSODI027YK17"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 70.4%; Score 784.4; DB 1; Length 786;
 Best Local Similarity 99.9%; Pred. No. 3.5e-205;
 Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 35 GAAGCCGGAAGCAGCCGCGCCAGTTCGGGAGACATGCGGGCGTTAAAGCTCTCGTG 94
 Db 1 GAAGCCGGAAGCAGCCGCGCCAGTTCGGGAGACATGCGGGCGTTAAAGCTCTCGTG 60
 Qy 95 GCATTATCTTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAGAG 154
 Db 61 GCATTATCTTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAGAG 120
 Qy 155 GATTATGCGGTTTACTGCGCCCTTATTCCTGCTGATTTTCCAGCCATCTCCCATCCCC 214
 Db 121 GATTATGCGGTTTACTGCGCCCTTATTCCTGCTGATTTTCCAGCCATCTCCCATCCCC 180
 Qy 215 CATTTCATTGCAAAAGAGTCCACCTATGACTCAGATGCAACAGTAGTGCCTGTGGGAA 274
 Db 181 CATTTCATTGCAAAAGAGTCCACCTATGACTCAGATGCAACAGTAGTGCCTGTGGGAA 240

QY	275	CTGGCATATTTCTTCACTACCTGGAATGTTGTTCTGCTTTGGATTTCCTGTTATTTCTT	334
Db	241	CTGGCATATTTCTTCACTACCTGGAATGTTGTTCTGCTTTGGATTTCCTGTTATTTCTT	300
QY	335	GCTCGTGGCTGTGATCAATGGGGAGCCCTGGGCTTGTGTTGGAGGCAATGCAAGTC	394
Db	301	GCTCGTGGCTGTGATCAATGGGGAGCCCTGGGCTTGTGTTGGAGGCAATGCAAGTC	360
QY	395	ATTTTCTTTACAATCAAGGGTTTTCTCTATATTTGGAAGAGGAGATGATTTAGCTGG	454
Db	361	ATTTTCTTTACAATCAAGGGTTTTCTCTATATTTGGAAGAGGAGATGATTTAGCTGG	420
QY	455	GAGCAGTGTAGCATTATTTCTGATTCAGTGCATTCGAATTTCTTGAACCTCATACTAT	514
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QY	515	CTGTATACATGTCATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTTAAT	574
Db	481	CTGTATACATGTCATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTTAAT	540
QY	575	ACCTTTATATATCATGTTCACTTTAAGAAAGCTTCATAGTGGAGATGAGTTTATTC	634
Db	541	ACCTTTATATATCATGTTCACTTTAAGAAAGCTTCATAGTGGAGATGAGTTTATTC	600
QY	635	TCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTAGTTTGGCT	694
Db	601	TCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTAGTTTGGCT	660
QY	695	GTTTCATGTAGTCACGGTGTCTCAGAAATATATTAACGCACTTGTAGGCACTGCCA	754
Db	661	GTTTCATGTAGTCACGGTGTCTCAGAAATATATTAACGCACTTGTAGGCACTGCCA	720
QY	755	CCTTATGCACTGATCGAAACCTTTTCTGTTGGGATGCTTGGAGGAGCAGTACGCT	814
Db	721	CCTTATGCACTGATCGAAACCTTTTCTGTTGGGATGCTTGGAGGAGCAGTACGCT	780
QY	815	GAAGCA 820	
Db	781	GAAGCA 786	

RESULT 7

AL709947

LOCUS

DEFINITION

DKFZp686B1965_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

AL709947

AL709947.1 GI:19693302

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 805)

AUTHORS

Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and Wiemann, S.

TITLE

EST (Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B. and Wiemann, S.)

JOURNAL

COMMENT

Unpublished (2001)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by MedGenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence available.

This clone (DKFZp686B1965) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..805

source

QY	43	AAGCAGCGCGGCCCGCCAGTTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATC	102
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QY	103	CTTCAGTGGGCTATTTGGACTGATTTTCTTATGCTGGGATGCTTGGAGGATTTATGG	162
Db	61	CTTCAGTGGGCTATTTGGACTGATTTTCTTATGCTGGGATGCTTGGAGGATTTATGG	120
QY	163	CGTTTACTGGCCCTTATTCGTCCTGATTTTCCAGCCCATCTCCCCCATCCCCCATTTTCAT	222
Db	121	CGTTTACTGGCCCTTATTCGTCCTGATTTTCCAGCCCATCTCCCCCATCCCCCATTTTCAT	180
QY	223	TGCCAAAGAGTCACTTATGATCAGATGCAACAGTAGTGCCTGTCGGGAACCTGGCATA	282
Db	181	TGCCAAAGAGTCACTTATGATCAGATGCAACAGTAGTGCCTGTCGGGAACCTGGCATA	240
QY	283	TTTCTTCACTACTCGGAATTTGTTGTTCTGCTTTGGATTTCTTCTGTTATTTCTTCTGCTGT	342
Db	241	TTTCTTCACTACTCGGAATTTGTTGTTCTGCTTTGGATTTCTTCTGTTATTTCTTCTGCTGT	300
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QY	463	GTAGCACTTTATCTGATTCAGTGCATTTCTTATAGAACTCATACTATCTGTATAC	522
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Db	481	ATGTGCACATGGCGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAACTCTTTAT	540
QY	583	ATATCATGTTCACTTTAAGAAAGACTTCATAGTAGGAGATGAGTTTATTTCTCAGCAA	642
Db	541	ATATCATGTTCACTTTAAGAAAGACTTCATAGTAGGAGATGAGTTTATTTCTCAGCAA	600
QY	643	TAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTATGTTGTTGGCTGTTTCATGT	702
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QY	821	GGCTCTCTCATGACCCAGGAGGCC 844	
Db	781	GGCTCTCTCATGACCCAGGAGGCC 804	

RESULT 8

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BX378815
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DEFINITION BX378815 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0D1026Y015 5-PRIME, mRNA sequence.
ACCESSION  BX378815
VERSION     BX378815.2 GI:46558410
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 811)
AUTHORS     Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30439226.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            384.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?c=CS0D1026Y015&c=384.f.
FEATURES             Location/Qualifiers
     source           1..811
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone="CS0D1026Y015"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo (dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and EcoR V sites of the pCMVSPORT 6
                     vector. Library was normalized."
ORIGIN
Query Match      69.6%; Score 775; DB 5; Length 811;
Best Local Similarity 99.0%; Pred. No. 1.4e-202;
Matches 789; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 GTCTGGCTTGGCAGGCTGCCGGGCGTGCAGGAGCGGAGAGCGAGCGGCGGCCAG 60
Db 15 GTCTGGCTTGGCAGGCTGCCGGGCGTGCAGGAGCGGAGAGCGGCGGCCAG 74

Qy 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGCCATTATCTTTCAGTGGGGCTATTGG 120
Db 75 CTCGGGAGACATGGCGGCGTTAAAGCTCTTGTGGCATTATCTTTCAGTGGGGCTATTGG 134

Qy 121 ACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATATGCGCTTACTGGCCCTATT 180
Db 135 ACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATATGCGCTTACTGGCCCTATT 194

Qy 181 CGTCTGATTTTCCAGGCGCATCTCCCGCATCCCGCATTTTCATTCGCAAGAGTCACCTA 240
Db 195 CGTCTGATTTTCCAGGCGCATCTCCCGCATCCCGCATTTTCATTCGCAAGAGTCACCTA 254

Qy 241 TGACTCAGATCAACCACTAGTGGCTGTGGGAACTGGCATATTCTTCTACTCTGGAAT 300
Db 255 TGACTCAGATCAACCACTAGTGGCTGTGGGAACTGGCATATTCTTCTACTCTGGAAT 314

Qy 301 TGTGTTTCTGCTTGTGATTTCTCTGTTATTTCTGCTGCTGCTGCTGATCAAAATGGGG 360
Db 315 TGTGTTTCTGCTTGTGATTTCTCTGTTATTTCTGCTGCTGCTGCTGATCAAAATGGGG 374

Qy 361 AGCTCGGGCTTGTGTTGGCAGCAATGCAGTCAATTTTCTCTTCAATTCAGGGTTTTT 420
Db 375 AGCTCGGGCTTGTGTTGGCAGCAATGCAGTCAATTTTCTCTTCAATTCAGGGTTTTT 434

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Qy 421 CCTTATATTTGGAGAGAGAGATGATTTTAGCTGGAGCAGTGGTAGCACTTTTATCTCAT 480
Db 435 CCTTATATTTGGAGAGAGAGATGATTTTAGCTGGAGCAGTGGTAGCACTTTTATCTCAT 494

Qy 481 TACAGTGCATTGAATTTCTTAGAAGCTCATCTATCTGTATACATGTGCACATGGGCATT 540
Db 495 TACAGTGCATTGAATTTCTTAGAAGCTCATCTATCTGTATACATGTGCACATGGGCATT 554

Qy 541 TTACTATGAATTTAATATATGCTGGGTTTTTAAATACCTTTTATATATCATGTTCACTTTAA 600
Db 555 TTACTATGAATTTAATATATGCTGGGTTTTTAAATACCTTTTATATATCATGTTCACTTTAA 614

Qy 601 GAAAGACTTCATAGTAGGAGATCAGCTTTTATCTCAGCAAAATAGACCTGTCAAAATTTAG 660
Db 615 GAAAGACTTCATAGTAGGAGATCAGCTTTTATCTCAGCAAAATAGACCTGTCAAAATTTAG 674

Qy 661 ATTATGTTACTCAAATATATGTTACTGTTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGA 720
Db 675 ATTATGTTACTCAAATATATGTTACTGTTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGA 734

Qy 721 AAATATATTAACGAGCTCTTTGTAGGAGCTGCCACC-TTATGCAAGTGCATCGAAACCTTT 779
Db 735 AAATATATTAACGAGCTCTTTGTAGGAGCTGCCACCCTTTATGCAAGTGCATCGAAACCTTT 794

Qy 780 TGCTTGGGGATGTCCTT 796
Db 795 TGCTTGGGGATGTCCTT 811

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RESULT 9
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LOCUS      BO959135      996 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT 10029380 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6482247
            5', mRNA sequence.
ACCESSION  BO959135
VERSION     BO959135.1 GI:22374613
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 996)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@rs-rcmail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LICM2664 row: o column: 16
            High quality sequence stop: 591.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6482247"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCAAGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

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Note: this is a NIH_MGC Library."

ORIGIN	ORGANISM	Homo sapiens
Query Match	Best Local Similarity	69.3%; Score 771.6; DB 5; Length 996;
Matches 811; Conservative 0; Mismatches 9; Indels 4; Gaps 3;		
QY	74	GGGGCGTTAAAGCTCTCGTGGCATATTCCTTCACTGGGGCTATTGGAGTCACTTTTCTT 133
Db	1	GGGGCGTTAAAGCTCTCGTGGCATATTCCTTCACTGGGGCTATTGGAGTCACTTTTCTT 60
QY	134	ATGCTGGGATGTGCTTGAAGATTTATGGCGTTTACTGGCCCTTATTCGTCTCTGATTTTC 193
Db	61	ATGCTGGGATGTGCTTGAAGATTTATGGCGTTTACTGGCCCTTATTCGTCTCTGATTTTC 120
QY	194	CACGCATCTCCCCATCCCAATTCATTTGTCACAAAGAGTCACTATGACTCAGATGCA 253
Db	121	CACGCATCTCCCCATCCCAATTCATTTGTCACAAAGAGTCACTATGACTCAGATGCA 180
QY	254	ACCAGTGTGCTGTGCGGAAGTGGCATATTTCTTCACTACTGGAATTTGTTTCTGCC 313
Db	181	ACCAGTGTGCTGTGCGGAAGTGGCATATTTCTTCACTACTGGAATTTGTTTCTGCC 240
QY	314	TTTGGATTTCTGTATTTCTGCTCGTGTGCTGTGATCAATGGGAGCCTGCGGCCTT 373
Db	241	TTTGGATTTCTGTATTTCTGCTCGTGTGCTGTGATCAATGGGAGCCTGCGGCCTT 300
QY	374	GTGTTGGGAGCAATGCAGTCAATTTCTTACAAATCAAGGTTTTTCTTATATTGGA 433
Db	301	GTGTTGGGAGCAATGCAGTCAATTTCTTACAAATCAAGGTTTTTCTTATATTGGA 360
QY	434	ACAGAGATGATTTTGTAGCTGGGAGAGTGTAGTCACTTTTCTGATTTACAGTCAATGA 493
Db	361	ACAGAGATGATTTTGTAGCTGGGAGAGTGTAGTCACTTTTCTGATTTACAGTCAATGA 420
QY	494	ATTTCTTAGAATCTACTATCTGTATATCATGTGCACATGCGGCATTTTACTATGAAAT 553
Db	421	ATTTCTTAGAATCTACTATCTGTATATCATGTGCACATGCGGCATTTTACTATGAAAT 480
QY	554	TAATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACCTTTAAGAAAGACTTCATA 613
Db	481	TAATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACCTTTAAGAAAGACTTCATA 540
QY	614	AGTAGAGATGATTTTATCTCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCA 673
Db	541	AGTAGAGATGATTTTATCTCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCA 600
QY	674	AATATGTTACTTGTGTTGCTGTTCATGTAGTCACGGTCTCTCAGAAAATATATTAACG 733
Db	601	AATATGTTACTTGTGTTGCTGTTCATGTAGTCACGGTCTCTCAGAAAATATATTAACG 660
QY	734	CAGTCTGTAGGAGCTGCACCTTATGCAAGTGCATCGAAACCTTTTGTCTGGGATGTG 793
Db	661	CAGTCTGTAGGAGCTGCACCTTATGCAAGTGCATCGAAACCTTTTGTCTGGGATGTG 720
QY	794	CTTGGAGAGCAGATAAAGCTGAAGCAGGCCTCTCATGACCCAGGAAGG - CCGGGGTGG 851
Db	721	CTTGGAGAGG - AGATAACCTCTGAGCAGGCCTCTCATGACCCAGGAAGGCGGGGGA 779
QY	852	ATCCCTCTTTGTTGTTAGTCCATG - CTATTAAGTGTGGGCC 894
Db	780	TCCCTCTTTGTTGTTAGACCATGCTATTAAAGTGTGGGCC 823
RESULT 10	LOCUS	BU189726
DEFINITION	AGENCOURT_7858388 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6168548	
ACCESSION	BU189726	5', mRNA sequence.
VERSION	BU189726.1	GI:22703710
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	

ORIGIN

Query Match 68.9%; Score 767.2; DB 5; Length 914;

Best Local Similarity 96.9%; Pred. No. 2e-200; Mismatches 24; Indels 2; Gaps 2;

Matches 800; Conservative 0;

QY 47 AGCCGCGGCCCCAGTTCGGGAGACATGCGGGCGTTAAAGCTCTCGTGGCAATTAATCCTTC 106

Db 1 AGCCGCGGCCCCAGTTCGGGAGACATGCGGGCGTTAAAGCTCTCGTGGCAATTAATCCTTC 60

QY 107 AGTGGGCTATTGGACTGACATCTTTCTTATGCTGGATGCTCTTAGAGGATTAATGCGTT 166

Db 61 AGTGGGCTATTGGACTGACATCTTTCTTATGCTGGATGCTCTTAGAGGATTAATGCGTT 120

QY 167 TACTGGCCCTTATTCGCTCTGATTTTCCAGCGCATCTCCCCCATCCCCCATTTCAATTGCC 226

Db 121 TACTGGCCCTTATTCGCTCTGATTTTCCAGCGCATCTCCCCCATCCCCCATTTCAATTGCC 180

QY 227 AAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGTGCTGTGCGGAACCTGGCATAATTC 286

Db 181 AAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGTGCTGTGCGGAACCTGGCATAATTC 240

QY 287 TTCACCTAGCAATTTGTTGTTCTGCTTTGGAATTTCTGTTATTTCTTGTCTGCTGGCT 346

Db 241 TTCACCTAGCAATTTGTTGTTCTGCTTTGGAATTTCTGTTATTTCTTGTCTGCTGGCT 300

QY 347 GTGATCAATGGGAGCCTGCGGCTGTGTTGGCAGCAATGCAAGTCAATTTTCTTTACA 406

Db 301 GTGATCAATGGGAGCCTGCGGCTGTGTTGGCAGCAATGCAAGTCAATTTTCTTTACA 360

QY 407 ATTCAAGGGTTTTTCTCTTATATTGGAGAGGAGATGATTTTGTGGGAGAGTGGTAG 466

Db 361 ATTCAAGGGTTTTTCTCTTATATTGGAGAGGAGATGATTTTGTGGGAGAGTGGTAG 420

QY 467 CACTTTATTTCTGATTTACAGTCAATTTCTTAGAATCTATCTATCTGTATACATCT 526

Db 421 CACTTTATTTCTGATTTACAGTCAATTTCTTAGAATCTATCTATCTGTATACATCT 480

QY 527 GCACATGCGGCATTTTACTATCAAAATTTAATATGCTGGGTTTTTAAATACCTTTATATAT 586

Db 481 GCACATGCGGCATTTTACTATCAAAATTTAATATGCTGGGTTTTTAAATACCTTTATATAT 540

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM613 row: g column: 23
High quality sequence stop: 589.

FEATURES

source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30528070"
/tissue_type="Human Placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_147"
/note="Organ: Placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamH; Oligo-dr primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

ORIGIN

Query Match 68.5%; Score 763.4; DB 7; Length 835;
Best Local Similarity 98.3%; Pred. No. 2.2e-199;
Matches 790; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

Qy 1 GTCTGGCTTGGGAGGCTGCGCGGCGTGGCAGGAAGCGGAGCAGCGGCGGCCAG 60
Db 37 GTCTGGCTTGGCAGGCTGCGCGGCGTGGCAGGAAGCGGAGCAGCGGCGGCCAG 96
Qy 61 TTGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCTTCAGTGGGCTATTGG 120
Db 97 TTGGGAGACATGGCGGCGTAAAGCTCTCGTGGCATTATCTTCAGTGGGCTATTGG 156
Qy 121 ACTGACTTTTCTTATGCTGGGATGCTGCTTAGAGGATATATGGCTTACTGGCCCTTATT 180
Db 157 ACTGACTTTTCTTATGCTGGGATGCTGCTTAGAGGATATATGGCTTACTGGCCCTTATT 216
Qy 181 CGTCCTGATTTTCCAGCGCATCTCCCATCCCATCTTCATTCGCAAAAGATGACCTA 240
Db 217 CGTCCTGATTTTCCAGCGCATCTCCCATCCCATCTTCATTCGCAAAAGATGACCTA 276
Qy 241 TGACTCAGATGCAACCGATAGTGCCTGTGCGGAATCGGCATATTTCTTCACTACTGGAAT 300
Db 277 TGACTCAGATGCAACCGATAGTGCCTGTGCGGAATCGGCATATTTCTTCACTACTGGAAT 336
Qy 301 TGTGTTTCTGCTTTGGATTTCTGTTTATTTCTGCTGCTGCTGCTGCTGATCAAAATGGG 360
Db 337 TGTGTTTCTGCTTTGGATTTCTGTTTATTTCTGCTGCTGCTGCTGCTGATCAAAATGGG 396
Qy 361 AGCTTCGGGCTTGTGTTGGCAGCAATGCAATCTTCTTCAATTCAGGCTTTT 420
Db 397 AGCTTCGGGCTTGTGTTGGCAGCAATGCAATCTTCTTCAATTCAGGCTTTT 456
Qy 421 CCTTATATTTGGAAGAGAGATGATTTTATGCTGGGAGCAGTGGTAGCATTTTATCTGAT 480
Db 457 CCTTATATTTGGAAGAGAGATGATTTTATGCTGGGAGCAGTGGTAGCATTTTATCTGAT 516
Qy 481 TACAGTGCATTAATTTCTTAGAATCATCTATCTATACATGTCACATGCGGCATT 540
Db 517 TACAGTGCATTAATTTCTTAGAATCATCTATCTATACATGTCACATGCGGCATT 576
Qy 541 TTACTATGAATTTTATATGCTGGGTTTTTAAATACCTTTTATATATCATGTTCACTTTAA 600
Db 577 TTACTATGAATTTTATATGCTGGGTTTTTAAATACCTTTTATATATCATGTTCACTTTAA 636

Qy 601 GAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACCTGTCAAATTTAG 660
Db 637 GAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACCTGTCAAATTTAG 696
Qy 661 ATTATGTTACTCAAATATGTTACTTGTGTTGCTGTTTATGTTAGTACCGTGTCTCTCAGA 720
Db 697 ATTATGTTACTCAAATATGTTACTTGTGTTGCTGTTTATGTTAGTACCGTGTCTCTCAGA 756
Qy 721 AATATATTAAACGAG-TCTTGTAGCAGCTGCCACCTTATGCGATGCAATCGAAA--CCT 777
Db 757 AATATATTAAACGAGTCTTGTAGCAGCTGCCACCTTAGCAGGCGATCGAAAACCTT 816
Qy 778 TTTGCTTTGGGATGTGCTT 796
Db 817 TTTGCTTTGGGATGTGCTT 835

RESULT 13

CB956304

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1 (bases 1 to 786)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM154 row: o column: 14

High quality sequence stop: 577.

Location/Qualifiers

1. .786

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="IMAGE:3053725"

/clone_lib="NIH_MGC_184"

/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1: SfiI (ggccattggcc); Site 2: SfiI (ggccctcgccg); Library is oligo-dr primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGGCGGATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 67.1%; Score 747.2; DB 6; Length 786;

Best Local Similarity 98.7%; Pred. No. 6.6e-195;

Matches 774; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 64 GGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTTATCTTCAGTGGGCTATTGGACT 123

Db 405 TATTAACGACGCTTTGTTGGACGCTGCCACCTTATGACAGTCATCGAAACCTTTTGCTTG 346
 QY 786 GGGATGCTTTGGAGAGGAGATACGCTGAGCAGGCGCTCTCATGACCCAGGAGGCG 845
 Db 345 GGGATGCTTTGGAGAGGAGATAC-CTGAAGCAGGCGCTCTCATGACCCAGGAGGCG 287
 QY 846 GGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTTAAAGTGTGGCCACACAGCAAGA 905
 Db 286 GGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTTAAAGTGTGGCCACACAGCAAGA 227
 QY 906 GCGTCAACATTTCTAGAGCCCTTATAGAAATGCGAATCTGAAGCCCGACCTTGGACCC 965
 Db 226 GCGTCAACATTTCTAGAGCCCTTATAGAAATGCGAATCTGAAGCCCGACCTTGGACCC 167
 QY 966 AGGACATTTTGATGATGATCCAAAGAGTGTGATGACATGAAAGTTTGAGAAGCATCATC 1025
 Db 166 AGGACATTTTGATGATGATCCAAAGAGTGTGATGACATGAAAGTTTGAGAAGCATCATC 107
 QY 1026 ATAGAGAACTAAACATCACACCAACTTCTCTTATCTTTCCAGTGGCTAAACCACTTAACC 1085
 Db 106 ATAGAGAACTAAACATCACACCAACTTCTCTTATCTTTCCAGTGGCTAAACCACTTAACC 47
 QY 1086 TCTCTGGTGTACCTGCTCATTTGTTTA 1114
 Db 46 TCTCTGGTGTACCTGCTCATTTGTTTA 18

RESULT 15
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 LOCUS DKF2p686G13116 r1 686 (synonym: hicc3) Homo sapiens cDNA clone
 DEFINITION DKF2p686G13116 5', mRNA sequence.
 ACCESSION AL699934
 VERSION DKF2p686G13116
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
 Wiemann, S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 No sl sequence available.
 This clone (DKF2p686G13116) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 1..739
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 cDNA-collection"

ORIGIN
 Query Match 65.5%; Score 729.6; DB 1; Length 739;
 Best Local Similarity 99.2%; Pred. No. 4.7e-190;
 Matches 732; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 28 GTGCGAGAAAGCCGGAAGACAGCCCGGCCCCAGTTCCGGAGACATGGCGGCGTTAAAGC 87
 Db 2 GTGCGAGAAAGCCGGAAGACAGCCCGGCCCCAGTTCCGGAGACATGGCGGCGTTAAAGC 61
 QY 88 TCTCGTGGCATTTACCTTCAGTGGGGCTATTGGGACTGACATTTTCTTATGCTGGGATGTGC 147
 Db 62 TCTCGTGGCATTTACCTTCAGTGGGGCTATTGGGACTGACATTTTCTTATGCTGGGATGTGC 121
 QY 148 CTTAGAGGATTTATGGCGGTTTACTGGCCCTTATTCGTCTGATTTTCCACGCCATCTCCCC 207
 Db 122 CTTAGAGGATTTATGGCGGTTTACTGGCCCTTATTCGTCTGATTTTCCACGCCATCTCCCC 181
 QY 208 CATCCCCCATTTTCAATGCGCAAAAGAGTCACATATGACTCAGATGCAACACCATGAGTGCCTG 267
 Db 182 CATCCCCCATTTTCAATGCGCAAAAGAGTCACATATGACTCAGATGCAACACCATGAGTGCCTG 241
 QY 268 TCGGGAACCTGCATATTTCTTCACTACTGGAATTTGTTCTGCTGCTTTGGATTTCCCTGT 327
 Db 242 TCGGGAACCTGCATATTTCTTCACTACTGGAATTTGTTCTGCTGCTTTGGATTTCCCTGT 301
 QY 328 TATTCTTCTGCTGTGCTGTGATCAAAATGGGAGCCCTGCGGCCCTTGTGTTGGCAGGCAA 387
 Db 302 TATTCTTCTGCTGTGCTGTGATCAAAATGGGAGCCCTGCGGCCCTTGTGTTGGCAGGCAA 361
 QY 388 TGCAGTCAATTTCTTACAAATCAAGGGTTTTTCCCTTATATTTGGAAGAGGAGATGATTT 447
 Db 362 TGCAGTCAATTTCTTACAAATCAAGGGTTTTTCCCTTATATTTGGAAGAGGAGATGATTT 421
 QY 448 TAGCTGGGAGCAGTGTAGCCTTTATTTCTGATTACAGTGCATTCGAAATTTCTTAGAATCTC 507
 Db 422 TAGCTGGGAGCAGTGTAGCCTTTATTTCTGATTACAGTGCATTCGAAATTTCTTAGAATCTC 481
 QY 508 ATACTATCTGTATACATGTGCAATGCGGCAATTTTACTATGAAATTTAATATGCTGGGTT 567
 Db 482 ATACTATCTGTATACATGTGCAATGCGGCAATTTTACTATGAAATTTAATATGCTGGGTT 541
 QY 568 TTTTAAATACCTTTATATATATCATGTTTCACTTTAAGAAAGACTTTCATAAGTAGGAGATGAGT 627
 Db 542 TTTTAAATACCTTTATATATATCATGTTTCACTTTAAGAAAGACTTTCATAAGTAGGAGATGAGT 601
 QY 628 TTTTATTTCTCAGCAATAGACCTGTCAAAATTTAGATTATGTTACTCAAAATTTATGTTACTTG 687
 Db 602 TTTTATTTCTCAGCAATAGACCTGTGTCAATTTAGATTATGTTACTCAAAATTTATGTTACTTG 661
 QY 688 TTTGGCTGTTCAATGATGATCAAGTGTCTCAGAAAATATATTTAACCAGTCTTGTAGGCA 747
 Db 662 TTTGGCTGTTCAATGATGATCAAGTGTCTCAGAAAATATATTTAACCAGTCTTGTAGGCA 721
 QY 748 GCTGCCACCTTTATGCACT 765
 Db 722 GCTGCCACCTTTATGCACT 739

Search completed: August 18, 2005, 02:51:55
 Job time : 4261 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 15:40:42 ; Search time 700 Seconds
(without alignments)
9420.845 Million cell updates/sec

Title: US-10-774-721-21

Perfect score: 1114

Sequence: 1 gctcggttgaggcaggctgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870567 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1114	100.0	1114	13 ADR27672	Adt71341 Human OB-
3	1111.6	99.8	2732	3 AAF18159	Aaf18159 Lung canc
4	1069	96.0	1080	4 AAK94760	Aak94760 Human ful
5	1069	96.0	1080	12 ADL31809	Adl31809 Full leng
6	1067	95.8	2388	10 ADF81560	Adf81560 Leukaemia
7	909.2	81.6	1134	5 AAS81135	Aas81135 DNA encod
8	869.6	78.1	874	2 AAV17683	Aav17683 cDNA enco
9	648	52.8	648	13 ADR27652	Adr27652 Leptin re
10	588.4	52.8	629	4 AAK93306	Aak93306 Human cDN
11	588.4	52.8	629	4 AAK91898	Aak91898 Human cDN
12	588.4	52.8	629	12 ADL29733	Adl29733 5' end of
13	588.4	52.8	629	12 ADL28325	Adl28325 5' end of
c 15	498.4	44.7	546	10 ADE85249	Ade85249 Farnesyl
c 16	498.4	44.7	546	4 AAK92657	Aak92657 Human cDN
17	396	35.5	396	6 ABS51017	Abes51017 Human cDN
18	396	35.5	396	13 ADR27654	Adr27654 Human lep
19	393	35.3	1128	13 ADR27658	Adr27658 OB-RGRP Y
20	393	35.3	1359	13 ADR27656	Adr27656 OB-RGRP L

21	357.4	32.1	447	10 ADB52971	Adb52971 Primary r
22	246	22.1	246	8 ACA56898	Aca56898 Human cDN
23	187.6	16.8	930	5 AAS81134	Aas81134 DNA encod
24	174.6	15.7	674	3 AAZ56536	Aaz56536 Human lep
25	174.6	15.7	697	3 AAA15907	Aaa15907 Human pro
26	174.6	15.7	770	2 AAX00682	Aax00682 Human sec
27	174.6	15.7	770	6 ABL89990	Ab189990 Human pol
28	174.6	15.7	2652	5 AAF93764	Aaf93764 Human cDN
29	174.6	15.7	2694	3 AAZ65052	Aaz65052 Membrane-
30	174.6	15.7	2694	4 AAS46028	Aas46028 Human DNA
31	174.6	15.7	2694	5 AAF44198	Aaf44198 Human PRO
32	174.6	15.7	2694	6 ABL88149	Ab188149 Human PRO
33	174.6	15.7	2694	6 ABL95638	Ab195638 Human ang
34	174.6	15.7	2694	8 ACA89478	Aca89478 cDNA enco
35	174.6	15.7	2694	8 ACA73488	ACA73488 Human sec
36	174.6	15.7	2694	8 ACA05803	ACA05803 Human sec
37	174.6	15.7	2694	8 ACA66637	ACA66637 cDNA enco
38	174.6	15.7	2694	8 ACA64344	ACA64344 Novel hum
39	174.6	15.7	2694	8 ACF20212	Acf20212 Human sec
40	174.6	15.7	2694	8 ACF19598	ACF19598 Human sec
41	174.6	15.7	2694	8 ACD21886	Acd21886 Human sec
42	174.6	15.7	2694	8 ACF13051	Acf13051 Human sec
43	174.6	15.7	2694	8 ACD25154	Acd25154 Human sec
44	174.6	15.7	2694	8 ACF00203	Acf00203 Human sec
45	174.6	15.7	2694	8 ACA72260	Aca72260 Novel hum

ALIGNMENTS

RESULT 1

ADR27672

ID ADR27672 standard; DNA; 1114 BP.

XX

AC ADR27672;

XX

DT 04-NOV-2004 (first entry)

XX

DE Leptin receptor related protein, OB-RGRP, nucleotide sequence, SEQ ID 21.

XX

KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

KW Leptin receptor related protein; OB-RGRP; leptin receptor;

KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;

KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;

KW thrombus formation; immunity; inflammation; fetal development; cancer;

XX human; ds.

XX

OS Homo sapiens.

XX

PN FR2850971-A1.

XX

PD 13-AUG-2004.

XX

PF 10-FEB-2003; 2003FR-00001543.

XX

PR 10-FEB-2003; 2003FR-00001543.

XX

PA (AVET) AVENTIS PHARMA SA.

XX

PI (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

PI Jockers R, Couturier C, Uhlmann E;

XX

DR WPI; 2004-595751/58.

XX

PT New oligonucleotides that inhibit expression of the leptin receptor

PT related protein, useful for treatment and prevention of e.g.

PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and

PT angiogenesis.

XX

PS Claim 12; SEQ ID NO 21; 104pp; French.

XX

CC The present invention relates to a leptin receptor related protein (OB-

CC	RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (siRNA) of 15-25 nt that hybridize specifically with ADR27672, and their expression of OB-RGRP. Also claimed are fusion proteins (FPs), and their coding sequences comprising OB-RGRP or MV047 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also related interfering RNA, are e.g. used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes; anorexia; disorders of sexual maturity, haematopoiesis, angiogenesis, thrombus formation, regulation of immunity CC and inflammation, fetal development and cancer.
XX	
SQ	Sequence 1114 BP; 266 A; 242 C; 259 G; 347 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1114; DB 13; Length 1114;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTCTGGCTTGGCGCAGGTCGCCGGCCGTGGCGAAGCCGGAGCGCCGCCGCCACG 60
DB	1 GTCTGGCTTGGCGCAGGTCGCCGGCCGTGGCGAAGCCGGAGCGCCGCCGCCACG 60
QY	61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCGCTATTGG 120
DB	61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCGCTATTGG 120
QY	121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATATGCGCTTTACTTGGCGCTTATT 180
DB	121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATATGCGCTTTACTTGGCGCTTATT 180
QY	181 CGTCTGATTTTCAACGCATCTCCCCATCCCCCATTTCAATGCCAAAAGAGTCACCTA 240
DB	181 CGTCTGATTTTCAACGCATCTCCCCATCCCCCATTTCAATGCCAAAAGAGTCACCTA 240
QY	241 TGACTCAGATCAACACAGTAGTGCCTGTCGGGAAC TGGCATAATTTCTTCACTACTGGAAT 300
DB	241 TGACTCAGATCAACACAGTAGTGCCTGTCGGGAAC TGGCATAATTTCTTCACTACTGGAAT 300
QY	301 TGTGTGTTCTGCTTTGGATTTTCGTGTTATCTTGTCTGCTGCTGTGTAACAATGGG 360
DB	301 TGTGTGTTCTGCTTTGGATTTTCGTGTTATCTTGTCTGCTGCTGTGTAACAATGGG 360
QY	361 AGCCTGCGGCCCTTGTTGGCGAGCAATGCAGTCAATTTTCCATTACAATCAAGGGTTTTT 420
DB	361 AGCCTGCGGCCCTTGTTGGCGAGCAATGCAGTCAATTTTCCATTACAATCAAGGGTTTTT 420
QY	421 CCTTATATTTGGAAGAGGATGATTTTAGCTGGGAGCGATGTTTCTCATTTTCTCAT 480
DB	421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCGATGTTTCTCATTTTCTCAT 480
QY	481 TCAGTGTCAATGGAATTTCTTAGAACCTCATACTATCTGTATACATGTGCAATGCGGCATT 540
DB	481 TCAGTGTCAATGGAATTTCTTAGAACCTCATACTATCTGTATACATGTGCAATGCGGCATT 540
QY	541 TTACTATGAAATTTAATATGCTGGGTTTTTAACTCTTTATATATCATGTTTCACTTTAA 600
DB	541 TTACTATGAAATTTAATATGCTGGGTTTTTAACTCTTTATATATCATGTTTCACTTTAA 600
QY	601 GAAAGACTTCAATAGTAGGAGATGAGTTTTTATTTCTCAGCAAAATPAGACCTGTCAAATTTAG 660
DB	601 GAAAGACTTCAATAGTAGGAGATGAGTTTTTATTTCTCAGCAAAATPAGACCTGTCAAATTTAG 660
QY	661 ATTATGTTACTCAAAATATGTTACTTGTGGCTGTTTCATGTAGTACCAGTGTCTTCAGA 720
DB	661 ATTATGTTACTCAAAATATGTTACTTGTGGCTGTTTCATGTAGTACCAGTGTCTTCAGA 720

CC active against loss or gain of weight or diabetes in humans or animals.
 CC The method comprises measuring the effect of a test compound on the
 CC expression of at least one of the genes LEPROTL1 (leptin receptor
 CC overlapping transcript-like 1) or OB-RGRP (leptin receptor gene related
 CC protein). Alternatively the method comprises measuring the effect of the
 CC compound on intracellular transport as far as the cell membrane (CM), the
 CC presence at CM, and internalisation from the membrane of proteins (X)
 CC encoded by the specified genes, or parts of them. Compounds of the
 CC invention are used to treat or prevent obesity, weight loss and diabetes.
 CC The current sequence represents the human OB-RGRP gene sequence.
 XX
 SQ Sequence 1114 BP; 266 A; 242 C; 259 G; 347 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1114; DB 13; Length 1114;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTCTGGCTTGGCAGGCTGCCCGGCGGTGCGAGGAGCGGAGCGCGGCCCGAG 60
 Db 1 GTCTGGCTTGGCAGGCTGCCCGGCGGTGCGAGGAGCGGAGCGCGGCCCGAG 60
 Qy 61 TTCCGGAGACATGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
 Db 61 TTCCGGAGACATGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
 Qy 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTTATGGCGTTTACTGGCCCTTATT 180
 Db 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTTATGGCGTTTACTGGCCCTTATT 180
 Qy 181 CGTCTGATTTTTCAGCGCATCTCCCGATCCCGCATTTTCATTCGCAAGAGTCACTTA 240
 Db 181 CGTCTGATTTTTCAGCGCATCTCCCGATCCCGCATTTTCATTCGCAAGAGTCACTTA 240
 Qy 241 TGACTCAGATCAACACAGTAGTGGCTGTCGGGAACTGSCATATTTCTTCACTAGTGAAT 300
 Db 241 TGACTCAGATCAACACAGTAGTGGCTGTCGGGAACTGSCATATTTCTTCACTAGTGAAT 300
 Qy 301 TGTGTTTCTGCTTGGATTTCTGTTTATTTCTTCTGCTGGTGTGATCAAAATGGG 360
 Db 301 TGTGTTTCTGCTTGGATTTCTGTTTATTTCTTCTGCTGGTGTGATCAAAATGGG 360
 Qy 361 AGCTTGGGCTTGTGTTGGCAGCAATGCACTATTTCTTCAATTCAGGGTTTTT 420
 Db 361 AGCTTGGGCTTGTGTTGGCAGCAATGCACTATTTCTTCAATTCAGGGTTTTT 420
 Qy 421 CCTTATATTTGGAAGAGAGATGATTTTGTGCGAGCAGTGGTAGCACTTTATCTGAT 480
 Db 421 CCTTATATTTGGAAGAGAGATGATTTTGTGCGAGCAGTGGTAGCACTTTATCTGAT 480
 Qy 481 TACAGTGCATTTGAATTTCTTAGAACTCATATCTGTATATCATGTGCATGCGCAT 540
 Db 481 TACAGTGCATTTGAATTTCTTAGAACTCATATCTGTATATCATGTGCATGCGCAT 540
 Qy 541 TTACTATGAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGTCTTTAA 600
 Db 541 TTACTATGAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGTCTTTAA 600
 Qy 601 GAAAGACTTCATAGTAGGAGATGATTTTATTTCTCAGCAATAGCTGTCAAATTTAG 660
 Db 601 GAAAGACTTCATAGTAGGAGATGATTTTATTTCTCAGCAATAGCTGTCAAATTTAG 660
 Qy 661 ATTATGTTACTCAAAATATGTTTACTTGTGTTGGCTGTTTCACTAGTTCAGGTCCTCAGA 720
 Db 661 ATTATGTTACTCAAAATATGTTTACTTGTGTTGGCTGTTTCACTAGTTCAGGTCCTCAGA 720
 Qy 721 AAATATATTAACGAGTCTTTAGGAGCTGCCACCTTATGCAATGCAATGCAATCTTTT 780
 Db 721 AAATATATTAACGAGTCTTTAGGAGCTGCCACCTTATGCAATGCAATGCAATCTTTT 780
 Qy 781 GCTTGGGAGTCTGTTGGAGAGGAGATTAACGCTGAGCAGGCTCTCATGACCCAGAA 840
 Db 781 GCTTGGGAGTCTGTTGGAGAGGAGATTAACGCTGAGCAGGCTCTCATGACCCAGAA 840

Qy 841 GGC CGGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTAAAGTGTGCCCCACAGAC 900
 Db 841 GGC CGGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTAAAGTGTGCCCCACAGAC 900
 Qy 901 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTCTGAAGCCCACTCTG 960
 Db 901 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTCTGAAGCCCACTCTG 960
 Qy 961 GACCCAGGACATTTTGTATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1020
 Db 961 GACCCAGGACATTTTGTATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1020
 Qy 1021 TCATCATAGAGAGTAAACATCACACCACTTCTTATCTTTCCAGTGGCTAAACCACT 1080
 Db 1021 TCATCATAGAGAGTAAACATCACACCACTTCTTATCTTTCCAGTGGCTAAACCACT 1080
 Qy 1081 TAACCTCTCTGGGTTTACCTGCTCATTTGTTTA 1114
 Db 1081 TAACCTCTCTGGGTTTACCTGCTCATTTGTTTA 1114
 RESULT 3
 AAF18159
 ID AAF18159 standard; DNA; 2732 BP.
 XX
 AC AAF18159;
 XX AC
 DT 14-MAR-2001 (first entry)
 XX
 DE Lung cancer associated polynucleotide sequence SEQ ID 178.
 XX
 KW Human; lung cancer associated protein; neuroprotective; cytostatic;
 KW cardioactive; immunomodulatory; muscular active; vulnary;
 KW gastrointestinal; nephrotropic; antineoplastic; gynecological;
 KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease; ds.
 XX
 OS Homo sapiens.
 XX OS
 PN WO200055180-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005918.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI (ROSE/) ROSEN C A.
 XX
 PI Ruben SM;
 XX
 DR WPI; 2000-587514/55.
 XX
 DR P-PSDB; AAB58283.
 XX
 PT Lung cancer associated gene sequences, referred to as lung cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as lung cancer.
 XX
 PS Claim 1; Page 642; 1425pp; English.
 XX
 CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
 CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
 CC associated proteins and polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective; cytostatic; cardioactive;
 CC immunomodulatory; muscular active general; vulnary; gastrointestinal
 CC general; nephrotropic; antineoplastic; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the protein
 CC or polynucleotide sequences. The lung cancer associated polynucleotide
 CC sequences may be used for detection of lung cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The proteins may be used to treat disorders such as
 CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,

Db	858	GGCCGGGTGGATCCCTCTTTGTTGTAGTCATCGTATTAAAGTGTGGCCACACAGC
Qy	901	CAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAACTCTGAAGCCCCACTCTG

33 AGGAAGCCGGAAGCAGCCGCGGCCCCAGTTCGGGAGACATGGCGGGCGGTAAAGCTCTCG

Db 1 AGGAAGCGGAGAGAGCGCGCGCCCGGAGATGCGCGGGCTTAAAGCTCTCG 60
Qy TGGCAATATCTTCAGTGGGGCTATTGACCTGACTTTTCTTATGCTGGATGTCCTTAG 152
Db TGGCAATATCTTCAGTGGGGCTATTGACCTGACTTTTCTTATGCTGGATGTCCTTAG 120
Qy AGGATTAATGCGGTTTACTGGCCCTTATTCGTCCTGATTTTCCAGCCATCTCCCCCATCC 212
Db AGGATTAATGCGGTTTACTGGCCCTTATTCGTCCTGATTTTCCAGCCATCTCCCCCATCC 180
Qy CCCATTTTCATTCGCAAGAGTACCTATGACTCAGATGCAACCAAGTAGTGCCTGTCGG 272
Db CCCATTTTCATTCGCAAGAGTACCTATGACTCAGATGCAACCAAGTAGTGCCTGTCGG 240
Qy AACTGGCATATTTCTTCACTACTGGAATTTGTTCTTCTGCTTTGGAATTTCTGTTATTC 332
Db AACTGGCATATTTCTTCACTACTGGAATTTGTTCTTCTGCTTTGGAATTTCTGTTATTC 300
Qy TTGCTCGTGGCTGTGATCAAAATGAGGAGCTCGGCGCTTGTGTCAGGCAATGAG 392
Db TTGCTCGTGGCTGTGATCAAAATGAGGAGCTCGGCGCTTGTGTCAGGCAATGAG 360
Qy TCATTTTCTTACAAATTCAGGTTTTCCTTATATTGGAAGAGAGATGATTTAGCT 452
Db TCATTTTCTTACAAATTCAGGTTTTCCTTATATTGGAAGAGAGATGATTTAGCT 420
Qy GGGAGCAGTGTAGCATTATTTCTGATTCAGTGCATTTGAAATTTCTTAGAATCTACT 512
Db GGGAGCAGTGTAGCATTATTTCTGATTCAGTGCATTTGAAATTTCTTAGAATCTACT 480
Qy ATCTGTATACATGTCATCGGCAATTTTCTTATGAAATTTAAATATGCTGGGTTTTTA 572
Db ATCTGTATACATGTCATCGGCAATTTTCTTATGAAATTTAAATATGCTGGGTTTTTA 540
Qy ATACTTTTATATATCATGTTCACTTTAAGAGAGCTTCATAAGTAGAGATGATTTAT 632
Db ATACTTTTATATATCATGTTCACTTTAAGAGAGCTTCATAAGTAGAGATGATTTAT 600
Qy TCTCAGCAATAGACCTGTCAAATTTAGATATGTTACTCAAATTTATGTTACTTGTGG 692
Db TCTCAGC-ATAGACCTGTCAAATTTAGATATGTTACTCAAATTTATGTTACTTGTGG 659
Qy CTGTTTCATGATGACCGTCTCTCAGAAAATATATTAAACGAGCTCTTGTAGGCGCTGC 752
Db CTGTTTCATGATGACCGTCTCTCAGAAAATATATTAAACGAGCTCTTGTAGGCGCTGC 719
Qy CACCTTATGCAATGTCATCGAATCTTTTCTTGGGATGCTTGGAGGCGCATTAACG 812
Db CACCTTATGCAATGTCATCGAATCTTTTCTTGGGATGCTTGGAGGCGCATTAACG 779
Qy CTGAAGCAGGCTCTCATGACCCAGGAGGCGGGTGGATCCCTCTTGTGTTGTAGTC 872
Db CTGAAGCAGGCTCTCATGACCCAGGAGGCGGGTGGATCCCTCTTGTGTTGTAGTC 839
Qy CATGCTATTAAGAGTGGCCCAAGAGGCTCAACATTTCTTAGAGCCTTATTA 932
Db CATGCTATTAAGAGTGGCCCAAGAGGCTCAACATTTCTTAGAGCCTTATTA 899
Qy GAAATGCAATCTGAAGCCCACTCTGGACCCAGGACATTTTGTATGATCCAAAGAG 992
Db GAAATGCAATCTGAAGCCCACTCTGGACCCAGGACATTTTGTATGATCCAAAGAG 959
Qy TTGTATGCATGAAAGTTTGAAGAGCATCATATAGAGAGTAAACATCACCCCACT 1052
Db TTGTATGCATGAAAGTTTGAAGAGCATCATATAGAGAGTAAACATCACCCCACT 1019
Qy TCCTTATCTTTCCAGTGGCTAAACCACTTAACTCTCTGGGTGTACTGCTCATTTGTT 1112
Db TCCTTATCTTTCCAGTGGCTAAACCACTTAACTCTCTGGGTGTACTGCTCATTTGTT 1079
Qy 1113 T 1113

Db 1080 T 1080
RESULT 5
ADL31809
ID ADL31809 standard; cDNA; 1080 BP.
XX ADL31809;
AC ADL31809;
DT 20-MAY-2004 (first entry)
XX Full length human cDNA clone SeqID 3842.
XX human; medicine; signal transduction; glycoprotein; transcription;
XX oligo-capping method; ss; gene.
XX Homo sapiens.
XX EPI396543-A2.
XX 10-MAR-2004.
XX 07-JUL-2000; 2003EP-00025638.
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183865.
XX 07-JUL-2000; 2000EP-00114089.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX MPI: 2004-204755/20.
XX P-PSDB; ADL31810.
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX length human cDNAs.
XX Example 1; SEQ ID NO 3842; 1340pp; English.
XX This invention relates to a novel primers useful for synthesizing full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction.
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This polynucleotide sequence is a
XX full length human cDNA clone of the invention.
XX Sequence 1080 BP; 263 A; 232 C; 244 G; 341 T; 0 U; 0 Other;
Query Match 96.0%; Score 1069; DB 12; Length 1080;
Best Local Similarity 99.9%; Pred. No. 7.1e-312;
Matches 1080; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 33 AGGAAGCGGAGAGAGCGCGCCCGGAGATGCGCGGGCTTAAAGCTCTCG 92
Db 1 AGGAAGCGGAGAGAGCGCGCCCGGAGATGCGCGGGCTTAAAGCTCTCG 60
Qy 93 TGGCAATATCTTCAGTGGGGCTATTGACCTGACTTTTCTTATGCTGGATGTCCTTAG 152
Db 61 TGGCAATATCTTCAGTGGGGCTATTGACCTGACTTTTCTTATGCTGGATGTCCTTAG 120
Qy 153 AGGATTAATGCGGTTTACTGGCCCTTATTCGTCCTGATTTTCCAGCCATCTCCCCCATCC 212
Db 121 AGGATTAATGCGGTTTACTGGCCCTTATTCGTCCTGATTTTCCAGCCATCTCCCCCATCC 180
Qy 213 CCCATTTTCATTCGCAAGAGTACCTATGACTCAGATGCAACCAAGTAGTGCCTGTCGG 272
Db 181 CCCATTTTCATTCGCAAGAGTACCTATGACTCAGATGCAACCAAGTAGTGCCTGTCGG 240

273 AACTGGCATATTTCTTCACTACTGGAATTTGTTGTTCTGCTTTGGATTTCTGTTATTC 332
241 AACTGGCATATTTCTTCACTACTGGAATTTGTTGTTCTGCTTTGGATTTCTGTTATTC 300
333 TTGCTCGTGGCTGTGATCAAAATGGGAGCTCGGCGCTTGTGTTGGCAGGCAATGCAG 392
301 TTGCTCGTGGCTGTGATCAAAATGGGAGCTCGGCGCTTGTGTTGGCAGGCAATGCAG 360
393 TCATTTTCTTACAAATCAAGGGTTTTTCCCTTATATTTGGAAGAGGATGATTTAGCT 452
361 TCATTTTCTTACAAATCAAGGGTTTTTCCCTTATATTTGGAAGAGGATGATTTAGCT 420
453 GGGAGAGGTGAGACATTTATCTGATTCAGATGCAATTTGAATTTCTTAGAATCTCACT 512
421 GGGAGAGGTGAGACATTTATCTGATTCAGATGCAATTTGAATTTCTTAGAATCTCACT 480
513 ATCTGTATACATGTGCACATCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA 572
481 ATCTGTATACATGTGCACATCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA 540
573 ATACCTTTATATATCAATTTCACTTTAAGAAAGCTTCTAAGTAGGAGATGAGTTTAT 632
541 ATACCTTTATATATCAATTTCACTTTAAGAAAGCTTCTAAGTAGGAGATGAGTTTAT 600
633 TCTCAGCAATAGACCTGTCAAACTTTTGTGATTTAGATTTACTTCAAAATTTATGTTTGG 692
601 TCTCAGC-AATAGACCTGTCAAACTTTTGTGATTTAGATTTACTTCAAAATTTATGTTTGG 659
693 CTGTTTCATGTAGTCAAGGTCTCTCAGAAATATATTAAGCAGCTTCTTAGCAGCTGC 752
660 CTGTTTCATGTAGTCAAGGTCTCTCAGAAATATATTAAGCAGCTTCTTAGCAGCTGC 719
753 CACCTTATGATGATCGAATCTTTTGTGATTTAGATTTACTTCAAAATTTATGTTTGG 812
720 CACCTTATGATGATCGAATCTTTTGTGATTTAGATTTACTTCAAAATTTATGTTTGG 779
813 CTGAAGCAGGCTCTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTTGTAGTC 872
780 CTGAAGCAGGCTCTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTTGTAGTC 839
873 CATGCTATTAAGTTGGCCCAAGACCCCTCAACATTTCTAGAGCTTTATTA 932
840 CATGCTATTAAGTTGGCCCAAGACCCCTCAACATTTCTAGAGCTTTATTA 899
933 GAAATGAGATCTGAAGCCCACTCTGGACCCAGGACATTTGATGAGATCCAAAGGAG 992
900 GAAATGAGATCTGAAGCCCACTCTGGACCCAGGACATTTGATGAGATCCAAAGGAG 959
993 TTGTTATGCAATGAAGTTTGAAGATCATCATAGAGAGTAAACATCACACCCCACT 1052
960 TTGTTATGCAATGAAGTTTGAAGATCATCATAGAGAGTAAACATCACACCCCACT 1019
1053 TCCTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGGTGTGTACCTGTCTATTTGTT 1112
1020 TCCTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGGTGTGTACCTGTCTATTTGTT 1079
1113 T 1113
1080 T 1080

RESULT 6
ADP81560
ID ADP81560 standard; DNA; 2388 BP.

XX AC ADP81560;
XX DT 26-FEB-2004 (first entry)
XX DE Leukaemia-related DNA sequence #2116.
XX KW Cytostatic; Gene therapy; leukaemia; sg.

XX OS Unidentified.
XX PN WO2003039443-A2.
XX PD 15-MAY-2003.
XX PA 04-NOV-2002; 2002WO-EP012303.
XX PF 05-NOV-2001; 2001EP-00126244.
XX PR 30-APR-2002; 2002EP-00009758.
XX PA (DEKE-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
XX PA (HAFE/) HAFERLACH T.
XX PA (SCHO/) SCHOCH C.
XX PA (KERN/) KERN W.
XX PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
PI Bils R, Brors B, Mergenthaler S;
XX WPI; 2003-505037/47.
XX DR
XX CC Determining the subtype of leukemia cells and whether a patient sample
CC contains leukemia cells or other cells, useful for treating leukemia,
CC comprises determining the expression profile of a group of markers in a
CC patient sample.
XX PS Disclosure; SEQ ID NO 2116; 2938pp; English.
XX CC The present invention relates to a method (M1) for determining the
CC subtype of leukemia cells and whether a patient sample contains
CC leukemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukaemia.
XX SQ Sequence 2388 BP; 683 A; 461 C; 477 G; 747 T; 0 U; 20 Other;
Query Match 95.8%; Score 1067; DB 10; Length 2388;
Best Local Similarity 99.4%; Pred. No. 4.4e-311; Indels 4; Gaps 4;
Matches 1111; Conservative 0; Mismatches 3;
QY 1 GTCTGCTTGGCAGCTGCGGCGCTTAAAGCTCTCGTGGCATTTATCTTCACTGGGCTATTG 119
Db 1 GTCTGCTTGGCAGCTGCGGCGCTTAAAGCTCTCGTGGCATTTATCTTCACTGGGCTATTG 120
QY 60 GTTCCGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTTATCTTCACTGGGCTATTG 119
Db 61 GNTCCGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTTATCTTCACTGGGCTATTG 120
QY 120 GACTGACTTTTCTTATGCTGGGATGCTTAAAGCTCTCGTGGCATTTATCTTCACTGGGCTATTG 179
Db 121 GACTGACTTTTCTTATGCTGGGATGCTTAAAGCTCTCGTGGCATTTATCTTCACTGGGCTATTG 180
QY 180 TCGTCTGATTTTCCACGCACTCTCCGCCATCCCAATTTTCATTTGCAAAAGAGTCACT 239
Db 181 TCGTCTGATTTTCCACGCACTCTCCGCCATCCCAATTTTCATTTGCAAAAGAGTCACT 240
QY 240 ATGACTCAGATGCAACAGTGTGCTTGGGAGCTGCGGCACTGATTTCTTCACTACTGGA 299
Db 241 ATGACTCAGATGCAACAGTGTGCTTGGGAGCTGCGGCACTGATTTCTTCACTACTGGA 300
QY 300 TTGTTGTTT-CTGCTTTTGGATT-TCCTGTTATTTCTTGTGCTGGCTGTGATCNAAT 356
Db 301 TTGTTGTTTCTGCTTTTGGATTNTCTGTTATTTCTTGTGCTGGCTGTGATCNAAT 360
QY 357 GGGGAGCTCGGCTTGTGTTGGCAGGCAATGCACTGATTTTCTTCACTACTGGA 416
Db 361 GGGGAGCTCGGCTTGTGTTGGCAGGCAATGCACTGATTTTCTTCACTACTGGA 420
QY 417 TTTTCTTATTTTGGAGAGGAGATCATTTTATGCTGGGAGCTGTGTGATCNAAT 476

[illegible]

Qy 481 TACAGTGAATTTGAATTTCTTAGAAGTCTATCTATCTGTATACATGTGACATGGGCAAT 540
 Db |||||
 Qy 481 TACAGTGAATTTGAATTTCTTAGAAGTCTATCTATCTGTATACATGTGACATGGGCAAT 540
 Db |||||
 Qy 541 TTACTATGAATTTAAATATGCTGGGTTTTTAAATACCTTTATATATCATGTGTTCACTTTAA 600
 Db |||||
 Qy 541 TTACTATGAATTTAAATATGCTGGGTTTTTAAATACCTTTATATATCATGTGTTCACTTTAA 600
 Db |||||
 Qy 601 GAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAATAGACCTGTCAAAATTTAG 660
 Db |||||
 Qy 601 GAAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAATAGACCTGTCAAAATTTAG 660
 Db |||||
 Qy 661 ATATGTTACTCAAAATATGTTACTGTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGA 720
 Db |||||
 Qy 661 ATATGTTACTCAAAATATGTTACTGTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGA 720
 Db |||||
 Qy 721 AAATATATTAACGAGCTCTGTAGGAGCTGCGACCTTATGTCAGTGTGATGCAACCTTTT 780
 Db |||||
 Qy 721 AAATATATTAACGAGCTCTGTAGGAGCTGCGACCTTATGTCAGTGTGATGCAACCTTTT 780
 Db |||||
 Qy 781 GCTTGGGAGTGTCTGGAGAGGAGATGATGATGCTGAAGCAGGCTCTCATGACCCAGGAA 840
 Db |||||
 Qy 781 GCTTGGGAGTGTCTGGAGAGGAGATGATGATGCTGAAGCAGGCTCTCATGACCCAGGAA 840
 Db |||||
 Qy 841 GGCCGGGGTGGATCCCTCTTTGTTGTTGTTAGTCCA 874
 Db |||||

RESULT 9

ADR27652
 ID ADR27652 standard; DNA; 648 BP.
 AC ADR27652;
 DT 04-NOV-2004 (first entry)
 XX Leptin receptor related protein, OB-RGRP, nucleotide sequence, SEQ ID 1.
 DE
 KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
 KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW Leptin receptor related protein; OB-RGRP; leptin receptor;
 KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW human; ds.
 XX Homo sapiens.
 XX
 XX FR2850971-A1.
 XX
 XX 13-AUG-2004.
 XX
 XX 10-FEB-2003; 2003FR-00001543.
 XX
 XX 10-FEB-2003; 2003FR-00001543.
 XX
 XX (AVET) AVENTIS PHARMA SA.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Jockers R, Couturier C, Uhlmann E;
 XX WPI; 2004-595751/58.
 XX
 XX New oligonucleotides that inhibit expression of the leptin receptor
 XX related protein, useful for treatment and prevention of e.g.
 XX osteoporosis, obesity, diabetes, anorexia, haematopoiesis, and
 XX angiogenesis.
 XX
 XX Claim 1; SEQ ID NO 1; 104pp; French.
 XX
 XX The present invention relates to a leptin receptor related protein (OB-

CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
 CC specifically with and inhibits the expression of ADR27652. The ON
 CC promotes expression of leptin receptors on the cell surface and may
 CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
 CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
 CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
 CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
 CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
 CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
 CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
 CC protein (YFP) for detecting compounds that modify the interaction between
 CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
 CC treat leptin-related disorders. ON, also related interfering RNA, are
 CC used for prevention and/or treatment of leptin-related disorders, e.g.
 CC osteoporosis (or other conditions involving reduced bone density);
 CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity;
 CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
 CC and inflammation, fetal development and cancer.

SQ Sequence 648 BP; 181 A; 133 C; 129 G; 205 T; 0 U; 0 Other;

Query Match 58.2%; Score 648; DB 13; Length 648;
 Best Local Similarity 100.0%; Pred. No. 8.8e-185;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 CACTTTATCTGATTAACAGTGCATGAAATTTCTTAGAACTCATCTATCTGTATACATGT 526
 Db 1 CACTTTATCTGATTAACAGTGCATGAAATTTCTTAGAACTCATCTATCTGTATACATGT 60
 Qy 527 GCACATGGCGCATTTTACTATGAAATTTAAATATGCTGGTTTTTAAATACCTTTATATAT 586
 Db 61 GCACATGGCGCATTTTACTATGAAATTTAAATATGCTGGTTTTTAAATACCTTTATATAT 120
 Qy 587 CATGTTCACTTTAAGAAAGACTTCAATAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGA 646
 Db 121 CATGTTCACTTTAAGAAAGACTTCAATAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGA 180
 Qy 647 CTTGTCAAAATTTAGATTAATGTTACTCAAAATATGTTACTGTTGGCTGTTTCATGTAGTC 706
 Db 181 CTTGTCAAAATTTAGATTAATGTTACTCAAAATATGTTACTGTTGGCTGTTTCATGTAGTC 240
 Qy 707 ACGTGTCTCTCAGAAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTATGACGTG 766
 Db 241 ACGTGTCTCTCAGAAATATATTAACGAGCTTTGTAGGAGCTGCCACCTTATGACGTG 300
 Qy 767 CATCGAAACCTTTTGTCTTGGGATGCTTGGAGAGCAGATACCGCTGAAGCAGGCCTC 826
 Db 301 CATCGAAACCTTTTGTCTTGGGATGCTTGGAGAGCAGATACCGCTGAAGCAGGCCTC 360
 Qy 827 TCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTTGTTGTTAGTCCATGCTATTTAAAG 886
 Db 361 TCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTTGTTGTTAGTCCATGCTATTTAAAG 420
 Qy 887 TGTGCCCCACAGACCAAGAGCTCAACATTTCTTAGAGCTTTATAGAAATGACAGAACT 946
 Db 421 TGTGCCCCACAGACCAAGAGCTCAACATTTCTTAGAGCTTTATAGAAATGACAGAACT 480
 Qy 947 GAAGCCCCACTCTCGAGCCAGGACATTTTGTATGATGATCCAAAGGAGTTGTATGCACATGA 1006
 Db 481 GAAGCCCCACTCTCGAGCCAGGACATTTTGTATGATGATCCAAAGGAGTTGTATGCACATGA 540
 Qy 1007 AAGTTTGAGAAGCATCATCATATAGAGAGTAAACATCACCCCACTTCTCTTATCTTTCCA 1066
 Db 541 AAGTTTGAGAAGCATCATCATATAGAGAGTAAACATCACCCCACTTCTCTTATCTTTCCA 600
 Qy 1067 GTGGCTAAACCACTTAACCTCTCTGGGTGTTTACCTGCTCATTTGTTTA 1114
 Db 601 GTGGCTAAACCACTTAACCTCTCTGGGTGTTTACCTGCTCATTTGTTTA 648

RESULT 10

AAK93306
 ID AAK93306 standard; cDNA; 629 BP.

Qy	332	CTTGCTCGTGGCTGTGATCAAAATGGGAGGCTCGGCCCTTGTTGTGGCAGGAATGCA	391
Dd	301	CTTGCTCGTGGCTGTGATCAAAATGGGAGGCTCGGCCCTTGTTGTGGCAGGAATGCA	360
Qy	392	GTCAATTTTCCTTAACAATTCAAAGGGTTTTCCCTTTATATTTTGGAGAAGAGATGATTTTAGC	451
Dd	361	NTCAATTTTCCTTAACAATTCAAAGGGTTTTCCCTTTATATTTTGGAANAAGAGATGATTTTAGC	420
Qy	452	TGGAGCAGTGGTAGCACCTTTATCTGATACAGTCAGTCAGTTGGAATTTCTTAGAACCTCATAC	511
Dd	421	TGGAGCAGTGGTAGCACCTTTATCTGATACAGTCAGTCAGTTGGAATTTCTTAGAACCTCATAC	480
Qy	512	TATCTGTATACATGTCACATGCGGCATTTTACTATGAAATTTTAATAATGCTGGGTTTTTT	571
Dd	481	TATCTGTATACATGTCACATGCGGCATTTTACTATGAAATTTTAATAATGCTGGGTTTTTT	540
Qy	572	AATACCTTTTATATCATATGTTCACTTTAAGAAAGACCTTCATTAAGTAGGAGATGAGTTTAA	631
Dd	541	AATACCTTTTATATCATATGTTCACTTTAAGAAAGAC-TCATAAGTAGGAGATGAGTTTAA	599
Qy	632	TTCTCAGCAATAGACCTGTCAAATTTAGAT	662
Dd	600	TTCTCANC-AATAGACCTGTCAAATTTAGAT	629
 RESULT 11 AAK91898			
ID	AAK91898	standard; cDNA; 629 BP.	
XX	AC	AAK91898;	
XX	DT	06-NOV-2001 (first entry)	
XX	DE	Human cDNA 5'-end sequence, SEQ ID NO: 358.	
XX	KW	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.	
XX	OS	Homo sapiens.	
XX	PN	EPI130094-A2.	
XX	PD	05-SEP-2001.	
XX	PF	07-JUL-2000; 2000EP-00114089.	
XX	PR	08-JUL-1999; 99JP-00194486.	
PR	11-JAN-2000; 2000JP-00118774.		
PR	02-MAY-2000; 2000JP-00183765.		
XX	PA	(HELI-) HELIX RES INST.	
XX	PI	Ota T, Nishikawa T, Isogai T, Hayashi K, Iehii S, Kawai Y;	
PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;		
XX	WPI; 2001-524255/58.		
DR	830	Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.	
XX	Claim 2;	SEQ ID NO 358; 1380pp + Sequence Listing; English.	
XX	The invention relates to primers for synthesising full length cDNA clones. 830	cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO	

XX	Sequence	629 BP; 144 A; 129 C; 140 G; 211 T; 0 U; 5 Other;
SQ	Query Match	52.8%; Score 588.4; DB 12; Length 629;
	Best Local Similarity	98.6%; Pred. No. 8.8e-167;
	Mismatches	622; Conservative 0; Mismatches 6; Indels 3; Gaps 3;
Qy	33	AGGAAGCCGGAACAGCGCGGCCAGTTC-GGGAGACATCGCGGGGTAAAGCTCTC 91
Db	1	AGGAAGCCGGAACAGCGCGGCCAGTTCGGGGAGACATCGCGGGGTAAAGCTCTC 60
Qy	92	GTGGCATTAATCCCTTCAGTGCGGCCTATTGGACTGACTTTTCTTATGCTGGGATGCGCTTA 151
Db	61	GTGGCATTAATCCCTTCAGTGCGGCCTATTGGACTGACTTTTCTTATGCTGGGATGCGCTTA 120
Qy	152	GAGGATTAATGGCGTTTACCTGGCCCTTATTCGCTGATTTTCCAGCCATCTCCCCCAATC 211
Db	121	GAGGATTAATGGCGTTTACCTGGCCCTTATTCGCTGATTTTCCAGCCATCTCCCCCAATC 180
Qy	212	CCCCATTTTCATGCCCAGAAGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTGG 271
Db	181	CCCCATTTTCATGCCCAGAAGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTGG 240
Qy	272	GAACTGGCATATTTCTTCACTACTGGAATTTGTTTCTGCTTGGATTTCTCTGTATT 331
Db	241	GAACTGGCATATTTCTTCACTACTGGAATTTGTTTCTGCTTGGATTTCTCTGTATT 300
Qy	332	CTTGTCTGCTGTGCTGTGATCAAATGGGAGCCTCGGCCCTTGTGTGCGAGGCAATGCA 391
Db	301	CTTGTCTGCTGTGCTGTGATCAAATGGGAGCCTCGGCCCTTGTGTGCGAGGCAATGCA 360
Qy	392	GTCAATTTTCTTACAATTCGAAGGTTTTTCTTATATTGGAAGAGGAGATGATTTTAGC 451
Db	361	NTCAATTTTCTTACAATTCGAAGGTTTTTCTTATATTGGAAGAGGAGATGATTTTAGC 420
Qy	452	TGGGACAGTGGTAGCACCTTTATCTGATTACAGTGCATTTAATCTTTAGAACCTCATAC 511
Db	421	TGGGACAGTGGTAGCACCTTTATCTGATTACAGTGCATTTAATCTTTAGAACCTCATAC 480
Qy	512	TATCTGTATACATGTGCATCGCGCATTTTACTATGAATTTAATATGCTGGGTTTTT 571
Db	481	TATCTGTATACATGTGCATCGCGCATTTTACTATGAATTTAATATGCTGGGTTTTT 540
Qy	572	AATACCTTTATATATCATGTTTCACTTTAAGAAGACTTCAATAAGTAGGAGATGAGTTT 631
Db	541	AATACCTTTATATATCATGTTTCACTTTAAGAAGACTTCAATAAGTAGGAGATGAGTTT 599
Qy	632	TTCTCAGCAATAGACTGTCAAATTTAGAT 662
Db	600	TTCTCANC-AATAGACTGTCAAATTTAGAT 629
RESULT 12		
ADL29733	ID	ADL29733 standard; cDNA; 629 BP.
XX	AC	ADL29733;
XX	DT	20-MAY-2004 (first entry)
XX	DE	5' end of a representative human cDNA cluster SeqID 1766.
XX	KW	human; medicine; signal transduction; glycoprotein; transcription;
XX	OS	oligo-capping method; ss.
XX	PV	Homo sapiens.
XX	PN	EPI396543-A2.
XX	PD	10-MAR-2004.
XX	PF	07-JUL-2000; 2003EP-00025638.
XX		

CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.

XX Sequence 647 BP; 174 A; 122 C; 144 G; 205 T; 0 U; 2 Other;

Query Match 51.8%; Score 577.4; DB 10; Length 647;

Best Local Similarity 98.6%; Pred. No. 1.9e-163;

Matches 644; Conservative 0; Mismatches 3; Indels 6; Gaps 6;

QY 352 CAATGGGGAGCTGCGGCTTGTGGCGAGCAATGCAATTCCTTCAAAATCA 411

Db 1 CAATGGGGAGCTGCGGCTTGTGGCGAGCAATGCAATTCCTTCAAAATCA 59

QY 412 AGGGTTTTTCTTATATTTGAAGGAGATGATTTAGCTGGGAGCTGGTACCACTT 471

Db 60 AGGGTTTTTCTTATATTTGAAGGAGATGATTTAGCTGGGAGCTGGTACCACTT 119

QY 472 TATTCGATTACAGTGCAATGAAATTTCTTAGAAGCTCATCTGTATACATGTCACA 531

Db 120 TATTCGATTACAGTGCAATGAAATTTCTTAGAAGCTCATCTGTATACATGTCACA 179

QY 532 TGCGCATTTTACTATGAATTTAATATGCTGGGTTTTTAATACCTTTATATATCATGT 591

Db 180 TGCGCATTTTACTATGAATTTAATATGCTGGGTTTTTAATACCTTTATATATCATGT 239

QY 592 TCACCTTTAAGAAAGCTTCATAGTACGAGATGATTTATTCAGCAATAGACCTGT 651

Db 240 TCACCTTTAAGAAAGCTTCATAGTACGAGATGATTTATTCAGCAATAGACCTGT 299

QY 652 CAATTTAGATTATGTTACTCAAAATTTACTTGTGGCTGTTCAATGATGACCGT 711

Db 300 CAATTTAGATTATGTTACTCAAAATTTACTTGTGGCTGTTCAATGATGACCGT 359

QY 712 GCTCTCAGAAATATATTACGAGCTTTGTAGGAGCTGCCACCTTATGAGTGCATCG 771

Db 360 GCTCTCAGAAATATATTACGAGCTTTGTAGGAGCTGCCACCTTATGAGTGCATCG 419

QY 772 AACCTTTTGTGGGATGCTTGGAGAGCAGATACCTGAGCAGGCTCTCATG 831

Db 420 AACCTTTTGTGGGATGCTTGGAGAGCAGATACCTGAGCAGGCTCTCATG 479

QY 832 ACCAGGAAGCGCGGGTGGATCCCTCTTGTGTGTGTAGTCCATGCTATTAAGTGTGG 891

Db 480 ACCAGGAAGCGCGGGTGGATCCCTCTTGTGTGTGTAGTCCATGCTATTAAGTGTGG 537

QY 892 CCCACAGACCAAGAGCTTCAACATTTCTAGAGCCTTATTAGAAATGAGAAATCTGAAGC 951

Db 538 CCCACAGACCAAGAGCTTCAACATTTCTAGAGCCTTATTAGAAATGAGAAATCTGAAG- 596

QY 952 CCCACTCTGGACCCAGGACATTTGATGAGATCCAAAGAGTTGATGCAT 1004

Db 597 CCCACTCTGGACCCAGGACA-TTTGATGAGATCC-AANGAGTTGATGCNCAT 647

RESULT 15

ID AAK92657/c

AD AAK92657 standard; cDNA; 546 BP.

XX AAK92657;

AC AAK92657;

XX 06-NOV-2001 (first entry)

XX Human cDNA 3'-end sequence, SEQ ID NO: 1117.

DE Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EP1130094-A2.

XX

PD 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX 830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.

XX Claim 3; SEQ ID NO 1117; 1380pp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 3'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from BPO

XX Sequence 546 BP; 160 A; 114 C; 115 G; 150 T; 0 U; 7 Other;

Query Match 44.7%; Score 498.4; DB 4; Length 546;

Best Local Similarity 96.2%; Pred. No. 1.3e-139;

Matches 528; Conservative 0; Mismatches 18; Indels 3; Gaps 2;

QY 565 GTTTTTTAATACCTTTATATATCATGTTCATCTTTAAGAAAGACTTCAAGTAGAGATG 624

Db 546 GGTITTTTAAANCCCTTAAATCAANGTCCCTTTAAGANG-CTTCATAGTAGNAGATG 488

QY 625 AGTTTATTTCTCAGCAATAGACCTGTCAAATTTAGATTATGTTACTCAAAATTATGTTAC 684

Db 487 AGTTTATTTCTCAGCAA--TAGCCTGTCAAATTTAGATTATGTTACTCAAAATTATGTTAC 430

QY 685 TTGTTTGGCTGTTTCAATGATGTCACGGTCTCTCAGAAAATATATTAACGCAAGTCTGTAG 744

Db 429 TTGTTTGGCTGTTTCAATGATGTCACGGTCTCTCAGAAAATATATTAACGCAAGTCTGTAG 370

QY 745 GCAGCTGCCACCTTATGATGTCAGTGCATCGAAACCTTTCTGGGGATGCTTGGAGAGGC 804

Db 369 GCAGCTGCCACCTTATGATGTCAGTGCATCGAAACCTTTCTGGGGATGCTTGGAGAGGC 310

QY 805 AGATAAGCGCTGAAGCAGGCTCTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTG 864

Db 309 AGATAAGCGCTGAAGCAGGCTCTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTG 250

QY 865 TTGTAGTCCATGCTATTAAAGTGTGGCCCAAGAGAGCTCAACATTTCTCTAGAG 924

Db 249 TTGTAGTCCATGCTATTAAAGTGTGGCCCAAGAGAGCTCAACATTTCTCTAGAG 190

QY 925 CCTTATTAGAAATCGAGAACTGAAGCCCACTCTGGACCCAGGACATTTTGTATGATCAGATC 984

Db 189 CCTTATTAGAAATCGAGAACTGAAGCCCACTCTGGACCCAGGACATTTTGTATGATCAGATC 130

QY 985 CAAAGGAGTTGTATGACATGAAAGTTTGAGAAGCATCATCATAGAGAAGTAACATCAC 1044

Db 129 CAAAGGAGTTGTATGACATGAAAGTTTGAGAAGCATCATCATAGAGAAGTAACATCAC 70

QY 1045 ACCCAACTTCTTATCTTTCCAGTGGCTTAAACCACTTAACCTCTCTGGGTGTACCTGCT 1104

||||| 69 ACCCACTTCCTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTG3GTGTACCTGCT 10

Db

QY 1105 CATTGTTT 1113

QY

|||||

Db

9 CATTGTTT 1

Search completed: August 18, 2005, 00:13:52
Job time : 709 secs

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:59:27 ; Search time 9 Seconds
(without alignments)
2.633 Million cell updates/sec

Title: US-10-774-721-21

Perfect score: 1114

Sequence: 1 gctgggtggcaggctgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 511 seqs, 10634 residues

Total number of hits satisfying chosen parameters: 1022

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 511 summaries

Database : pubdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	2.2	25	1	US-10-956-157-58121
2	25	2.2	25	1	US-10-956-157-58122
3	25	2.2	25	1	US-10-956-157-58123
4	25	2.2	25	1	US-10-956-157-58124
5	25	2.2	25	1	US-10-956-157-58125
6	25	2.2	25	1	US-10-956-157-58126
7	25	2.2	25	1	US-10-956-157-58127
8	25	2.2	25	1	US-10-956-157-58128
9	25	2.2	25	1	US-10-956-157-58129
10	25	2.2	25	1	US-10-956-157-58130
11	25	2.2	25	1	US-10-956-157-58131
12	25	2.2	25	1	US-10-956-157-58132
13	25	2.2	25	1	US-10-956-157-58133
14	25	2.2	25	1	US-10-956-157-58134
15	25	2.2	25	1	US-10-956-157-58135
16	25	2.2	25	1	US-10-956-157-58136
17	25	2.2	25	1	US-10-956-157-58137
18	25	2.2	25	1	US-10-956-157-58138
19	25	2.2	25	1	US-10-956-157-58139
20	25	2.2	25	1	US-10-956-157-58140
21	25	2.2	25	1	US-10-956-157-58141
22	25	2.2	25	1	US-10-956-157-58142
23	25	2.2	25	1	US-10-956-157-58143
24	25	2.2	25	1	US-10-956-157-58144
25	25	2.2	25	1	US-10-956-157-58145
26	25	2.2	25	1	US-10-956-157-58146
27	25	2.2	25	1	US-10-956-157-58147
28	25	2.2	25	1	US-10-956-157-58148
29	25	2.2	25	1	US-10-956-157-58149
30	25	2.2	25	1	US-10-956-157-58150
31	25	2.2	25	1	US-10-956-157-58151
32	25	2.2	25	1	US-10-956-157-58152
33	25	2.2	25	1	US-10-956-157-58153

34	25	2.2	25	1	US-10-956-157-198286	Sequence 198286,
35	25	2.2	25	1	US-10-956-157-198863	Sequence 198863,
36	25	2.2	25	1	US-10-956-157-199300	Sequence 199300,
37	25	2.2	25	1	US-10-956-157-204733	Sequence 204733,
38	25	2.2	25	1	US-10-956-157-209653	Sequence 209653,
39	25	2.2	25	1	US-10-956-157-214737	Sequence 214737,
40	25	2.2	25	1	US-10-956-157-215150	Sequence 215150,
41	25	2.2	25	1	US-10-956-157-216427	Sequence 216427,
42	25	2.2	25	1	US-10-956-157-225248	Sequence 225248,
43	25	2.2	25	1	US-10-956-157-225301	Sequence 225301,
44	25	2.2	25	1	US-10-956-157-231080	Sequence 231080,
45	25	2.2	25	1	US-10-956-157-239117	Sequence 239117,
46	25	2.2	25	1	US-10-956-157-239416	Sequence 239416,
47	25	2.2	25	1	US-10-956-157-244137	Sequence 244137,
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51	25	2.2	25	1	US-10-956-157-254092	Sequence 254092,
52	25	2.2	25	1	US-10-956-157-261903	Sequence 261903,
53	25	2.2	25	1	US-10-956-157-265849	Sequence 265849,
54	25	2.2	25	1	US-10-956-157-267654	Sequence 267654,
55	25	2.2	25	1	US-10-956-157-269226	Sequence 269226,
56	25	2.2	25	1	US-10-956-157-292875	Sequence 292875,
57	25	2.2	25	1	US-10-956-157-298706	Sequence 298706,
58	25	2.2	25	1	US-10-956-157-301719	Sequence 301719,
59	25	2.2	25	1	US-10-956-157-304297	Sequence 304297,
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61	25	2.2	25	1	US-10-956-157-309122	Sequence 309122,
62	25	2.2	25	1	US-10-956-157-316779	Sequence 316779,
63	25	2.2	25	1	US-10-956-157-317103	Sequence 317103,
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65	23.4	2.1	25	1	US-10-719-956-674672	Sequence 674672,
66	22.4	2.0	25	1	US-10-719-956-345761	Sequence 345761,
67	22	2.0	22	1	US-10-774-721-32	Sequence 32, Appl
68	21.8	2.0	25	1	US-10-719-900-377733	Sequence 377733,
69	21.8	2.0	25	1	US-10-719-956-92898	Sequence 92898, A
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73	20.8	1.9	25	1	US-10-719-956-445812	Sequence 445812,
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76	20.2	1.8	25	1	US-10-719-900-377731	Sequence 377731,
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78	20.2	1.8	25	1	US-10-719-956-133887	Sequence 133887,
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81	20	1.8	20	1	US-10-774-721-23	Sequence 23, Appl
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83	20	1.8	20	1	US-10-774-721-25	Sequence 25, Appl
84	20	1.8	20	1	US-10-774-721-26	Sequence 26, Appl
85	20	1.8	20	1	US-10-774-721-27	Sequence 27, Appl
86	20	1.8	20	1	US-10-774-721-28	Sequence 28, Appl
87	20	1.8	20	1	US-10-774-721-29	Sequence 29, Appl
88	20	1.8	20	1	US-10-774-721-30	Sequence 30, Appl
89	20	1.8	20	1	US-10-774-721-31	Sequence 31, Appl
90	20	1.8	20	1	US-10-774-721-32	Sequence 32, Appl
91	20	1.8	20	1	US-10-774-721-33	Sequence 33, Appl
92	20	1.8	20	1	US-10-774-721-34	Sequence 34, Appl
93	19.8	1.8	20	1	US-10-774-721-38	Sequence 38, Appl
94	19.8	1.8	25	1	US-09-918-702-59	Sequence 59, Appl
95	19.4	1.7	25	1	US-10-719-956-178975	Sequence 178975,
96	19.2	1.7	25	1	US-10-774-721-37	Sequence 37, Appl
97	19.2	1.7	25	1	US-10-719-956-48484	Sequence 48484, A
98	19.2	1.7	25	1	US-10-719-956-445813	Sequence 445813,
99	19	1.7	25	1	US-10-719-956-456462	Sequence 456462,
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101	18.8	1.7	25	1	US-10-809-189-107033	Sequence 107033,
102	18.8	1.7	25	1	US-10-956-157-97217	Sequence 97217, A
103	18.8	1.7	25	1	US-10-956-157-97220	Sequence 97220, A
104	18.6	1.7	25	1	US-10-719-956-553897	Sequence 553897,
105	18.6	1.7	25	1	US-10-098-2638-110792	Sequence 110792,
106	18.6	1.7	25	1	US-10-719-900-262562	Sequence 262562,
					US-10-719-900-464383	Sequence 464383,

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107	18.6	1.7	25	1	US-10-809-189-125800	Sequence 125800,	c 180	16	1.4	20	1	US-10-280-183A-284	Sequence 284, App
c 108	18.6	1.7	25	1	US-10-956-157-97213	Sequence 97213, A	c 181	16	1.4	20	1	US-10-280-183A-286	Sequence 286, App
109	18.6	1.7	25	1	US-10-956-157-314866	Sequence 314866,	c 182	15.8	1.4	19	1	US-10-923-516-391	Sequence 391, App
c 110	18.6	1.7	25	1	US-10-719-956-16848	Sequence 16848, A	c 183	15.8	1.4	19	1	US-10-923-516-805	Sequence 805, App
111	18.6	1.7	25	1	US-10-719-956-133888	Sequence 133888,	c 184	15.8	1.4	20	1	US-10-160-807-48	Sequence 48, Appl
112	18.6	1.7	25	1	US-10-719-956-231988	Sequence 231988,	c 185	15.8	1.4	20	1	US-10-160-807-196	Sequence 196, App
113	18.6	1.7	25	1	US-10-719-956-255221	Sequence 255221,	c 186	15.8	1.4	20	1	US-10-655-847-48	Sequence 48, Appl
114	18.6	1.7	25	1	US-10-719-956-365165	Sequence 365165,	c 187	15.8	1.4	20	1	US-10-655-847-196	Sequence 196, App
c 115	18.2	1.6	25	1	US-10-098-263B-63072	Sequence 63072, A	c 188	15.8	1.4	21	1	US-09-816-814-7	Sequence 7, Appl
c 116	18.2	1.6	25	1	US-10-719-900-707	Sequence 707, App	c 189	15.8	1.4	21	1	US-10-786-720-15221	Sequence 15221, A
c 117	18.2	1.6	25	1	US-10-719-900-18782	Sequence 18782, A	c 190	15.8	1.4	21	1	US-10-751-736-45418	Sequence 45418, A
c 118	18.2	1.6	25	1	US-10-956-157-250112	Sequence 250112,	c 191	15.8	1.4	22	1	US-10-032-585-4031	Sequence 4031, Ap
c 119	18.2	1.6	25	1	US-10-843-527-4769	Sequence 4769, Ap	c 192	15.8	1.4	22	1	US-10-032-585-4031	Sequence 382, App
c 120	18.2	1.6	25	1	US-10-843-527-233408	Sequence 233408,	c 193	15.6	1.4	20	1	US-10-035-978A-29	Sequence 29, Appl
c 121	18.2	1.6	25	1	US-10-719-956-178976	Sequence 178976,	c 194	15.6	1.4	20	1	US-10-263-594-29	Sequence 93, Appl
c 122	18	1.6	18	1	US-08-779-457-30	Sequence 30, Appl	c 195	15.6	1.4	22	1	US-10-795-667-93	Sequence 95, Appl
c 123	18	1.6	18	1	US-08-779-457-31	Sequence 31, Appl	c 196	15.6	1.4	22	1	US-10-797-333A-95	Sequence 97, Appl
c 124	18	1.6	18	1	US-10-214-802-30	Sequence 30, Appl	c 197	15.4	1.4	18	1	US-10-349-143-11660	Sequence 11660, A
c 125	18	1.6	18	1	US-10-214-802-31	Sequence 31, Appl	c 198	15.4	1.4	20	1	US-10-281-479A-9	Sequence 9, Appl
c 126	18	1.6	18	1	US-10-921-710-30	Sequence 30, Appl	c 199	15.4	1.4	20	1	US-10-275-180A-9	Sequence 9, Appl
c 127	18	1.6	18	1	US-10-921-710-31	Sequence 31, Appl	c 200	15.4	1.4	20	1	US-10-286-132A-9	Sequence 9, Appl
c 128	17.8	1.6	25	1	US-10-719-900-30059	Sequence 30059,	c 201	15.4	1.4	20	1	US-10-688-706-2397	Sequence 2397, Ap
c 129	17.8	1.6	25	1	US-10-719-900-708562	Sequence 708562,	c 202	15.4	1.4	20	1	US-10-688-706-2465	Sequence 2465, Ap
c 130	17.8	1.6	25	1	US-10-719-900-793561	Sequence 793561,	c 203	15.4	1.4	20	1	US-10-688-706-2492	Sequence 2492, Ap
c 131	17.8	1.6	25	1	US-10-719-900-979209	Sequence 979209,	c 204	15.4	1.4	20	1	US-10-688-706-2639	Sequence 2639, Ap
c 132	17.8	1.6	25	1	US-10-719-956-152720	Sequence 152720,	c 205	15.2	1.4	20	1	US-09-817-913-33	Sequence 33, Appl
c 133	17.8	1.6	25	1	US-10-719-956-356718	Sequence 356718,	c 206	15.2	1.4	20	1	US-09-817-538-33	Sequence 33, Appl
c 134	17.8	1.6	25	1	US-10-719-956-427749	Sequence 427749,	c 207	15.2	1.4	20	1	US-10-052-390B-18	Sequence 18, Appl
c 135	17.8	1.6	25	1	US-10-719-956-571667	Sequence 571667,	c 208	15.2	1.4	20	1	US-10-448-836-219	Sequence 219, App
c 136	17.6	1.6	24	1	US-09-841-368A-60	Sequence 60, Appl	c 209	15.2	1.4	20	1	US-10-167-034-103	Sequence 103, App
c 137	17.6	1.6	24	1	US-09-992-665-263	Sequence 63, App	c 210	15.2	1.4	20	1	US-10-167-034-103	Sequence 219, App
c 138	17.6	1.6	24	1	US-10-314-810-60	Sequence 60, Appl	c 211	15.2	1.4	20	1	US-10-448-914A-219	Sequence 219, App
c 139	17.6	1.6	25	1	US-10-098-263B-87092	Sequence 87092, A	c 212	15.2	1.4	20	1	US-10-289-762-6064	Sequence 6064, Ap
c 140	17.6	1.6	25	1	US-10-719-900-143190	Sequence 143190,	c 213	15.2	1.4	20	1	US-10-429-95	Sequence 429, App
c 141	17.6	1.6	25	1	US-10-719-900-217495	Sequence 217495,	c 214	15.2	1.4	20	1	US-10-210-429-95	Sequence 210, App
c 142	17.6	1.6	25	1	US-10-719-900-266991	Sequence 266991,	c 215	15.2	1.4	20	1	US-10-189-818B-30	Sequence 30, Appl
c 143	17.6	1.6	25	1	US-10-719-900-646382	Sequence 646382,	c 216	15.2	1.4	20	1	US-10-673-886A-9	Sequence 9, Appl
c 144	17.6	1.6	25	1	US-10-719-900-685910	Sequence 685910,	c 217	15.2	1.4	20	1	US-10-870-587-33	Sequence 33, Appl
c 145	17.6	1.6	25	1	US-10-719-900-762876	Sequence 762876,	c 218	15.2	1.4	20	1	US-10-913-280-249	Sequence 249, App
c 146	17.6	1.6	25	1	US-10-719-900-762876	Sequence 762876,	c 219	15.2	1.4	20	1	US-10-913-280-249	Sequence 18, Appl
c 147	17.6	1.6	25	1	US-10-719-900-767443	Sequence 767443,	c 220	15.2	1.4	20	1	US-10-498-505A-18	Sequence 14585, A
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c 149	17.6	1.6	25	1	US-10-719-900-878694	Sequence 878694,	c 222	15.2	1.4	20	1	US-10-831-901A-14586	Sequence 15629, A
c 150	17.6	1.6	25	1	US-10-719-900-884508	Sequence 884508,	c 223	15.2	1.4	20	1	US-10-831-901A-15629	Sequence 26184, A
c 151	17.6	1.6	25	1	US-10-719-900-898908	Sequence 898908,	c 224	15.2	1.4	20	1	US-10-831-901A-26184	Sequence 26186, A
c 152	17.6	1.6	25	1	US-10-719-900-20048	Sequence 20048, A	c 225	15.2	1.4	20	1	US-10-831-901A-26186	Sequence 26187, A
c 153	17.6	1.6	25	1	US-10-956-157-97212	Sequence 97212, A	c 226	15.2	1.4	20	1	US-10-831-901A-26187	Sequence 26189, A
c 154	17.6	1.6	25	1	US-10-956-157-97218	Sequence 97218, A	c 227	15.2	1.4	20	1	US-10-831-901A-26189	Sequence 26189, A
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c 156	17.6	1.6	25	1	US-10-956-157-316449	Sequence 316449,	c 229	15.2	1.4	21	1	US-10-786-720-7299	Sequence 7299, Ap
c 157	17.6	1.6	25	1	US-10-843-527-8674	Sequence 8674, Ap	c 230	15.2	1.4	21	1	US-10-786-720-9567	Sequence 9567, Ap
c 158	17.6	1.6	25	1	US-10-843-527-132401	Sequence 132401,	c 231	15.2	1.4	21	1	US-10-786-720-15109	Sequence 15109, A
c 159	17.6	1.6	25	1	US-10-843-527-229503	Sequence 229503,	c 232	15.2	1.4	21	1	US-10-786-720-15111	Sequence 15111, A
c 160	17.6	1.6	25	1	US-10-681-773-16943	Sequence 16943, A	c 233	15.2	1.4	21	1	US-10-751-736-44459	Sequence 44459, A
c 161	17.6	1.6	25	1	US-10-681-773-16944	Sequence 16944, A	c 234	15.2	1.4	21	1	US-10-751-736-44459	Sequence 632, App
c 162	17.6	1.6	25	1	US-10-681-773-103264	Sequence 103264,	c 235	15.2	1.4	21	1	US-10-847-918-8793	Sequence 8793, Ap
c 163	17.6	1.6	25	1	US-10-719-956-48483	Sequence 48483, A	c 236	15	1.3	21	1	US-10-847-918-882	Sequence 26321, A
c 164	17.6	1.6	25	1	US-10-719-956-276484	Sequence 276484,	c 237	15	1.3	21	1	US-10-751-736-26321	Sequence 6, Appl
c 165	17.6	1.6	25	1	US-10-719-956-357405	Sequence 357405,	c 238	14.8	1.3	18	1	US-09-749-709-6	Sequence 16, Appl
c 166	17.6	1.6	25	1	US-10-719-956-649616	Sequence 649616,	c 239	14.8	1.3	20	1	US-09-734-847A-16	Sequence 152, App
c 167	17.6	1.6	25	1	US-10-719-956-685651	Sequence 685651,	c 240	14.8	1.3	20	1	US-09-800-629A-152	Sequence 152, App
c 168	16.8	1.5	21	1	US-10-231-778-208	Sequence 208, App	c 241	14.8	1.3	20	1	US-09-858-152A-9	Sequence 52, Appl
c 169	16.8	1.5	24	1	US-09-911-088-1	Sequence 1, Appl	c 242	14.8	1.3	20	1	US-10-002-974-52	Sequence 68, Appl
c 170	16.8	1.5	24	1	US-10-913-085-1	Sequence 1, Appl	c 243	14.8	1.3	20	1	US-10-012-984-68	Sequence 314, App
c 171	16.6	1.5	23	1	US-10-032-585-4596	Sequence 4596, Ap	c 244	14.8	1.3	20	1	US-10-444-206-314	Sequence 67, Appl
c 172	16.2	1.5	21	1	US-10-751-736-44458	Sequence 44458, A	c 245	14.8	1.3	20	1	US-10-462-691-67	Sequence 68, Appl
c 173	16.2	1.5	23	1	US-09-990-940-23	Sequence 23, Appl	c 246	14.8	1.3	20	1	US-10-317-478-40	Sequence 40, Appl
c 174	16.2	1.5	23	1	US-10-681-199-23	Sequence 23, Appl	c 247	14.8	1.3	20	1	US-10-673-523-68	Sequence 96, Appl
c 175	16.2	1.5	23	1	US-10-913-280-633	Sequence 63, Appl	c 248	14.8	1.3	20	1	US-10-317-478-96	Sequence 152, App
c 176	16.2	1.5	23	1	US-11-038-360-23	Sequence 23, Appl	c 249	14.8	1.3	20	1	US-10-679-532-152	Sequence 9, Appl
c 177	16	1.4	16	1	US-10-774-721-45	Sequence 45, Appl	c 250	14.8	1.3	20	1	US-10-783-415-9	Sequence 1118, Ap
c 178	16	1.4	17	1	US-10-339-793-47	Sequence 47, Appl	c 251	14.8	1.3	20	1	US-10-619-739-1118	Sequence 47, Appl
c 179	16	1.4	20	1	US-10-159-339-21	Sequence 21, Appl	c 252	14.8	1.3	20	1	US-10-659-473-47	Sequence 47, Appl

C 253	14.8	1.3	20	1	US-10-641-962-314	Sequence 314, App	326	14.2	1.3	19	1	US-10-389-431-48	Sequence 48, Appl
C 254	14.8	1.3	20	1	US-10-773-678-222	Sequence 222, App	327	14.2	1.3	19	1	US-10-858-500-599	Sequence 599, App
C 255	14.8	1.3	20	1	US-10-831-901A-15630	Sequence 15630, A	328	14.2	1.3	19	1	US-10-478-633A-147	Sequence 147, App
C 256	14.8	1.3	20	1	US-10-831-901A-15631	Sequence 15631, A	329	14.2	1.3	19	1	US-10-783-128-527	Sequence 527, App
C 257	14.8	1.3	20	1	US-10-831-901A-25596	Sequence 25596, A	330	14.2	1.3	19	1	US-10-783-128-642	Sequence 642, App
C 258	14.8	1.3	20	1	US-10-831-901A-25597	Sequence 25597, A	331	14.2	1.3	19	1	US-10-783-128-1088	Sequence 1088, App
C 259	14.8	1.3	20	1	US-10-831-901A-25598	Sequence 25598, A	C 332	14.2	1.3	19	1	US-10-783-128-2279	Sequence 2279, App
C 260	14.8	1.3	20	1	US-10-831-901A-26089	Sequence 26089, A	C 333	14.2	1.3	19	1	US-10-783-128-2279	Sequence 2279, App
C 261	14.8	1.3	20	1	US-10-831-901A-26090	Sequence 26090, A	C 334	14.2	1.3	19	1	US-10-783-128-2394	Sequence 2394, App
C 262	14.8	1.3	20	1	US-10-831-901A-26091	Sequence 26091, A	C 335	14.2	1.3	19	1	US-10-783-128-2840	Sequence 2840, App
C 263	14.8	1.3	20	1	US-10-831-901A-26185	Sequence 26185, A	336	14.2	1.3	20	1	US-09-771-357-79	Sequence 79, Appl
C 264	14.8	1.3	20	1	US-10-831-901A-26185	Sequence 26185, A	337	14.2	1.3	20	1	US-09-918-187-73	Sequence 73, Appl
C 265	14.8	1.3	20	1	US-10-831-901A-26490	Sequence 26490, A	338	14.2	1.3	20	1	US-10-054-225-12	Sequence 12, Appl
C 266	14.8	1.3	20	1	US-10-956-373-29	Sequence 29, Appl	C 339	14.2	1.3	20	1	US-10-024-450-12	Sequence 12, Appl
C 267	14.8	1.3	20	1	US-10-627-253A-299	Sequence 299, App	C 340	14.2	1.3	20	1	US-10-006-883A-73	Sequence 73, Appl
C 268	14.8	1.3	21	1	US-10-627-253A-300	Sequence 300, App	C 341	14.2	1.3	20	1	US-10-059-579-79	Sequence 79, Appl
C 269	14.8	1.3	21	1	US-10-627-253A-301	Sequence 301, App	C 342	14.2	1.3	20	1	US-10-348-485-86	Sequence 86, Appl
C 270	14.8	1.3	21	1	US-10-627-253A-302	Sequence 302, App	C 343	14.2	1.3	20	1	US-10-428-617-12	Sequence 12, Appl
C 271	14.8	1.3	21	1	US-10-627-253A-303	Sequence 303, App	C 344	14.2	1.3	20	1	US-10-240-046A-56	Sequence 56, Appl
C 272	14.8	1.3	21	1	US-10-627-253A-304	Sequence 304, App	C 345	14.2	1.3	20	1	US-10-154-708-86	Sequence 86, Appl
C 273	14.8	1.3	21	1	US-10-786-720-15220	Sequence 15220, A	C 346	14.2	1.3	20	1	US-10-154-708-86	Sequence 86, Appl
C 274	14.8	1.3	21	1	US-10-786-720-15222	Sequence 15222, A	C 347	14.2	1.3	20	1	US-10-300-683-333	Sequence 333, App
C 275	14.8	1.3	21	1	US-10-751-736-29451	Sequence 29451, A	C 348	14.2	1.3	20	1	US-10-395-031-5	Sequence 5, Appl
C 276	14.8	1.3	21	1	US-10-751-736-31083	Sequence 31083, A	C 349	14.2	1.3	20	1	US-10-349-143-9409	Sequence 9409, App
C 277	14.8	1.3	21	1	US-10-751-736-45419	Sequence 45419, A	C 350	14.2	1.3	20	1	US-10-188-470-69	Sequence 69, Appl
C 278	14.8	1.3	21	1	US-10-484-577-293	Sequence 293, App	C 351	14.2	1.3	20	1	US-10-190-366-111	Sequence 111, App
C 279	14.8	1.3	21	1	US-10-484-577-294	Sequence 294, App	C 352	14.2	1.3	20	1	US-10-190-366-308	Sequence 308, App
C 280	14.8	1.3	21	1	US-10-484-577-295	Sequence 295, App	C 353	14.2	1.3	20	1	US-10-289-762-2125	Sequence 2125, App
C 281	14.8	1.3	21	1	US-10-484-577-296	Sequence 296, App	C 354	14.2	1.3	20	1	US-10-289-762-4121	Sequence 4121, App
C 282	14.8	1.3	21	1	US-10-847-918-4920	Sequence 4920, App	C 355	14.2	1.3	20	1	US-10-289-762-5159	Sequence 5159, App
C 283	14.4	1.3	16	1	US-09-866-108-2565	Sequence 6, Appl	C 356	14.2	1.3	20	1	US-10-289-762-5166	Sequence 5166, App
C 284	14.4	1.3	17	1	US-09-866-108-2566	Sequence 2566, App	C 357	14.2	1.3	20	1	US-10-289-762-5681	Sequence 5681, App
C 285	14.4	1.3	17	1	US-09-866-108-2566	Sequence 2566, App	C 358	14.2	1.3	20	1	US-10-317-500-76	Sequence 76, Appl
C 286	14.4	1.3	17	1	US-09-877-478-948	Sequence 948, App	C 359	14.2	1.3	20	1	US-10-731-739-310	Sequence 310, App
C 287	14.4	1.3	17	1	US-09-930-423-478	Sequence 478, App	C 360	14.2	1.3	20	1	US-10-424-041-105	Sequence 105, App
C 288	14.4	1.3	17	1	US-09-930-423-1012	Sequence 1012, App	C 361	14.2	1.3	20	1	US-10-424-041-179	Sequence 179, App
C 289	14.4	1.3	17	1	US-09-745-237A-478	Sequence 478, App	C 362	14.2	1.3	20	1	US-10-477-238A-310	Sequence 310, App
C 290	14.4	1.3	17	1	US-09-745-237A-1012	Sequence 1012, App	C 363	14.2	1.3	20	1	US-10-680-287A-310	Sequence 310, App
C 291	14.4	1.3	17	1	US-10-342-902-948	Sequence 948, App	C 364	14.2	1.3	20	1	US-10-476-960-4	Sequence 4, Appl
C 292	14.4	1.3	17	1	US-10-138-674-7395	Sequence 7395, App	C 365	14.2	1.3	20	1	US-10-484-442-73	Sequence 73, Appl
C 293	14.4	1.3	17	1	US-10-287-949A-7395	Sequence 7395, App	C 366	14.2	1.3	20	1	US-10-858-500-205	Sequence 205, App
C 294	14.4	1.3	17	1	US-10-689-841-948	Sequence 948, App	C 367	14.2	1.3	20	1	US-10-858-500-381	Sequence 381, App
C 295	14.4	1.3	17	1	US-10-723-361-2565	Sequence 2565, App	C 368	14.2	1.3	20	1	US-10-643-775-1061	Sequence 1061, App
C 296	14.4	1.3	17	1	US-10-723-361-2566	Sequence 2566, App	C 369	14.2	1.3	20	1	US-10-619-253-73	Sequence 73, Appl
C 297	14.4	1.3	17	1	US-10-712-633-347	Sequence 347, App	C 370	14.2	1.3	20	1	US-10-477-173-310	Sequence 310, App
C 298	14.4	1.3	19	1	US-09-969-373-2494	Sequence 2494, App	C 371	14.2	1.3	20	1	US-10-831-901A-10393	Sequence 10393, A
C 299	14.4	1.3	19	1	US-10-731-739-588	Sequence 588, App	C 372	14.2	1.3	20	1	US-10-831-901A-10394	Sequence 10394, A
C 300	14.4	1.3	19	1	US-10-477-238A-588	Sequence 588, App	C 373	14.2	1.3	20	1	US-10-831-901A-11295	Sequence 11295, A
C 301	14.4	1.3	19	1	US-10-680-287A-588	Sequence 588, App	C 374	14.2	1.3	20	1	US-10-831-901A-12114	Sequence 12114, A
C 302	14.4	1.3	19	1	US-10-477-173-588	Sequence 588, App	C 375	14.2	1.3	20	1	US-10-831-901A-12115	Sequence 12115, A
C 303	14.4	1.3	19	1	US-10-834-377-588	Sequence 588, App	C 376	14.2	1.3	20	1	US-10-831-901A-14584	Sequence 14584, A
C 304	14.4	1.3	20	1	US-09-854-883-297	Sequence 297, App	C 377	14.2	1.3	20	1	US-10-831-901A-14587	Sequence 14587, A
C 305	14.4	1.3	20	1	US-09-917-963-91	Sequence 91, Appl	C 378	14.2	1.3	20	1	US-10-831-901A-15287	Sequence 15287, A
C 306	14.4	1.3	20	1	US-09-953-318-37	Sequence 37, Appl	C 379	14.2	1.3	20	1	US-10-831-901A-15288	Sequence 2183, A
C 307	14.4	1.3	20	1	US-10-085-906-317	Sequence 317, App	C 380	14.2	1.3	20	1	US-10-831-901A-26183	Sequence 26188, A
C 308	14.4	1.3	20	1	US-10-446-373-37	Sequence 37, Appl	C 381	14.2	1.3	20	1	US-10-831-901A-26188	Sequence 26188, A
C 309	14.4	1.3	20	1	US-10-360-510-297	Sequence 297, App	C 382	14.2	1.3	20	1	US-10-831-901A-26488	Sequence 26488, A
C 310	14.4	1.3	20	1	US-10-349-143-6795	Sequence 6795, App	C 383	14.2	1.3	20	1	US-10-831-901A-26896	Sequence 26896, A
C 311	14.4	1.3	20	1	US-10-289-762-1803	Sequence 1803, App	C 384	14.2	1.3	20	1	US-10-831-901A-26897	Sequence 26897, A
C 312	14.4	1.3	20	1	US-10-455-229-23	Sequence 23, Appl	C 385	14.2	1.3	20	1	US-10-476-264-189	Sequence 189, App
C 313	14.4	1.3	20	1	US-10-293-864-44	Sequence 44, Appl	C 386	14.2	1.3	20	1	US-10-834-377-310	Sequence 310, App
C 314	14.4	1.3	20	1	US-10-293-864-45	Sequence 45, Appl	C 387	14.2	1.3	20	1	US-10-980-850-1	Sequence 1, Appl
C 315	14.4	1.3	20	1	US-10-293-864-120	Sequence 120, App	C 388	14.2	1.3	20	1	US-11-039-629-125	Sequence 125, App
C 316	14.4	1.3	20	1	US-10-293-864-121	Sequence 121, App	C 389	14.2	1.3	20	1	US-10-774-721-43	Sequence 43, Appl
C 317	14.4	1.3	20	1	US-10-688-706-2537	Sequence 2537, App	C 390	14.2	1.3	20	1	US-09-504-231A-706	Sequence 706, App
C 318	14.4	1.3	20	1	US-10-688-706-2670	Sequence 2670, App	C 391	14.2	1.3	20	1	US-09-274-553D-706	Sequence 706, App
C 319	14.4	1.3	20	1	US-10-831-901A-4408	Sequence 4408, App	C 392	14.2	1.3	20	1	US-10-349-443-5553	Sequence 5553, App
C 320	14.4	1.3	20	1	US-10-831-901A-4409	Sequence 4409, App	C 393	14.2	1.3	20	1	US-10-719-993-55163	Sequence 55163, A
C 321	14.4	1.3	20	1	US-10-831-901A-4410	Sequence 4410, App	C 394	14.2	1.3	20	1	US-09-802-669-156	Sequence 156, App
C 322	14.4	1.3	20	1	US-10-831-901A-4411	Sequence 4411, App	C 395	14.2	1.3	20	1	US-10-172-911-55	Sequence 55, Appl
C 323	14.4	1.3	20	1	US-10-831-901A-4412	Sequence 4412, App	C 396	14.2	1.3	20	1	US-10-349-143-4185	Sequence 4185, App
C 324	14.4	1.3	20	1	US-10-008-747-297	Sequence 297, App	C 397	14.2	1.3	20	1	US-10-349-143-5624	Sequence 5624, App
C 325	14.2	1.3	19	1	US-10-388-578-48	Sequence 48, Appl	C 398	14.2	1.3	20	1	US-10-619-220-156	Sequence 156, App
												US-10-831-901A-18964	Sequence 18964, A


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RESULT 2
US-10-956-157-58122
; Sequence 58122, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58122

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1011 TTGAGAGCATCATCATAGAGAAGT 1035
      |||||
Db      1 TTGAGAGCATCATCATAGAGAAGT 25

RESULT 3
US-10-956-157-58123
; Sequence 58123, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58123
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58123

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      723 ATATATTAAACCGAGTCTTGTTAGGCA 747
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Db      1 ATATATTAAACCGAGTCTTGTTAGGCA 25

RESULT 4
US-10-956-157-58124
; Sequence 58124, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 58124
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58124

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1012 TGAGAGCATCATCATAGAGAAGTA 1036
      |||||
Db      1 TGAGAGCATCATCATAGAGAAGTA 25

RESULT 5
US-10-956-157-58125
; Sequence 58125, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58125
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58125

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1013 GAGAGCATCATCATAGAGAAGTAA 1037
      |||||
Db      1 GAGAGCATCATCATAGAGAAGTAA 25

RESULT 6
US-10-956-157-58126
; Sequence 58126, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58126
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58126

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1035 TAAACATCACACCCCACTTCTTAT 1059
      |||||
Db      1 TAAACATCACACCCCACTTCTTAT 25
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RESULT 7
US-10-956-157-58127
; Sequence 58127, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58127
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58127

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1024 TCATAGAGAAGTAAACATCACACCC 1048
Db 1 TCATAGAGAAGTAAACATCACACCC 25

RESULT 8
US-10-956-157-58128
; Sequence 58128, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58128

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CATAGAGAAGTAAACATCACACCCA 1049
Db 1 CATAGAGAAGTAAACATCACACCCA 25

RESULT 9
US-10-956-157-58129
; Sequence 58129, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58129
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58129

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 ATAGAGAAGTAAACATCACACCCA 1050
Db 1 ATAGAGAAGTAAACATCACACCCA 25

RESULT 10
US-10-956-157-58130
; Sequence 58130, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58130

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 TAGAGAAGTAAACATCACACCCAAC 1051
Db 1 TAGAGAAGTAAACATCACACCCAAC 25

RESULT 11
US-10-956-157-58131
; Sequence 58131, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58131

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 ATTATGTTACTTGTGGCTGTTC 699
Db 1 ATTATGTTACTTGTGGCTGTTC 25

RESULT 12
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US-10-956-157-58132
; Sequence 58132, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58132
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58132

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1040 ATCACACCCCAACTTCCTTATCTTTC 1064
Db      1 ATCACACCCCAACTTCCTTATCTTTC 25

RESULT 13
US-10-956-157-58133
; Sequence 58133, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58133

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1039 CATCACACCCCAACTTCCTTATCTTT 1063
Db      1 CATCACACCCCAACTTCCTTATCTTT 25

RESULT 14
US-10-956-157-58134
; Sequence 58134, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58134
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58134

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1034 GTAAACATCATCACCCCAACTTCCTTTA 1058
Db      1 GTAAACATCATCACCCCAACTTCCTTTA 25

RESULT 15
US-10-956-157-58135
; Sequence 58135, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58135

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      676 TTATGTTACTTGTGTTGGCTGTTCAT 700
Db      1 TTATGTTACTTGTGTTGGCTGTTCAT 25

RESULT 16
US-10-956-157-58136
; Sequence 58136, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58136
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58136

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1036 AAACATCATCACCCCAACTTCCTTATC 1060
Db      1 AAACATCATCACCCCAACTTCCTTATC 25

RESULT 17
US-10-956-157-58137
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; Sequence 58137, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58137

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1051 CTTCCCTTATCTTCCAGTGGCTTAA 1075
Db      1 CTTCCCTTATCTTCCAGTGGCTTAA 25

RESULT 18
US-10-956-157-58138
; Sequence 58138, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58138

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1052 TTCCTTATCTTCCAGTGGCTTAA 1076
Db      1 TTCCTTATCTTCCAGTGGCTTAA 25

RESULT 19
US-10-956-157-58139
; Sequence 58139, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58139
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58139

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; ORGANISM: Probe Sequence
US-10-956-157-58139

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1008 AGTTTGAGAAGCATCATCATAGAGA 1032
Db      1 AGTTTGAGAAGCATCATCATAGAGA 25

RESULT 20
US-10-956-157-58140
; Sequence 58140, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58140

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1023 ATCATAGAGAAGTAACATCACACC 1047
Db      1 ATCATAGAGAAGTAACATCACACC 25

RESULT 21
US-10-956-157-58141
; Sequence 58141, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58141
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58141

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      725 ATATTACGCAGTCTTGTAGGCAGC 749
Db      1 ATATTACGCAGTCTTGTAGGCAGC 25

RESULT 22
US-10-956-157-58142
; Sequence 58142, Application US/10956157

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; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58142
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58142

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      674 AATTATGTTACTTGTGGCTGTTTC 698
      |||||||
Db      1 AATTATGTTACTTGTGGCTGTTTC 25

RESULT 23
US-10-956-157-58143
; Sequence 58143, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58143
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58143

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1038 ACATCACACCACTTCCTTATCTT 1062
      |||||||
Db      1 ACATCACACCACTTCCTTATCTT 25

RESULT 24
US-10-956-157-58144
; Sequence 58144, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58144

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1037 AACATCACACCACTTCCTTATCTT 1061
      |||||||
Db      1 AACATCACACCACTTCCTTATCTT 25

RESULT 25
US-10-956-157-126134
; Sequence 126134, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-126134

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      723 ATATATTAAACGCACTCTGTAGGCA 747
      |||||||
Db      1 ATATATTAAACGCACTCTGTAGGCA 25

RESULT 26
US-10-956-157-133680
; Sequence 133680, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-133680

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      820 AGGCCTCTCATGACCCAGGAGGCC 844
      |||||||
Db      1 AGGCCTCTCATGACCCAGGAGGCC 25

RESULT 27
US-10-956-157-137776
; Sequence 137776, Application US/10956157
; Publication No. US20050118625A1
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US-10-956-157-58144

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1037 AACATCACACCACTTCCTTATCTT 1061
      |||||||
Db      1 AACATCACACCACTTCCTTATCTT 25

RESULT 25
US-10-956-157-126134
; Sequence 126134, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-126134

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      723 ATATATTAAACGCACTCTGTAGGCA 747
      |||||||
Db      1 ATATATTAAACGCACTCTGTAGGCA 25

RESULT 26
US-10-956-157-133680
; Sequence 133680, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-133680

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      820 AGGCCTCTCATGACCCAGGAGGCC 844
      |||||||
Db      1 AGGCCTCTCATGACCCAGGAGGCC 25

RESULT 27
US-10-956-157-137776
; Sequence 137776, Application US/10956157
; Publication No. US20050118625A1
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Fri Aug 19 11:00:02 2005

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137776
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-13776

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      869 AGTCCATGCTATTAAAGGTGGCC 893
      |||||||
Db      1 AGTCCATGCTATTAAAGGTGGCC 25

RESULT 28
US-10-956-157-140388
; Sequence 140388, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140388
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-140388

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      644 AGACCTGTCAAATTTAGATTATGTT 668
      |||||||
Db      1 AGACCTGTCAAATTTAGATTATGTT 25

RESULT 29
US-10-956-157-140715
; Sequence 140715, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140715
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-140715

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Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      897 AGACCAAGAGCCTCAACATTTCCCTA 921
      |||||||
Db      1 AGACCAAGAGCCTCAACATTTCCCTA 25

RESULT 30
US-10-956-157-146569
; Sequence 146569, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-146569

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      575 ACCTTTATATCATGTTCACTTTA 599
      |||||||
Db      1 ACCTTTATATCATGTTCACTTTA 25

RESULT 31
US-10-956-157-158472
; Sequence 158472, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158472
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-158472

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCACACAGACCAAGAG 906
      |||||||
Db      1 AAAAGTGTGGCCACACAGACCAAGAG 25

RESULT 32
US-10-956-157-168122
; Sequence 168122, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-168122

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 674 AATTATGTTACTTGTGGCTGTTTC 698
    |||||||
Db 1 AATTATGTTACTTGTGGCTGTTTC 25

RESULT 33
US-10-956-157-182572
; Sequence 182572, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182572
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-182572

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 776 CTTTGTGGGATGCTGGAG 800
    |||||||
Db 1 CTTTGTGGGATGCTGGAG 25

RESULT 34
US-10-956-157-198286
; Sequence 198286, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-198286
```

```
Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 823 CCTCTCATGACCCAGGAAGCCGG 847
    |||||||
Db 1 CCTCTCATGACCCAGGAAGCCGG 25

RESULT 35
US-10-956-157-198863
; Sequence 198863, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198863
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-198863

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 855 CCTTTGTGTGTAGTCCATGCTA 879
    |||||||
Db 1 CCTTTGTGTGTAGTCCATGCTA 25

RESULT 36
US-10-956-157-199300
; Sequence 199300, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199300
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-199300

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1054 CCTTATCTTCCAGTGGCTAAACCA 1078
    |||||||
Db 1 CCTTATCTTCCAGTGGCTAAACCA 25

RESULT 37
US-10-956-157-204733
; Sequence 204733, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

Fri Aug 19 11:00:02 2005

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; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 204733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-204733

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      766 GCATCGAAACCTTTTCTTGGGGAT 790
      |||||||
Db      1 GCATCGAAACCTTTTCTTGGGGAT 25

RESULT 38
US-10-956-157-209653
; Sequence 209653, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209653
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-209653

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      748 GCTGCCACCTTATGCGATGCGATCGA 772
      |||||||
Db      1 GCTGCCACCTTATGCGATGCGATCGA 25

RESULT 39
US-10-956-157-214737
; Sequence 214737, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214737
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-214737

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      748 GCTGCCACCTTATGCGATGCGATCGA 772
      |||||||
Db      1 GCTGCCACCTTATGCGATGCGATCGA 25
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      761 GCAGTGCATCGAAACCTTTTCTTGG 785
      |||||||
Db      1 GCAGTGCATCGAAACCTTTTCTTGG 25

RESULT 40
US-10-956-157-215150
; Sequence 215150, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215150
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-215150

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      745 GCAGTGCACCTTATGCGATGCGAT 769
      |||||||
Db      1 GCAGTGCACCTTATGCGATGCGAT 25

RESULT 41
US-10-956-157-216427
; Sequence 216427, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 216427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-216427

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      527 GCACATGCGGCATTTTACTATGAAA 551
      |||||||
Db      1 GCACATGCGGCATTTTACTATGAAA 25

RESULT 42
US-10-956-157-225248
; Sequence 225248, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225248
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225248

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 771 GAAACCTTTTCTGGGGATGCT 795
|||||
Db 1 GAAACCTTTTCTGGGGATGCT 25

RESULT 43

US-10-956-157-225301
; Sequence 225301, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225301

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1005 GAAAGTTTGAGAGCATCATAG 1029
|||||
Db 1 GAAAGTTTGAGAGCATCATAG 25

RESULT 44

US-10-956-157-231080
; Sequence 231080, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-231080

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 904 GAGCCTCAACATTTTCCTAGAGCCTT 928
|||||
Db 1 GAGCCTCAACATTTTCCTAGAGCCTT 25

RESULT 45

US-10-956-157-239117
; Sequence 239117, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-239117

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 981 GATCCAAAGGAGTTGTATGCACATG 1005
|||||
Db 1 GATCCAAAGGAGTTGTATGCACATG 25

RESULT 46

US-10-956-157-239416
; Sequence 239416, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239416
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-239416

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 806 GATAACGCTGAAGCAGGCCTCTCAT 830
|||||
Db 1 GATAACGCTGAAGCAGGCCTCTCAT 25

RESULT 47

US-10-956-157-244137
; Sequence 244137, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 244137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-244137

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 244137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-244137
Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 695 GTTCATGTAGTCACGGTGCTCTCAG 719
Db 1 GTTCATGTAGTCACGGTGCTCTCAG 25
RESULT 48
US-10-956-157-246391
; Sequence 246391, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 246391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-246391
Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 687 GTTTGGCTGTTTCATGTAGTCACGGT 711
Db 1 GTTTGGCTGTTTCATGTAGTCACGGT 25
RESULT 49
US-10-956-157-247073
; Sequence 247073, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 247073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-247073
Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 GTAGTCACGGTGCTCTCAGAAAAATA 725
Db 1 GTAGTCACGGTGCTCTCAGAAAAATA 25
RESULT 50
US-10-956-157-250507
; Sequence 250507, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250507
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-250507
Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 GTACACGGTGCTCTCAGAAAAATATAT 728
Db 1 GTACACGGTGCTCTCAGAAAAATATAT 25
RESULT 51
US-10-956-157-254092
; Sequence 254092, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-254092
Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 791 GTGCTTGGAGAGCGCATACCGCTG 815
Db 1 GTGCTTGGAGAGCGCATACCGCTG 25
RESULT 52
US-10-956-157-261903
; Sequence 261903, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 261903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-261903
Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 261903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-261903

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 785 GGGGATGCTTGGAGAGGACAGATA 809
Db 1 GGGGATGCTTGGAGAGGACAGATA 25

RESULT 53

US-10-956-157-265849
; Sequence 265849, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 265849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-265849

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 850 GGATCCCTCTTGTGTTGTTAGTCCA 874
Db 1 GGATCCCTCTTGTGTTGTTAGTCCA 25

RESULT 54

US-10-956-157-267654
; Sequence 267654, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 267654
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-267654

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 GGAGATGAGTTTATTCTCAGCAA 642
Db 1 GGAGATGAGTTTATTCTCAGCAA 25

RESULT 55

US-10-956-157-269226
; Sequence 269226, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269226
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-269226

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 960 GGACCCAGGACATTTTGATGAGATC 984
Db 1 GGACCCAGGACATTTTGATGAGATC 25

RESULT 56

US-10-956-157-292875
; Sequence 292875, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-292875

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1088 TCTGGGTGTACCTGCTCATTTGTT 1112
Db 1 TCTGGGTGTACCTGCTCATTTGTT 25

RESULT 57

US-10-956-157-298706
; Sequence 298706, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)

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Fri Aug 19 11:00:02 2005

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; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 2004-10-04
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 298706
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-298706

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 TCAACATTTCTAGAGCCTTATTAG 933
      ||||||||||||||||||||||||
Db 1 TCAACATTTCTAGAGCCTTATTAG 25

RESULT 58
US-10-956-157-301719
; Sequence 301719, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301719
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-301719

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 TACATGTGCACATGCGCATTTTAC 544
      ||||||||||||||||||||||||
Db 1 TACATGTGCACATGCGCATTTTAC 25

RESULT 59
US-10-956-157-304297
; Sequence 304297, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 304297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-304297

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 TAGAAGTAACATCACCCCAAC 1051
      ||||||||||||||||||||||||
Db 1 TAGAAGTAACATCACCCCAAC 25

RESULT 60
US-10-956-157-308375
; Sequence 308375, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 308375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-308375

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 630 TATTCTCAGCAATAGACCTGTCAA 654
      ||||||||||||||||||||||||
Db 1 TATTCTCAGCAATAGACCTGTCAA 25

RESULT 61
US-10-956-157-309122
; Sequence 309122, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 309122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-309122

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 TTGTGTTCTAGTCCATGCTATTA 883
      ||||||||||||||||||||||||
Db 1 TTGTGTTCTAGTCCATGCTATTA 25

RESULT 62
US-10-956-157-316779
; Sequence 316779, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 316779
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-316779

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 TAGAAGTAACATCACCCCAAC 1051
      ||||||||||||||||||||||||
Db 1 TAGAAGTAACATCACCCCAAC 25
```



```
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 316779
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-316779

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      916  TTCCTAGAGCCTTATTAGAAATGCA 940
          |||||
Db      1    TTCCTAGAGCCTTATTAGAAATGCA 25

RESULT 63
US-10-956-157-317103
; Sequence 317103, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 317103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-317103

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1052 TTCCTATATCTTCAGTGGCTAAAC 1076
          |||||
Db      1    TTCCTATATCTTCAGTGGCTAAAC 25

RESULT 64
US-10-719-956-417007
; Sequence 417007, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417007
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-417007

Query Match      2.1%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 36;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      271  GGAAGCTGGCATATTTCTTCACTACT 295
          |||||
```

```
Db      1    GGAAGCTGGCATATTTCTTCACTACT 25

RESULT 65
US-10-719-956-674672
; Sequence 674672, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674672
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-674672

Query Match      2.1%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 36;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      330  TTCTTGCTCGTGTGGCTGTGATCAA 354
          |||||
Db      1    TTCTTGCTCGTGTGGCTGTGATCAA 25

RESULT 66
US-10-719-956-345761
; Sequence 345761, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 345761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-345761

Query Match      2.0%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      152  GAGGATTATGGCGTTTACTGGCCC 175
          |||||
Db      1    GAGGACTATGGCGTTTACTGGCCC 24

RESULT 67
US-10-774-721-32/c
; Sequence 32, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Eugen
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAY2003/0005 US NP
```

Fri Aug 19 11:00:02 2005

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; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS11
US-10-774-721-32

Query Match      2.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      264 CCTGTCGGGAAGTGGCATATTT 285
      |||||
Db      22 CCTGTCGGGAAGTGGCATATTT 1

RESULT 68
US-10-719-900-377733
; Sequence 377733, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 377733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-377733

Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1085 CTCTCTGGGTGTACTGCTCATTT 1109
      |||||
Db      1 CTCTCTGGGTGTGCAATGCTCATTT 25

RESULT 69
US-10-719-956-92898
; Sequence 92898, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 92898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-92898

Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      330 TTCTTGCTCGTGGCTGTGATCAA 354
      |||||
Db      1 TTCTTGCTCGGAGGCTGTGATCAA 25

RESULT 70
US-10-719-956-417006
; Sequence 417006, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-417006

Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      271 GGAAGTGGCATATTTCTTCACTACT 295
      |||||
Db      1 GGAAGTGGCATATTTCTTCACTACT 25

RESULT 71
US-10-719-956-674671
; Sequence 674671, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-674671

Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      330 TTCTTGCTCGTGGCTGTGATCAA 354
      |||||
Db      1 TTCTTGCTCGGAGGCTGTGATCAA 25

RESULT 72
US-10-719-956-345760
; Sequence 345760, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

```
Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      254 ACCAGTAGTCCTCTCGGAACTGG 278
      |||||
Db      1 ACTAGCAGTCCTCTCGGAACTGG 25

RESULT 70
US-10-719-956-417006
; Sequence 417006, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-417006

Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      271 GGAAGTGGCATATTTCTTCACTACT 295
      |||||
Db      1 GGAAGTGGCATATTTCTTCACTACT 25

RESULT 71
US-10-719-956-674671
; Sequence 674671, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-674671

Query Match      2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      330 TTCTTGCTCGTGGCTGTGATCAA 354
      |||||
Db      1 TTCTTGCTCGGAGGCTGTGATCAA 25

RESULT 72
US-10-719-956-345760
; Sequence 345760, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 345760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-345760

Query Match      1.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 GAGGATTATGCGTTTACTGCCCC 175
      ||||| ||||| ||||| ||||| |||||
Db 1 GAGGACTATGCGCTTTACTGCCCC 24

RESULT 73
US-10-719-956-445812
; Sequence 445812, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 445812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-445812

Query Match      1.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 379 GGCAGGCAATGCAGTCATTTTCCT 402
      ||||| ||||| ||||| ||||| |||||
Db 1 GGCTGGCAATGCAGTTATTTTCCT 24

RESULT 74
US-10-719-956-456463
; Sequence 456463, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 456463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-456463
```

```
Query Match      1.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 76 GGGCGTTAAAGCTCTCGTGCCATT 99
      ||||| ||||| ||||| ||||| |||||
Db 1 GGGCGTTAAAGCTCTTGTGGCACT 24

RESULT 75
US-10-098-263B-110791
; Sequence 110791, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110791

Query Match      1.8%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 179 TTGTCCTCGATTTTCCACGCCATCT 203
      ||||| ||||| ||||| ||||| |||||
Db 1 TTCATCTGAGTTTCCACGCCGCT 25

RESULT 76
US-10-719-900-377731
; Sequence 377731, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 377731
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-377731

Query Match      1.8%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1085 CTCTCTGGGTGTTACCTGCTCATTT 1109
      ||||| ||||| ||||| ||||| |||||
Db 1 CTCTCTGGGTGTTACGATGCTCATTT 25

RESULT 77
US-10-719-956-92897
; Sequence 92897, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
```

; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS02
US-10-774-721-23

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 CCCAGTTCGGGAGACATGGC 75
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCCAGTTCGGGAGACATGGC 1

RESULT 82

US-10-774-721-24/c
; Sequence 24, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR FILING DATE: 2004-02-09
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS03
US-10-774-721-24

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 CGGAGACATGGCGGCGTT 82
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CGGAGACATGGCGGCGTT 1

RESULT 83

US-10-774-721-25/c
; Sequence 25, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR FILING DATE: 2003-04-07

; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS04
US-10-774-721-25

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 ATGGCGGGCGTTAAAGCTCT 90
| | | | | | | | | | | | | | | | | | | | | |
Db 20 ATGGCGGGCGTTAAAGCTCT 1

RESULT 84

US-10-774-721-26/c
; Sequence 26, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS05
US-10-774-721-26

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 AGCTCTCGTGCATTATCC 103
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AGCTCTCGTGCATTATCC 1

RESULT 85

US-10-774-721-27/c
; Sequence 27, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR FILING DATE: 60/461,005

Fri Aug 19 11:00:02 2005

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; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS06
US-10-774-721-27

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 CTTATGCTGGGATGTGCCTT 150
| | | | | | | | | | | | | | | | | |
Db 20 CTTATGCTGGGATGTGCCTT 1

RESULT 86
US-10-774-721-28/c
; Sequence 28, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAY2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS07
US-10-774-721-28

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGTGCTTAGAGGATATG 162
| | | | | | | | | | | | | | | | | |
Db 20 TGTGCTTAGAGGATATG 1

RESULT 87
US-10-774-721-29/c
; Sequence 29, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAY2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09

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; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS08
US-10-774-721-29

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 GAGGATTATGGCGTTTACTG 171
| | | | | | | | | | | | | | | | | |
Db 20 GAGGATTATGGCGTTTACTG 1

RESULT 88
US-10-774-721-30/c
; Sequence 30, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAY2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS09
US-10-774-721-30

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GCGTTTACTGGCCCTTATT 180
| | | | | | | | | | | | | | | | | |
Db 20 GCGTTTACTGGCCCTTATT 1

RESULT 89
US-10-774-721-31/c
; Sequence 31, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of The OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAY2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721

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; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS10
US-10-774-721-31

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TGCCTGTCGGGAACGTGGCAT 281
|||||
Db 20 TGCCTGTCGGGAACGTGGCAT 1

RESULT 90

US-10-774-721-33/c
; Sequence 33, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS12
US-10-774-721-33

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 269 CGGGAACGTGGCATATTTCTT 288
|||||
Db 20 CGGGAACGTGGCATATTTCTT 1

RESULT 91

US-10-774-721-34/c
; Sequence 34, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP

; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS13
US-10-774-721-34

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 CCTTGTGTGGCAGCAATG 389
|||||
Db 20 CCTTGTGTGGCAGCAATG 1

RESULT 92

US-10-774-721-38/c
; Sequence 38, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-38

Query Match 1.8%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 AGTGCCTGTGGGAACCTGGC 279
|||||
Db 20 AGTGCCTGTGGGAACCTGGC 1

RESULT 93

US-09-918-702-59/c
; Sequence 59, Application US/09918702
; Patent No. US20020146678A1
; GENERAL INFORMATION:
; APPLICANT: Benvenisty, Nissim
; TITLE OF INVENTION: Directed Differentiation of Embryonic Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 1822/113
; CURRENT APPLICATION NUMBER: US/09/918,702
; CURRENT FILING DATE: 2001-07-31

```
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: 3' primer of Parathyroid Hormone
US-09-918-702-59

Query Match      1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 794 CTTGGAGAGCGCAGATAACGCTGA 816
Db 23 CTTGGAGAGCGCAGACAAAGCTGA 1

RESULT 94
US-10-719-956-178975
; Sequence 178975, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 178975
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-178975

Query Match      1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 308 TCTGCTTTTGGATTTCCTGTTAT 330
Db 2 TCAGCCTCTGATTTCCTGTTAT 24

RESULT 95
US-10-774-721-37
; Sequence 37, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FR2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Artificial
US-10-774-721-37

Query Match      1.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 76;
Matches 16; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 261 GTGCTGTGCGGAACCTGCAT 281
Db 1 GUGCCUGUGGGGACUGGCTT 21

RESULT 96
US-10-719-956-48484
; Sequence 48484, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-48484

Query Match      1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 229 AAGAGTCACCTATGACTCAGATGC 252
Db 1 AAGGTCACCTATGACTCGGACGC 24

RESULT 97
US-10-719-956-445813
; Sequence 445813, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 445813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-445813

Query Match      1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 379 GCGAGCAATGCGATCATTTTCT 402
Db 1 GGCTGGCAATGCTGTTATTTCCT 24

RESULT 98
US-10-719-956-456462
; Sequence 456462, Application US/10719956
```



```
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 456462
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-456462

Query Match          1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 76 GGGCGTTAAAGCTCTCGTGGCATT 99
Db 1 GGGCGTTAAAGCACTTGTGGCACT 24

RESULT 99
US-10-719-956-511569/c
; Sequence 511569, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 511569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-511569

Query Match          1.7%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 TCTGTAGGCAGCTGCCAC 755
Db 19 TCTGTAGGCAGCTGCCAC 1

RESULT 100
US-10-809-189-107033/c
; Sequence 107033, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107033
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-107033

Query Match          1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 626 GTTTTATTCTCAGCAATAGAC 647
Db 25 GTTTTATTCTCAGCCAGAGAC 4

RESULT 101
US-10-956-157-97217/c
; Sequence 97217, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97217
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97217

Query Match          1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 926 CTTATTAGAAATGCAGATCTG 947
Db 22 CTTGTTAGAAATGCAGAGTCTG 1

RESULT 102
US-10-956-157-97220/c
; Sequence 97220, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97220
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97220

Query Match          1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 926 CTTATTAGAAATGCAGATCTG 947
Db 23 CTTGTTAGAAATGCAGAGTCTG 2
```

Fri Aug 19 11:00:02 2005

```
; SEQ ID NO 262562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-262562

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 84.0%; Pred. No. 1.3e+02; Mismatches 4; Indels 0; Gaps 0;

QY 874 ATGCTATTAAAGTGTGCCACAG 898
    ||||| ||||| ||||| |||||
Db 1 ATGCTTTTCAAGTGTGCTCCACAG 25

RESULT 106
US-10-719-900-464383
; Sequence 464383, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 464383
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-464383

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 84.0%; Pred. No. 1.3e+02; Mismatches 4; Indels 0; Gaps 0;

QY 318 GATTTCCTGTTATCTTGTCTCGTGT 342
    ||||| ||||| ||||| |||||
Db 1 GACTTCATGTTATTTCTTGCTAGTTT 25

RESULT 107
US-10-809-189-125800
; Sequence 125800, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-125800

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 84.0%; Pred. No. 1.3e+02; Mismatches 4; Indels 0; Gaps 0;

; SEQ ID NO 262562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-262562

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 84.0%; Pred. No. 1.3e+02; Mismatches 4; Indels 0; Gaps 0;

QY 179 TTGCTCTGATTTTCCACGCCATCT 203
    ||||| ||||| ||||| |||||
Db 1 TTGCTCTGATTTTCCACGCCATCT 25

RESULT 105
US-10-719-900-262562
; Sequence 262562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
Qy 864 GTTGATGTCATGCTATTAAAGTG 888
| ||||| ||||| ||||| ||||| |||||
Db 1 GCTGTACTTCTGCTGTTAAAGTG 25

RESULT 108
US-10-956-157-97213/c
; Sequence 97213, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97213
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97213

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 922 GAGCTTATTAGAAATGCAGATCT 946
| || ||||| ||||| ||||| |||||
Db 25 GAAACTTGTAGAAATGCAGATCT 1

RESULT 109
US-10-956-157-314866
; Sequence 314866, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 314866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-314866

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 284 TTCTTCACTACTGGAATTTGTTT 308
| ||||| ||||| ||||| ||||| |||||
Db 1 TTCTTCACTACTGGAATTTGCTATT 25

RESULT 110
US-10-719-956-16848/c
; Sequence 16848, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719.956
; CURRENT FILING DATE: 2003-11-20
```

```
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-16848

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 374 GTGTTGGCAGCAATGCAGTCATTT 398
| ||||| ||||| ||||| ||||| |||||
Db 25 GGGCTGTCAGGCACTGCAGTCATTT 1

RESULT 111
US-10-719-956-133888
; Sequence 133888, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719.956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 133888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-133888

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 59 AGTTCGGGAGACATGGCGGCGTTA 83
| || ||||| ||||| ||||| |||||
Db 1 AGCTCCAGAGACTTGGCGGCGTTA 25

RESULT 112
US-10-719-956-231988
; Sequence 231988, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719.956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 231988
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-231988

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 32 CAGGAAGCCGGAAGCAGCCGCGCC 56
```



```
Db 1 AAGTTTCTTCCTTGTTGGCTG 23

RESULT 118
US-10-956-157-250112/c
; Sequence 250112, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250112
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-250112

Query Match 1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 104 TTCAGTGGGGCTATTGGACTGCAC 126
|||||
Db 23 TTCAGTGGGAGTATGGTCTGAC 1

RESULT 119
US-10-843-527-4769/c
; Sequence 4769, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 4769
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-4769

Query Match 1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 892 CCCACAGACCAAGAGCCTCAACA 914
|||||
Db 24 CCCACAGACCAAGAGCATCGAGA 2

RESULT 120
US-10-843-527-233408
; Sequence 233408, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
```

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; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 233408
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-233408

Query Match 1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 892 CCCACAGACCAAGAGCCTCAACA 914
|||||
Db 2 CCCACAGACCAAGAGCATCGAGA 24

RESULT 121
US-10-719-956-178976
; Sequence 178976, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 178976
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-178976

Query Match 1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 308 TCTCCCTTTGGATTTCCTGTTAT 330
|||||
Db 2 TCAGCCTCTGGTTTTCCTGTTAT 24

RESULT 122
US-08-779-457-30/c
; Sequence 30, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
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;
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-779-457-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 18 GCTGGGATGTCCTTAGA 1

RESULT 123
US-08-779-457-31
; Sequence 31, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodriguez, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-10-214-802-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18

RESULT 124
US-10-214-802-30/c
; Sequence 30, Application US/10214802
; Publication No. US20030004109A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/214,802
; FILING DATE: 06-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-97
; APPLICATION NUMBER: 60/
; FILING DATE: 08-Jan-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-10-214-802-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-779-457-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 18 GCTGGGATGTCCTTAGA 1

RESULT 123
US-08-779-457-31
; Sequence 31, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodriguez, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-10-214-802-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18

RESULT 124
US-10-214-802-30/c
; Sequence 30, Application US/10214802
; Publication No. US20030004109A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/214,802
; FILING DATE: 06-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-97
; APPLICATION NUMBER: 60/
; FILING DATE: 08-Jan-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-10-214-802-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 136 GCTGGGATGTCCTTAGA 153
Db 18 GCTGGGATGTCCTTAGA 1

RESULT 125
US-10-214-802-31
; Sequence 31, Application US/10214802
; Publication No. US20030004109A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/214,802
; FILING DATE: 06-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-97
; APPLICATION NUMBER: 60/
; FILING DATE: 08-Jan-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-214-802-31

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18

RESULT 126
US-10-921-710-30/c
; Sequence 30, Application US/10921710
; Publication No. US20050019325A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Matthews, William
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT
```

```
; TITLE OF INVENTION: DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN
; TITLE OF INVENTION: OBESE ANIMAL
; FILE REFERENCE: GENENT.53CP2C1
; CURRENT APPLICATION NUMBER: US/10/921,710
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 08/779457
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 60/064855
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/585005
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/667197
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide sequence
US-10-921-710-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 18 GCTGGGATGTCCTTAGA 1

RESULT 127
US-10-921-710-31
; Sequence 31, Application US/10921710
; Publication No. US20050019325A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Matthews, William
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT
; TITLE OF INVENTION: DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN
; FILE REFERENCE: GENENT.53CP2C1
; CURRENT APPLICATION NUMBER: US/10/921,710
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 08/779457
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 60/064855
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/585005
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/667197
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide sequence
US-10-921-710-31

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18
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; NUMBER OF SEQ ID NOS: 982914
COMMAND: micarray probe Sequence Listing Generator V 1.1

```



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RESULT 133
US-10-719-956-356718/c
; Sequence 356718, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-356718

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1019 CATCATCATAGAGAGTAAC 1039
Db      23 CAGCACCATAGAGAGTAAC 3

RESULT 134
US-10-719-956-427749/c
; Sequence 427749, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 427749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-427749

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      995 GTATGCACATGAAGATTGAG 1015
Db      25 GTAAGCACATGAAGATTGAG 5

RESULT 135
US-10-719-956-571667
; Sequence 571667, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 571667

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      921 AGAGCCCTTATTAGAAATGCAGAAAT 944
Db      24 AGAGCCATAGTTAAATGCAGAAAT 1

RESULT 136
US-09-841-366A-60/c
; Sequence 60, Application US/09841366A
; Patent No. US20020058265A1
; GENERAL INFORMATION:
; APPLICANT: Bacher, Jeffery W.
; APPLICANT: Flanagan, Laura
; APPLICANT: Nassif, Nadine
; TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN
; FILE REFERENCE: 16026-9287
; CURRENT APPLICATION NUMBER: US/09/841,366A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/663,020
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BAT-25 primer
US-09-841-366A-60

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      921 AGAGCCCTTATTAGAAATGCAGAAAT 944
Db      24 AGAGCCATAGTTAAATGCAGAAAT 1

RESULT 137
US-09-992-665-263
; Sequence 263, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-263

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;

US-10-719-956-356718/c
; Sequence 356718, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-356718

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1019 CATCATCATAGAGAGTAAC 1039
Db      23 CAGCACCATAGAGAGTAAC 3

RESULT 134
US-10-719-956-427749/c
; Sequence 427749, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 427749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-427749

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      995 GTATGCACATGAAGATTGAG 1015
Db      25 GTAAGCACATGAAGATTGAG 5

RESULT 135
US-10-719-956-571667
; Sequence 571667, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 571667

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      921 AGAGCCCTTATTAGAAATGCAGAAAT 944
Db      24 AGAGCCATAGTTAAATGCAGAAAT 1

RESULT 136
US-09-841-366A-60/c
; Sequence 60, Application US/09841366A
; Patent No. US20020058265A1
; GENERAL INFORMATION:
; APPLICANT: Bacher, Jeffery W.
; APPLICANT: Flanagan, Laura
; APPLICANT: Nassif, Nadine
; TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN
; FILE REFERENCE: 16026-9287
; CURRENT APPLICATION NUMBER: US/09/841,366A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/663,020
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BAT-25 primer
US-09-841-366A-60

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      921 AGAGCCCTTATTAGAAATGCAGAAAT 944
Db      24 AGAGCCATAGTTAAATGCAGAAAT 1

RESULT 137
US-09-992-665-263
; Sequence 263, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-263

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
```

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Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 834 CCAGGAAGCGCGGGTGGATCCCT 857
Db 1 CCAGTATGCCGGGATGATACCT 24

RESULT 138
US-10-314-810-60/c
; Sequence 60, Application US/10314810
; Publication No. US20030180758A1
; GENERAL INFORMATION:
; APPLICANT: Bacher, Jeffery W.
; APPLICANT: Flanagan, Laura
; APPLICANT: Nassif, Nadine
; TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN
; TITLE OF INVENTION: DIAGNOSIS OF TUMORS
; FILE REFERENCE: 16026-9267
; CURRENT APPLICATION NUMBER: US/10/314,810
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/841,366
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/663,020
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BAT-25 primer
US-10-314-810-60

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 921 AGAGCCTTATTAGAAATGCAGAT 944
Db 24 AGAGCCATAGTTAAATGCAGAT 1

RESULT 139
US-10-098-263B-87092/c
; Sequence 87092, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87092

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 652 CAAATTTAGATTATGTACTCAAA 675
Db 24 CAAATTTAACTATGTCTACTGAA 1

RESULT 140
US-10-719-900-143190
; Sequence 143190, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 143190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-143190

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 297 GAATGTGTTTCTGCTTGGAT 320
Db 2 GAAGTGTGTTTCTGCTATGTAT 25

RESULT 141
US-10-719-900-217495
; Sequence 217495, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 217495
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-217495

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 885 AGTGTGGCCACAGACCAAGGCC 908
Db 1 AGTGGGTTCACAGACCAATAGCC 24

RESULT 142
US-10-719-900-266991/c
; Sequence 266991, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 266991
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-266991

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   813 CTGAAGCAGCCCTTCATGACCA 836
     ||||| ||||| ||||| |||||
Db   25  CTGAGCTGCCTCATATGACCA 2

RESULT 143
US-10-719-900-646382
; Sequence 646382, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 646382
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-646382

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   517 GTATACATGTGCATCGGCATT 540
     ||||| ||||| ||||| |||||
Db   2  GTATACATGTCAATTGCACATT 25

RESULT 144
US-10-719-900-685910
; Sequence 685910, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 685910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-685910

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   750 TGGCACCTTATGAGTGCAATCGAA 773
     ||||| ||||| ||||| |||||
Db   2  TCCCACTGAAGCAGTGCAATGAA 25

RESULT 145
US-10-719-900-718042
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; ORGANISM: Mus musculus
US-10-719-900-876443

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 121 ACTGACTTTCTTATGCTGGGATG 144
      ||||| ||||| ||||| ||||| |||||
Db 2 ACTGACTTTCTTGTACTGGGCTG 25

RESULT 148
US-10-719-900-878694
; Sequence 878694, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 878694
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-878694

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 295 TGGAAATTCGTTTCTGCGTTGG 318
      ||||| ||||| ||||| ||||| |||||
Db 1 TGGAAATTCGTTTCTGCGTTGG 24

RESULT 149
US-10-719-900-884508
; Sequence 884508, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 884508
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-884508

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1068 TGGCTAAACCACTTAACCTCTCG 1091
      ||||| ||||| ||||| ||||| |||||
Db 1 TGGCAAATCACTTCACTCCCTG 24

RESULT 150
US-10-719-900-899808/c
; Sequence 899808, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 899808
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-899808

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGAAAGACTTCA 611
      ||||| ||||| ||||| ||||| |||||
Db 24 ATGTCACCTCTAAGAAACACTACA 1

RESULT 151
US-10-809-189-20048/c
; Sequence 20048, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20048
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-20048

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 957 TCTGACCCAGGACATTTTGATGA 980
      ||||| ||||| ||||| ||||| |||||
Db 25 TCTTGACCCAGACACTTTGGTGA 2

RESULT 152
US-10-956-157-97212/c
; Sequence 97212, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
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Fri Aug 19 11:00:02 2005

```
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-105776

Query Match
Best Local Similarity 1.6%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 398 TTCCTTACAAATTCAGGGTTTTC 421
DB 25 TTCGTTACAATTCACAGGTTTGC 2

RESULT 158
US-10-843-527-132401
; Sequence 132401, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132401
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-132401

Query Match
Best Local Similarity 1.6%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 398 TTCCTTACAAATTCAGGGTTTTC 421
DB 1 TTCGTTACAATTCACAGGTTTGC 24

RESULT 159
US-10-843-527-229503/c
; Sequence 229503, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 229503
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-229503

Query Match
Best Local Similarity 1.6%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 920 TAGAGCCTTATTAGAAATGCAGAA 943

; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-105776

Query Match
Best Local Similarity 1.6%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 398 TTCCTTACAAATTCAGGGTTTTC 421
DB 25 TTCGTTACAATTCACAGGTTTGC 2

RESULT 160
US-10-681-773-16943
; Sequence 16943, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-16943

Query Match
Best Local Similarity 1.6%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1043 ACACCCAACTTCCTTATCTTTCCA 1066
DB 1 ACTCCCAATCTCGTTATCTTTCCA 24

RESULT 161
US-10-681-773-16944
; Sequence 16944, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-16944

Query Match
Best Local Similarity 1.6%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1043 ACACCCAACTTCCTTATCTTTCCA 1066
DB 1 ACTCCCAATCTCGTTATCTTTCCA 24

RESULT 162
```

```
US-10-681-773-103264/c
; Sequence 103264, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 103264
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-103264
Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1000 CACATGAAGTTTCAGAGCATCA 1023
Db 24 CACTTAAACATTGAGAGCTTCA 1

RESULT 163
US-10-719-956-48483
; Sequence 48483, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48483
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-48483
Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 229 AAGAGTCACCTATGACTCAGATGC 252
Db 1 AAGGTCACCTAAGACTCGGACGC 24

RESULT 164
US-10-719-956-276484
; Sequence 276484, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 276484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-276484
Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 229 AAGAGTCACCTATGACTCAGATGC 252
Db 1 AAGGTCACCTAAGACTCGGACGC 24

RESULT 165
US-10-719-956-357405/c
; Sequence 357405, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 357405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-357405
Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 975 TGATGATGCCAAAGAGGTGTAT 998
Db 25 TGATGAGTCCAAACGAGTGTAT 2

RESULT 166
US-10-719-956-649616/c
; Sequence 649616, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 649616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-649616
Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 446 TTTAGCTGGGAGCAGTGTAGCAC 469
Db 1 TTTAGCTGGGAGCAGTGTAGCAC 469
```

Query Match 1.5%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 606 ACTTCATAGTAGGAGATGA 625
DB 20 ACTTCATAGGAGAGATGA 1

RESULT 169
US-09-911-088-1
; Sequence 1, Application US/09911088
; Patent No. US20020123145A1
; GENERAL INFORMATION:
; APPLICANT: OW, DAVID
; TITLE OF INVENTION: METHODS FOR THE REPLACEMENT, TRANSLLOCATION, AND
; FILE REFERENCE: 16313-0052
; CURRENT APPLICATION NUMBER: US/09/911,088
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 60/220,062
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-911-088-1

Query Match 1.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTCTTCTGCC 313
DB 5 CTGGAATTGTTCTTCTGCC 24

RESULT 170
US-10-913-085-1
; Sequence 1, Application US/10913085
; Publication No. US20050009182A1
; GENERAL INFORMATION:
; APPLICANT: OW, DAVID
; TITLE OF INVENTION: METHODS FOR THE REPLACEMENT, TRANSLLOCATION, AND
; FILE REFERENCE: 16313-0052
; CURRENT APPLICATION NUMBER: US/10/913,085
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/09/911,088
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 60/220,062
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-913-085-1

Query Match 1.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTCTTCTGCC 313
DB 5 CTGGAATTGTTCTTCTGCC 24

25 TTTAGCTGACAGCAAGGTAGCAC 2

RESULT 167
US-10-719-956-685651/c
; Sequence 685651, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 685651
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-685651

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 874 ATGCTATTAAAGTGTGGCCACA 897
DB 25 ATGCTGATACAGTGTGGTCCACA 2

RESULT 168
US-10-231-778-208/c
; Sequence 208, Application US/10231778
; Publication No. US20030126647A1
; GENERAL INFORMATION:
; APPLICANT: Bilodeau, Pierre
; APPLICANT: Chaudhury, Abdul M.
; APPLICANT: Dennis, Elizabeth S.
; APPLICANT: Koltunow, Anna M.G.
; APPLICANT: Luo, Ming
; APPLICANT: Peacock, William J.
; TITLE OF INVENTION: Method for inducing seed development by down-regulating
; FILE REFERENCE: 72-98A
; CURRENT APPLICATION NUMBER: US/10/231,778
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 09/398,237
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 60/101,184
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: AU PP6061
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: AU PP6062
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: AU PP6063
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: AU PQ1345
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: AU PQ1346
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer
US-10-231-778-208


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RESULT 171
US-10-032-585-4596/c
; Sequence 4596, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4596
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4596

Query Match          1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 477 TGATTACAGTCGATTGAATTTCT 499
|||||
Db 23 TGATTGCAGTCGTTGAAATTT 1

RESULT 172
US-10-751-736-44458/c
; Sequence 44458, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44458
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-44458

Query Match          1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 281 TATTTCTTCACTACTGGAATT 301
|||||
Db 21 TCTTTCTTCAACACTGGAATT 1

RESULT 173
US-09-990-940-23/c
; Sequence 23, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
```

```
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TGR342Right PCR
US-09-990-940-23

Query Match          1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 117 TTGGACTGACTTTTCTTATGC 137
|||||
Db 22 TTGGAATGCCCTTTCTTATTC 2

RESULT 174
US-10-681-199-23
; Sequence 23, Application US/10681199
; Publication No. US20040138441A1
; GENERAL INFORMATION:
; APPLICANT: KERE, Juha
; TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
; FILE REFERENCE: 0933-0214P
; CURRENT APPLICATION NUMBER: US/10/681,199
; CURRENT FILING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER EKNI-1R
US-10-681-199-23

Query Match          1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1000 CACATGAAGTTTCGAGAAGCA 1020
|||||
Db 1 CACACCAAGTTTGAGAACCA 21

RESULT 175
US-10-913-280-633/c
; Sequence 633, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
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Fri Aug 19 11:00:02 2005

APPLICANT: Gimms, Edward I.
APPLICANT: Galdzicka, Marzena
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
FILE REFERENCE: 07917-238001
CURRENT APPLICATION NUMBER: US/10/913,280
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 60/493,238
PRIOR FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US 60/568,958
PRIOR FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 920
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 633
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-10-913-280-633

Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 91 CGTGGCATTATCTTCAGTGG 111
||||| ||||| ||||| |||||
DB 21 CGTGGCCTTCTCCCTCAGTGG 1

RESULT 176
US-11-038-360-23/c
Sequence 23, Application US/11038360
Publication No. US20050170397A1
GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Zhao, Jiayang
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: An, Songzhu
APPLICANT: Dai, Kang
APPLICANT: Gupte, Jamila S.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Novel Receptors
FILE REFERENCE: 018781-007410US
CURRENT APPLICATION NUMBER: US/11/038,360
CURRENT FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US/09/990,940
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/252,841
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/257,636
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/261,377
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/279,554
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/280,696
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 23
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:TGR342Right PCR
OTHER INFORMATION: expression profiling primer
US-11-038-360-23

Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 117 TTGGACTGACTTTTCTTATGC 137
||||| ||||| ||||| |||||
DB 22 TTGGAATGCTTTTCTTATTC 2

RESULT 177
US-10-774-721-45/c
Sequence 45, Application US/10774721
Publication No. US20050009042A1
GENERAL INFORMATION:
APPLICANT: JOCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: UHLMANN, Eugen
TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
FILE REFERENCE: FRAV2003/0005 US NP
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/461,005
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patent In version 3.1
SEQ ID NO 45
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial
US-10-774-721-45

Query Match 1.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 CTTGCTCGTGTGGCTG 347
||||| ||||| ||||| |||||
DB 16 CTTGCTCGTGTGGCTG 1

RESULT 178
US-10-339-793-47
Sequence 47, Application US/10339793
Publication No. US20030180764A1
GENERAL INFORMATION:
APPLICANT: Lynx Therapeutics, Inc.
APPLICANT: Shang, Jin
APPLICANT: Bowen, Benjamin
TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
FILE REFERENCE: 37-000310US
CURRENT APPLICATION NUMBER: US/10/339,793
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 443
SOFTWARE: Patent In version 3.1
SEQ ID NO 47
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-339-793-47

Query Match 1.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGTTGT 996
||||| ||||| ||||| |||||
DB 1 GATCCAAAGGAGTTGT 16

RESULT 179

US-10-159-339-21
; Sequence 21, Application US/10159339
; Publication No. US20030166540A1

GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
; TITLE OF INVENTION: HGPBHM30
; FILE REFERENCE: D0169NP
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US/10/159,339
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21

LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-339-21

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1092 GGTGTACCTGCTCAT 1107
|||||
Db 5 GGTGTACCTGCTCAT 20

RESULT 180

US-10-280-183A-284/c
; Sequence 284, Application US/10280183A
; Publication No. US20040081964A1

GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETENERS

FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 284

LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-280-183A-284

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1092 GGTGTACCTGCTCAT 1107
|||||
Db 16 GGTGTACCTGCTCAT 1

RESULT 181

US-10-280-183A-286/c
; Sequence 286, Application US/10280183A
; Publication No. US20040081964A1

GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.

; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETENERS
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 286

LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-280-183A-286

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1092 GGTGTACCTGCTCAT 1107
|||||
Db 16 GGTGTACCTGCTCAT 1

RESULT 182

US-10-923-516-391
; Sequence 391, Application US/10923516
; Publication No. US20050176025A1

GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of B-Cell CLL/Lymphoma-2
; TITLE OF INVENTION: (BCL2) Gene Expression Using Short Interfering Nucleic Acid (si

FILE REFERENCE: 400/173 (MBHB02-714-F)
; CURRENT APPLICATION NUMBER: US/10/923,516
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US 03/04908
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/396,905
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 882
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 391

```

; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/160,807
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-807-48

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGGATGCTTGGAGA 801
||| |||||
DB 1 TTGTAGATGTGCTTGGAGA 19

RESULT 185
US-10-160-807-196/C
; Sequence 196, Application US/10160807
; Publication No. US20030224514A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/160,807
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 196
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-160-807-196

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGGATGCTTGGAGA 801
||| |||||
DB 20 TTGTAGATGTGCTTGGAGA 2

RESULT 186
US-10-655-847-48
; Sequence 48, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/655,847
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US/10/160,807
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA

```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-48

Query Match          1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 783 TTGGGGATGTCCTGGAGA 801
    ||| ||||| ||||| |||||
Db 1 TTGTAGATGTCCTGGAGA 19

RESULT 187
US-10-655-847-196/c
; Sequence 196, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Preter
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/655,847
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US/10/160,807
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 196
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-655-847-196

Query Match          1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 783 TTGGGGATGTCCTGGAGA 801
    ||| ||||| ||||| |||||
Db 20 TTGTAGATGTCCTGGAGA 2

RESULT 188
US-09-816-814-7/c
; Sequence 7, Application US/09816814
; Publication No. US20030027136A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-816-814-7

Query Match          1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 GCCGGACGACCGCGGCC 56
    ||| ||||| ||||| |||||
Db 21 GCTGGAACGACCGCGGCC 3

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-48

Query Match          1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 783 TTGGGGATGTCCTGGAGA 801
    ||| ||||| ||||| |||||
Db 1 TTGTAGATGTCCTGGAGA 19

RESULT 189
US-10-786-720-15221/c
; Sequence 15221, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15221
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-786-720-15221

Query Match          1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 932 AGAAATGCAGAAATCTGAAG 950
    ||| ||||| ||||| |||||
Db 20 AGACATGCAGAAATCTCAAG 2

RESULT 190
US-10-751-736-45418/c
; Sequence 45418, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45418
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-45418

Query Match          1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 283 TTTCTTCACTACTGGAATT 301
    ||| ||||| ||||| |||||
Db 20 TTTCTTCACTACTGGAATT 2

RESULT 191
US-10-032-585-4031/c
; Sequence 4031, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
```

```

; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032.585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4031
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Candida albicans
; OTHER INFORMATION: P451 vacA-derived probe
US-10-032-585-4031

Query Match      1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAA 355
Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 192
US-10-882-104-382/c
; Sequence 382, Application US/10882104
; Publication No. US20050079619A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Targets Discovery
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/10/882,104
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: US/09/792,024
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer
US-10-882-104-382

Query Match      1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAA 355
Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 193
US-10-035-978A-29
; Sequence 29, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
; TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; FILE REFERENCE: INNOG2.001C1
; CURRENT APPLICATION NUMBER: US/10/035.978A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/284,725
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: EP 97870133.2

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; PRIOR FILING DATE: 1997-09-09
; PRIOR APPLICATION NUMBER: EP 96870131.8
; PRIOR FILING DATE: 1996-10-16
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P451 vacA-derived probe
US-10-035-978A-29

Query Match      1.4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 103 CTTCACTGGGGCTATTGG 120
Db 2 CTTTAGTRGGGYTATTGG 19

RESULT 194
US-10-263-594-29
; Sequence 29, Application US/10263594
; Publication No. US20030175746A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: Probes, methods and kits for detection and
; TITLE OF INVENTION: typing of Helicobacter pylori nucleic acids in biological
; samples.
; NUMBER OF SEQUENCES: 280
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/263,594
; APPLICATION NUMBER: US/10/263,594
; FILING DATE: 02-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,725
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP96/870131.8
; FILING DATE: 16-OCT-1996
; APPLICATION NUMBER: PCT/EP97/05614
; FILING DATE: 10-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel B.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: INNOG2.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 760-0404
; TELEFAX: (949) 760-9395
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-263-594-29

```

```

Query Match      1.4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 103 CTCAGTGGGCTATTGG 120
    |||||:|||||
Db 2 CTTTAGTRGGGYATTGG 19

RESULT 195
US-10-795-667-93
; Sequence 93, Application US/10795667
; Publication No. US20040209298A1
; GENERAL INFORMATION:
; APPLICANT: KAMBEROV, EMMANUEL
; APPLICANT: SUN, TONG
; APPLICANT: BRUENING, ERIC EGON
; APPLICANT: PINTER, JONATHON H.
; APPLICANT: SLEPTSOVA, IRINA
; APPLICANT: KURIHARA, TAKAO
; APPLICANT: MAKAROV, VLADIMIR L.
; TITLE OF INVENTION: AMPLIFICATION AND ANALYSIS OF WHOLE GENOME AND WHOLE
; TITLE OF INVENTION: TRANSCRIPTOME LIBRARIES GENERATED BY A DNA
; TITLE OF INVENTION: POLYMERIZATION PROCESS
; FILE REFERENCE: RUBC:022US
; CURRENT APPLICATION NUMBER: US/10/795,667
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/453,060
; PRIOR FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 93
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-795-667-93

Query Match      1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 297 GAATTGTTGTTCTGCGCTTTGG 318
    |||||:|||||
Db 1 GAATTTGGTTCTTGCTTTGG 22

RESULT 196
US-10-797-333A-95
; Sequence 95, Application US/10797333A
; Publication No. US20040209299A1
; GENERAL INFORMATION:
; APPLICANT: PINTER, JONATHON H.
; APPLICANT: KURIHARA, TAKAO
; APPLICANT: SLEPTSOVA, IRINA
; APPLICANT: BRUENING, ERIC EGON
; APPLICANT: ZIEHLER, WILLIAM
; APPLICANT: MAKAROV, VLADIMIR L.
; TITLE OF INVENTION: IN VITRO DNA IMMORTALIZATION AND WHOLE GENOME
; TITLE OF INVENTION: AMPLIFICATION USING LIBRARIES GENERATED FROM RANDOMLY
; TITLE OF INVENTION: FRAGMENTED DNA
; FILE REFERENCE: RUBC:021US
; CURRENT APPLICATION NUMBER: US/10/797,333A
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/453,071
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 95
; LENGTH: 22

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-797-333A-95

Query Match      1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 297 GAATTGTTGTTCTGCGCTTTGG 318
    |||||:|||||
Db 1 GAATTTGGTTCTTGCTTTGG 22

RESULT 197
US-10-349-143-11660
; Sequence 11660, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11660
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-21246 for SEQ 3795, in compl
US-10-349-143-11660

Query Match      1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 104 TTCAGTGGGCTATTGG 120
    |||||:|||||
Db 2 TTCAGTGGGCTATTGG 18

RESULT 198
US-10-281-479A-9
; Sequence 9, Application US/10281479A
; Publication No. US2003013932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THE
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6

```

APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
FILE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U7 US/10/286,132A
CURRENT APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 20
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-9

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
|||||
Db 3 GTTGTATGCACATGAGA 19

RESULT 199
US-10-275-180A-9
Sequence 9, Application US/10275180A
Publication No. US20030190687A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Koopman, William J.
APPLICANT: Kimberly, Robert P.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U5
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
US-10-275-180A-9

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
|||||
Db 3 GTTGTATGCACATGAGA 19

RESULT 200
US-10-286-132A-9
Sequence 9, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Lobuglio, Albert S.

APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
FILE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U7 US/10/286,132A
CURRENT APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 20
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-9

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
|||||
Db 3 GTTGTATGCACATGAGA 19

RESULT 201
US-10-688-706-2397
Sequence 2397, Application US/10688706
Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Brochard, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 2397
LENGTH: 20
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: human GFAT antisense
US-10-688-706-2397

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 553 TTAATATGCTGGGTTT 569
|||||
Db 4 TTAATAAGCTGGGTTT 20

RESULT 202
US-10-688-706-2465
Sequence 2465, Application US/10688706
Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Brochard, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706


```
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2455
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2465

Query Match      1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      553 TTAATATGCTGGGTTTT 569
Db      2 TTAATAAGCTGGGTTTT 18

RESULT 203
US-10-688-706-2492
; Sequence 2492, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2492
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2492

Query Match      1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      553 TTAATATGCTGGGTTTT 569
Db      3 TTAATAAGCTGGGTTTT 19

RESULT 204
US-10-688-706-2639
; Sequence 2639, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2639
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial

; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2455
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2639

Query Match      1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      553 TTAATATGCTGGGTTTT 569
Db      1 TTAATAAGCTGGGTTTT 17

RESULT 205
US-09-817-913-33
; Sequence 33, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfills, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-33

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      743 AGCAGCTGCCACCTTATGC 762
Db      1 AGCCAGCTGCCATTGATGC 20

RESULT 206
US-09-817-538-33
; Sequence 33, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfills, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-33

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      743 AGCAGCTGCCACCTTATGC 762
Db      1 AGCCAGCTGCCATTGATGC 20
```

Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 207
US-10-052-390B-18
; Sequence 18, Application US/10052390B
; Publication No. US20030148970A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavioie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-18

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGCCAGCTGCCACTTGATGC 762
||| ||||| ||||| |||||

Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 208
US-10-051-819B-18
; Sequence 18, Application US/10051819B
; Publication No. US20030152557A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavioie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-18

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGCCAGCTGCCACTTGATGC 762
||| ||||| ||||| |||||

Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 209
US-10-448-836-219
; Sequence 219, Application US/10448836
; Publication No. US20030207313A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,836
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 219
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
; OTHER INFORMATION: diernhoferi
US-10-448-836-219

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 998 TGCACATGAAAGTTTGAGAA 1017
||||| ||||| ||||| |||||

Db 1 TGCACACAAACTTTGAGAA 20

RESULT 210
US-10-167-034-32/c
; Sequence 32, Application US/10167034
; Publication No. US20030228690A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1 EXPRESSION
; FILE REFERENCE: PTS-0003
; CURRENT APPLICATION NUMBER: US/10/167,034
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 142
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-167-034-32

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCTCTCATGACCCA 836
||| ||||| ||||| |||||

Db 20 AGGAGGCTCTCTATGACCCA 1

RESULT 211

US-10-167-034-103
; Sequence 103, Application US/10167034
; Publication No. US20030228690A1
; GENERAL INFORMATION:

; APPLICANT: Brenda P. Baker
; APPLICANT: Susan M. Preier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1 EXPRESSION
; FILE REFERENCE: PTS-0003
; CURRENT APPLICATION NUMBER: US/10/167,034
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 142
; SEQ ID NO 103

; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-167-034-103

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 817 AGCAGGCCTCTCTATGACCCA 836

Db 1 AGGAGGCTCTCTATGACCCA 20

RESULT 212

US-10-448-914A-219
; Sequence 219, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:

; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,914A
; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 219

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
US-10-448-914A-219

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 998 TGCACATGAAGTTTGAGAA 1017

||||| ||| |||||||

Db 1 TGCACAACAACACTTTGAGAA 20

RESULT 213

US-10-289-762-6064/c
; Sequence 6064, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:

; APPLICANT: Griffsais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6064

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6064

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 459 AGTGGTAGCACTTTATTCTG 478

Db 20 AGCGGTAGCAGTTTCTCTG 1

RESULT 214

US-10-210-429-24/c
; Sequence 24, Application US/10210429
; Publication No. US20040023379A1
; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION
; FILE REFERENCE: PTS-0048
; CURRENT APPLICATION NUMBER: US/10/210,429
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 24

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-429-24

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 801 AGCGAGATAACGCTGAAGCA 820

Db 20 AGCGAGAAACCCCTGAAGGA 1

RESULT 215

US-10-210-429-95
; Sequence 95, Application US/10210429
; Publication No. US20040023379A1
; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION
; FILE REFERENCE: PTS-0048
; CURRENT APPLICATION NUMBER: US/10/210,429
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 95

Fri Aug 19 11:00:02 2005

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-210-429-95

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 801 AGGCAGATAAGCCTGAAGCA 820
Db 1 AGGCAGAAAACCTGAAGCA 20

RESULT 216
US-10-189-818B-30
; Sequence 30, Application US/10189818B
; Publication No. US20040072770A1
; GENERAL INFORMATION:
; APPLICANT: ZUOMEI, LI
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACETYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-30

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGGCAGCTGCCACTTGAUC 20

RESULT 217
US-10-673-886A-9/c
; Sequence 9, Application US/10673886A
; Publication No. US20040132139A1
; GENERAL INFORMATION:
; APPLICANT: GENODYSSEE
; TITLE OF INVENTION: New Polynucleotides and Polypeptides of the IFNalpha-21 Gene
; FILE REFERENCE: BIF022965 PCT
; CURRENT APPLICATION NUMBER: US/10/673,886A
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: FR 0 104 404
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-673-886A-9

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 608 TTCATAAGTAGGAGATGAGT 627
Db 20 TTCCCAAGTAGCAGATGAGT 1

RESULT 218
US-10-870-587-33
; Sequence 33, Application US/10870587
; Publication No. US20040266718A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/10/870,587
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US/09/817,913
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-870-587-33

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGGCAGCTGCCACTTGTATGC 20

RESULT 219
US-10-913-280-249/c
; Sequence 249, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Ginns, Edward I.
; APPLICANT: Galdzicka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 07917-238001
; CURRENT APPLICATION NUMBER: US/10/913,280
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-913-280-249

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 92 GTGGCATTATCCTTCAGTGC 111
Db 20 GTGGCCTTCTCCCTCAGTGC 1
```

```
RESULT 220
US-10-498-505A-18
; Sequence 18, Application US/10498505A
; Publication No. US20050090642A1
; GENERAL INFORMATION:
; APPLICANT: MIYAWAKI, Atsushi
; APPLICANT: KARASAWA, Satoshi
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: P25481
; CURRENT APPLICATION NUMBER: US/10/498.505A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/JP02/13363
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-498-505A-18

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 497 TCTTAGAACTCATCTATCT 516
Db 1 TCTTCGAACTCAAACTTCT 20

RESULT 221
US-10-831-901A-14585
; Sequence 14585, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL000808US)
; CURRENT APPLICATION NUMBER: US/10/831.901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14585
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14586

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1004 TGAAGTTTGAGAGCATCA 1023
Db 1 TGACAGTTTGAAGCAACAT 20

RESULT 223
US-10-831-901A-15629
; Sequence 15629, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
```

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; OTHER INFORMATION: Antisense compound
US-10-831-901A-14585

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1005 GAAAGTTTGAGAGCATCAT 1024
Db 1 GACAGTTTGAAGCAACAT 20

RESULT 222
US-10-831-901A-14586
; Sequence 14586, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL000808US)
; CURRENT APPLICATION NUMBER: US/10/831.901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14586
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14586

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1004 TGAAGTTTGAGAGCATCA 1023
Db 1 TGACAGTTTGAAGCAACAT 20

RESULT 223
US-10-831-901A-15629
; Sequence 15629, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
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; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15629
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-15629

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1016 AAGCATCATCATGAGAGT 1035
Db 1 AAGATCATCATGAGAAAT 20

RESULT 224
US-10-831-901A-26184/c
; Sequence 26184, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26184
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26186

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 320 TTTCCTGTTATTCTTGCTG 339
Db 20 TTTCGTGGTATTCTTGCTAG 1

RESULT 226
US-10-831-901A-26187/c
; Sequence 26187, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26186
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26186

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 320 TTTCCTGTTATTCTTGCTG 339
Db 20 TTTCGTGGTATTCTTGCTAG 1

RESULT 226
US-10-831-901A-26187/c
; Sequence 26187, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26186
```

```

; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL000808)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 3063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26187

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      321  TTCCTGTTATCTTCCTCGT 340
          ||| ||| ||| ||| ||| ||| ||| |||
Db      20  TTCGTGGTATCTTCCTAGT 1

RESULT 227
US-10-831-901A-26489/c
; Sequence 26489, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL000808)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770

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; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26489
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26489

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      658  TAGATTATGTTACTCAAAATT 677
          ||| ||| ||| ||| ||| ||| ||| |||
Db      20  TGGATTATGTTACTACAATT 1

RESULT 228
US-10-257-158A-4773/c
; Sequence 4773, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Zirvi, Monib
; APPLICANT: Gerry, Norman P.
; APPLICANT: Favis, Reyna
; APPLICANT: Kliman, Richard
; TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC AC
; TITLE OF INVENTION: SEQUENCE DIFFERENCES USING LIGASE DETECTION REACTION
; FILE REFERENCE: 19603/2834
; CURRENT APPLICATION NUMBER: US/10/257,158A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/US01/10958
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/197,271
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 9544
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4773
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
US-10-257-158A-4773

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      767  CATCGAAACCTTTGCTTGG 786
          ||| ||| ||| ||| ||| ||| ||| |||
Db      20  CATCGACACCGTTTGCTTCG 1

RESULT 229
US-10-786-720-7299
; Sequence 7299, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

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Query Match 1.4%; Score 15.2; DB 1; Length 21;

RESULT 234
US-10-913-280-632/c

Fri Aug 19 11:00:02 2005

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-749-709-6

Query Match      1.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 934 AAATGCAATCTGAAGC 951
Db 1 AAATGCAATCTGAAGC 18

RESULT 239
US-09-734-847A-16
; Sequence 16, Application US/09734847A
; Patent No. US20020049173A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Monia, Brett P.
; APPLICANT: Freix, Susan
; APPLICANT: McKay, Robert
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation of mRNA
; FILE REFERENCE: ISPH-0524
; CURRENT APPLICATION NUMBER: US/09/734,847A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-734-847A-16

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 240
US-09-800-629A-152
; Sequence 152, Application US/09800629A
; Patent No. US20020128216A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G.
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/09/800,629A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/07318
; PRIOR FILING DATE: 2000-03-17

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-800-629A-152

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 241
US-09-858-152A-9/c
; Sequence 9, Application US/09858152A
; Publication No. US2003004419A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: Marchetti, Antonio
; APPLICANT: Buttitta, Fianna
; APPLICANT: Smith, Gilbert H.
; APPLICANT: Callahan, Robert
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6
; FILE REFERENCE: 4239-59122
; CURRENT APPLICATION NUMBER: US/09/858,152A
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-858-152A-9

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 926 CTTATTAGAAATGCAGAA 943
Db 20 CTAATTAATAAATGCAGAA 3

RESULT 242
US-10-002-974-52/c
; Sequence 52, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Inohara, Naohiro
; APPLICANT: Nunez, Gabriel
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-002-974-52

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      784 TGGGATGTGCTTGAGA 801
      |||||
Db      18 TGGGATGTGTTGAAGA 1

RESULT 243
US-10-012-984-68/c
; Sequence 68, Application US/10012984
; Publication No. US20030118561A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
; FILE REFERENCE: RTS-0334
; CURRENT APPLICATION NUMBER: US/10/012,984
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-012-984-68

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      418 TTGCTTATATTGGAAG 435
      |||||
Db      18 TTGCTTATATTGGAAG 1

RESULT 244
US-10-444-206-314/c
; Sequence 314, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 314
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-444-206-314
; Sequence 314, Application US/10673523
; Publication No. US20040110713A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
; FILE REFERENCE: RTS-0334
; CURRENT APPLICATION NUMBER: US/10/673,523
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US/10/012,984
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-673-523-68

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      418 TTCCCTTATATTGGAAG 435
      |||||
Db      18 TTGCTTATATTGGAAG 1

RESULT 247
```

```
US-10-317-478-40/c
; Sequence 40, Application US/10317478
; Publication No. US20040115636A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF INTERLEUKIN 18 EXPRESSION
; FILE REFERENCE: PTS-0025
; CURRENT APPLICATION NUMBER: US/10/317,478
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
;
US-10-317-478-40
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 748 GCTGCCACCTTATGCAGT 765
Db 20 GCTGCCACCTGTCGAGT 3

RESULT 248
US-10-317-478-96
; Sequence 96, Application US/10317478
; Publication No. US20040115636A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF INTERLEUKIN 18 EXPRESSION
; FILE REFERENCE: PTS-0025
; CURRENT APPLICATION NUMBER: US/10/317,478
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
;
US-10-317-478-96
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 748 GCTGCCACCTTATGCAGT 765
Db 1 GCTGCCACCTGTCGAGT 18

RESULT 249
US-10-679-532-152
; Sequence 152, Application US/10679532
; Publication No. US20040121376A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G.
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muchiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/10/679,532
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/800,629A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/07318

US-10-679-532-152
; Sequence 152, Application US/10679532
; Publication No. US20040121376A1
; GENERAL INFORMATION:
; APPLICANT: Christians, Frederick C.
; TITLE OF INVENTION: Synthetic Tag Genes
; FILE REFERENCE: 3502.1
; CURRENT APPLICATION NUMBER: US/10/619,739
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,530
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 2068
; SOFTWARE: FastSeq for Windows Version 4.0

US-10-619-739-1118
; Sequence 1118, Application US/10619739
; Publication No. US2004017519A1
; GENERAL INFORMATION:
; APPLICANT: Christians, Frederick C.
; TITLE OF INVENTION: Synthetic Tag Genes
; FILE REFERENCE: 3502.1
; CURRENT APPLICATION NUMBER: US/10/619,739
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,530
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 2068
; SOFTWARE: FastSeq for Windows Version 4.0

US-10-783-415-9/c
; Sequence 9, Application US/10783415
; Publication No. US20040141918A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Marchetti, Antonio
; APPLICANT: Buttitta, Flamma
; APPLICANT: Smith, Gilbert H.
; APPLICANT: Callahan, Robert
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6
; FILE REFERENCE: 4239-59122
; CURRENT APPLICATION NUMBER: US/10/783,415
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 09/856,152
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
;
US-10-783-415-9
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 CTTATTAGAAATGCAGAA 943
Db 20 CTAATTAAATGCAGAA 3

RESULT 251
US-10-619-739-1118
; Sequence 1118, Application US/10619739
; Publication No. US2004017519A1
; GENERAL INFORMATION:
; APPLICANT: Christians, Frederick C.
; TITLE OF INVENTION: Synthetic Tag Genes
; FILE REFERENCE: 3502.1
; CURRENT APPLICATION NUMBER: US/10/619,739
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,530
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 2068
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 1118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-739-1118

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 597 TCATGTAGTACGGTGCT 714
|||||
Db 2 TCATGTAGTGACAGTGCT 19

RESULT 252

US-10-659-473-47
; Sequence 47, Application US/10659473
; Publication No. US20040197906A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA REGULATORY SUBUNIT RII BETA EXPRESSION
; FILE REFERENCE: RTS-0218
; CURRENT APPLICATION NUMBER: US/10/659,473
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/915,485A
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-659-473-47

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 663 TATGTACTCAAAATATG 680
|||||
Db 3 TATGTACTGACATTATG 20

RESULT 253

US-10-641-962-314/c
; Sequence 314, Application US/10641962
; Publication No. US20040235164A1
; GENERAL INFORMATION:

; APPLICANT: Bennett et al.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: 30566/39578
; CURRENT APPLICATION NUMBER: US/10/641,962
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 314
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-641-962-314

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 640 AAATAGACCTGCTCAATT 657
|||||
Db 20 AAATAGACCTCTCAATT 3

RESULT 254

US-10-773-678-222/c
; Sequence 222, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:

; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 222
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-222

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 548 GAAATTTAATATGCTGGG 565
|||||
Db 18 GAAATTTAATATGCTGGG 1

RESULT 255

US-10-831-901A-15630
; Sequence 15630, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Maguire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10

Fri Aug 19 11:00:02 2005

```
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15630
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15630

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1016 AAGCATCATCATAGAGAA 1033
    ||| ||||| |||||
Db 2 AAGATCATCATGGAGAA 19

RESULT 256
US-10-831-901A-15631
; Sequence 15631, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-04-30
; PRIOR FILING DATE: 2003-04-30
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-06-10
; PRIOR FILING DATE: 2003-06-10
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15631
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15631

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1016 AAGCATCATCATAGAGAA 1033
    ||| ||||| |||||
Db 3 AAGATCATCATGGAGAA 20

RESULT 257
```

```
US-10-831-901A-25596
; Sequence 25596, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-04-30
; PRIOR FILING DATE: 2003-04-30
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-06-10
; PRIOR FILING DATE: 2003-06-10
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25596
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-25596

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 718 AGAAATATATTAACGCA 735
    ||||| ||||| |||||
Db 1 AGAAATATATCAAGGCA 18

RESULT 258
US-10-831-901A-25597
; Sequence 25597, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
```

; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25597
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-25597

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 718 AGAAATATATTAACGCA 735
|||
Db 2 AGAAATATATCAAGGCA 19

RESULT 259
US-10-831-901A-25598
; Sequence 25598, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25598
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-25598

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 718 AGAAATATATTAACGCA 735
|||
Db 3 AGAAATATATCAAGGCA 20

RESULT 260
US-10-831-901A-26089/c
; Sequence 26089, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26089
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26089

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 993 TTGTATGCACATGAAGT 1010
|||
Db 18 TTGTAAGCAACAAGT 1

RESULT 261
US-10-831-901A-26090/c
; Sequence 26090, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

```

;
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26091

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      993 TTGTATGCACATGAAGT 1010
      ||||| ||||| ||||| |||||
Db      20 TTGTAAGCACAGAAGT 3

RESULT 263
US-10-831-901A-26185/c
; Sequence 26185, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26185

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      320 TTTCCTGTTATTCTTGCT 337
      ||||| ||||| ||||| |||||
Db      19 TTTCGTGGTATTCTTGCT 2

RESULT 264
US-10-831-901A-26490/c
; Sequence 26490, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26091

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      993 TTGTATGCACATGAAGT 1010
      ||||| ||||| ||||| |||||
Db      19 TTGTAAGCACAGAAGT 2

RESULT 262
US-10-831-901A-26091/c
; Sequence 26091, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26090

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      993 TTGTATGCACATGAAGT 1010
      ||||| ||||| ||||| |||||
Db      19 TTGTAAGCACAGAAGT 2
```



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; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: IS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26490
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26490

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 GATTATGTTACTCAAAATT 677
Db 19 GATTATGTTACTCAAAATT 2

RESULT 265
US-10-831-901A-26491/c
; Sequence 26491, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: IS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
```

```
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26491
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26491

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 GATTATGTTACTCAAAATT 677
Db 20 GATTATGTTACTCAAAATT 3

RESULT 266
US-10-956-373-29
; Sequence 29, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL Erbb-2 POLYPEPTIDES AND KITS AND
; TITLE OF INVENTION: METHODS USING SAME
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-956-373-29

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 359 GGAGCCTGCGGCCTTG 376
Db 3 GGAGCCTGCGGCCTTG 20

RESULT 267
US-10-627-253A-299
; Sequence 299, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
```

Fri Aug 19 11:00:02 2005

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; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-299

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
   ||||| ||||| |||||
Db 4 AATCACTCAACCTCTCTG 21

RESULT 268
US-10-627-253A-300/c
; Sequence 300, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 300
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-300

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
   ||||| ||||| |||||
Db 4 AATCACTCAACCTCTCTG 21

RESULT 269
US-10-627-253A-301
; Sequence 301, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24

; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-301

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
   ||||| ||||| |||||
Db 4 AATCACTMAACCTCTCTG 21

RESULT 270
US-10-627-253A-302/c
; Sequence 302, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 302
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-302

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
   ||||| ||||| |||||
Db 18 AATCACTMAACCTCTCTG 1

RESULT 271
US-10-627-253A-303
; Sequence 303, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
```

```
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 303
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-303

Query Match          1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTAAACCTCTCTG 21
|||||
|

RESULT 272
US-10-627-253A-304/c
; Sequence 304, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: MORHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 304
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-304

Query Match          1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTAAACCTCTCTG 1
|||||
|

RESULT 273
US-10-786-720-15220/c
; Sequence 15220, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
```

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; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15220
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-786-720-15220

Query Match          1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 933 GAAATGCAGAAATCTGAAG 950
Db 21 GACATGCAGAAATCTCAAG 4
|||||
|

RESULT 274
US-10-786-720-15222
; Sequence 15222, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15222
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
; US-10-786-720-15222

Query Match          1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 72.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 933 GAAATGCAGAAATCTGAAG 950
Db 1 GACAUGCAGAAUCUCAAG 18
|||||
|

RESULT 275
US-10-751-736-29451
; Sequence 29451, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29451
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
; US-10-751-736-29451

Query Match          1.3%; Score 14.8; DB 1; Length 21;
```

Fri Aug 19 11:00:02 2005

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Best Local Similarity 44.4%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 8; Conservative 8; Mismatches 2;

QY 495 TTCTTAGAAGCTCATACT 512
Db 1 UUUUUAAGAUUCUUAACU 18

RESULT 276
US-10-751-736-31083/c
; Sequence 31083, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31083
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-31083

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 597 TTAAGAAAGACTTCATAA 614
Db 18 TCAGAAAGACGTCATAA 1

RESULT 277
US-10-751-736-45419/c
; Sequence 45419, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45419
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-45419

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 283 TTCTTCACACTGGAAAT 300
Db 18 TTCTTCACACTGGAAAT 1

RESULT 278
US-10-484-577-293
; Sequence 293, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
; TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGT1A
; FILE REFERENCE: F2285PCT-1
; CURRENT APPLICATION NUMBER: US/10/484,577
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/08220
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: EP 01 11 7608.8
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: EP 02011710.7
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 683
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 293
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-484-577-293

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTAAACCTCTCTG 21

RESULT 279
US-10-484-577-294/c
; Sequence 294, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
; TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGT1A
; FILE REFERENCE: F2285PCT-1
; CURRENT APPLICATION NUMBER: US/10/484,577
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/08220
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: EP 01 11 7608.8
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: EP 02011710.7
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 683
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 294
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-484-577-294

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTAAACCTCTCTG 1

RESULT 280
US-10-484-577-295
; Sequence 295, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft


```

/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aeomica Sequence Listing Engine
/ SEQ ID NO 2565
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108-2565

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 743 AGGCAGCTGCCACCTT 758
DB 17 AGGCAGCTGCCGCCTT 2

RESULT 285
US-09-866-108-2566/c
/ Sequence 2566, Application US/09866108
/ Patent No. US2002004800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2566
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2566

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e-02;
Matches 15; Conservative 0; Mismatches 1; Indels

Qy 743 AGGCAGCTGCCACCTT 758
   ||| ||||| |||||
Db 16 AGGCAGCTGCCGCCTT 1

RESULT 286
US-09-877-478-948
; Sequence 948, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04

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; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 948
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
; US-10-342-902-948

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      569 TTTAATACCTTTATAT 584
DB      1 UUUUAUGCCUUUAU 16

RESULT 292
US-10-138-674-7395/c
; Sequence 7395, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7395
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-138-674-7395

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTTATTCTCAGCAA 641
DB      17 GTTTTATGCTCAGCAA 2

RESULT 293
US-10-287-949A-7395/c
; Sequence 7395, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7395
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-287-949A-7395

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTTATTCTCAGCAA 641
DB      17 GTTTTATGCTCAGCAA 2

RESULT 294
US-10-669-841-948
; Sequence 948, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCI/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 948
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
; US-10-669-841-948
```


Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATAT 584
::||: ||::||:|
Db 1 UUUAAUGCCUUUAU 16

RESULT 295

US-10-723-361-2565/c
; Sequence 2565, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2565
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2566

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
|||||||
Db 16 AGGCAGCTGCCACCTT 1

RESULT 297

US-10-712-633-347/c
; Sequence 347, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: MHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
|||||||
Db 17 AGGCAGCTGCCACCTT 2

RESULT 296

US-10-723-361-2566/c
; Sequence 2566, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

Fri Aug 19 11:00:02 2005

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-731-739-588

Query Match          1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TCGAATTGTTGTTCT 310
        |||||
Db       1 TCGAATTGTTGTTCT 16

RESULT 300
US-10-477-238A-588
; Sequence 588, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
; APPLICANT: Yaworsky, Paul
; APPLICANT: Babi, Philip
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-212
; CURRENT APPLICATION NUMBER: US/10/477,238A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-238A-588

Query Match          1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TCGAATTGTTGTTCT 310
        |||||
Db       1 TCGAATTGTTGTTCT 16

RESULT 301
US-10-680-287A-588
; Sequence 588, Application US/10680287A
; Publication No. US2004024069A1
; GENERAL INFORMATION:
; APPLICANT: Yaworsky, Paul
; APPLICANT: Babi, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-238A-588

Query Match          1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      314 TTGGATTTCCTGTTA 329
        |||||
Db       1 TTGGATTTCCTGTTA 16

RESULT 299
US-10-731-739-588
; Sequence 588, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/10/731,739
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-633-347

Query Match          1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTATTCTCAGCAA 641
        |||||
Db       17 GTTTATTCTCAGCAA 2

RESULT 298
US-09-969-373-2494
; Sequence 2494, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2494
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2494

Query Match          1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      314 TTGGATTTCCTGTTA 329
        |||||
Db       1 TTGGATTTCCTGTTA 16

RESULT 299
US-10-731-739-588
; Sequence 588, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/10/731,739
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
```

; PRIOR APPLICATION NUMBER: US 60/353,058
 ; PRIOR FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: US 60/361,293
 ; PRIOR FILING DATE: 2002-03-04
 ; NUMBER OF SEQ ID NOS: 812
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 588
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-680-287A-588

Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TGGAAATTGTTGTTCT 310
 |||||
 Db 1 TGGAAATTGTTGTTCT 16

RESULT 302

US-10-477-173-588
 ; Sequence 588 Application US/10477173
 ; Publication No. US20050070699A1

; GENERAL INFORMATION:
 ; APPLICANT: Genome Therapeutics Corporation and
 ; APPLICANT: Allen, Kristina M.
 ; APPLICANT: Yaworsky, Paul
 ; APPLICANT: Morales, Arturo J.
 ; APPLICANT: Graham, James R.
 ; APPLICANT: Anisowicz, Anthony
 ; APPLICANT: Liu, Wei

; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels

; FILE REFERENCE: 032796-135
 ; CURRENT APPLICATION NUMBER: US/10/477,173
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: US 60/290,071
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US 60/291,311
 ; PRIOR FILING DATE: 2001-05-17
 ; PRIOR APPLICATION NUMBER: US 60/353,058
 ; PRIOR FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: US 60/361,293
 ; PRIOR FILING DATE: 2002-03-04
 ; NUMBER OF SEQ ID NOS: 1086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 588
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-477-173-588

Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TGGAAATTGTTGTTCT 310
 |||||
 Db 1 TGGAAATTGTTGTTCT 16

RESULT 303

US-10-834-377-588
 ; Sequence 588 Application US/10834377
 ; Publication No. US20050142617A1

; GENERAL INFORMATION:
 ; APPLICANT: Carulli, John P.
 ; APPLICANT: Little, Randall D.
 ; APPLICANT: Recker, Robert R.
 ; APPLICANT: Johnson, Mark L.
 ; TITLE OF INVENTION: High bone mass gene of 11q13.3
 ; FILE REFERENCE: 032796-014

; CURRENT APPLICATION NUMBER: US/10/834,377
 ; CURRENT FILING DATE: 2004-04-29
 ; PRIOR APPLICATION NUMBER: US/09/543,771B
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 09/229,319
 ; PRIOR FILING DATE: 1999-01-13
 ; PRIOR APPLICATION NUMBER: US 60/071,449
 ; PRIOR FILING DATE: 1998-01-13
 ; PRIOR APPLICATION NUMBER: US 60/105,511
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 641
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 588
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-834-377-588

Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TGGAAATTGTTGTTCT 310
 |||||
 Db 1 TGGAAATTGTTGTTCT 16

RESULT 304

US-09-854-883-297
 ; Sequence 297 Application US/09854883
 ; Patent No. US20020055479A1

; GENERAL INFORMATION:

; APPLICANT: Lex M. Cowser
 ; APPLICANT: Jacqueline Wyatt
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Madeline M. Butler
 ; APPLICANT: Robert McKay

; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

; FILE REFERENCE: ISPH-0576
 ; CURRENT APPLICATION NUMBER: US/09/854,883
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 09/629,644
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 09/487,368
 ; PRIOR FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 389
 ; SEQ ID NO 297
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-854-883-297

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 GGCTGTGATCAATGG 358
 |||||
 Db 1 GGCTGTGATCAATGG 16

RESULT 305

US-09-917-963-91/c
 ; Sequence 91 Application US/09917963
 ; Publication No. US20030086912A1

; GENERAL INFORMATION:

; APPLICANT: Rosanne M. Crooke
 ; APPLICANT: Mark J. Graham

; TITLE OF INVENTION: ANTISENSE EXPRESSION

; FILE REFERENCE: 032796-014

; FILE REFERENCE: ISPH-0591
 ; CURRENT APPLICATION NUMBER: US/09/917,963
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 91
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-917-963-91

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 130 TCTTATGCTGGCATGT 145
 Db 18 TCTTATGCTGGCATGT 3

RESULT 306
 US-09-953-318-37
 ; Sequence 37, Application US/09953318
 ; Publication No. US20030105036A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
 ; TITLE OF INVENTION: EXPRESSION
 ; FILE REFERENCE: RFS-0232
 ; CURRENT APPLICATION NUMBER: US/09/953,318
 ; CURRENT FILING DATE: 2001-09-13
 ; NUMBER OF SEQ ID NOS: 154
 ; SEQ ID NO 37
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-953-318-37

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATCTCAGCAA 641
 Db 4 GTTTTATCTCAGCAA 19

RESULT 307
 US-10-085-906-317
 ; Sequence 317, Application US/10085906
 ; Publication No. US20030054371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ying, Vincent
 ; APPLICANT: Wu, Paul
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
 ; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
 ; FILE REFERENCE: GNN-5343CP2
 ; CURRENT APPLICATION NUMBER: US/10/085,906
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 60/126,215
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: US 09/534,061
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/07938
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 545
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 317

; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-906-317

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 721 AAATATATTAAACGAG 736
 Db 5 AAATATATTAAACGAG 20

RESULT 308
 US-10-446-373-37
 ; Sequence 37, Application US/10446373
 ; Publication No. US20030204076A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
 ; TITLE OF INVENTION: EXPRESSION
 ; FILE REFERENCE: RFS-0232
 ; CURRENT APPLICATION NUMBER: US/10/446,373
 ; CURRENT FILING DATE: 2003-05-28
 ; PRIOR APPLICATION NUMBER: US/09/953,318
 ; PRIOR FILING DATE: 2001-09-13
 ; NUMBER OF SEQ ID NOS: 154
 ; SEQ ID NO 37
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-446-373-37

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATCTCAGCAA 641
 Db 4 GTTTTATCTCAGCAA 19

RESULT 309
 US-10-360-510-297
 ; Sequence 297, Application US/10360510
 ; Publication No. US20030220282A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowser
 ; APPLICANT: Jacqueline Wyatt
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Madeline M. Butler
 ; APPLICANT: Robert McKay
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
 ; FILE REFERENCE: ISPH-0576
 ; CURRENT APPLICATION NUMBER: US/10/360,510
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US/09/854,883
 ; PRIOR FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 09/629,644
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 09/487,368
 ; PRIOR FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 389
 ; SEQ ID NO 297
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-297

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 GGCTGTGATCAAAATGG 358
Db 1 GGCTGTGATCAAAAGG 16

RESULT 310
US-10-349-143-6795
; Sequence 6795, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6795
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-19464 for SEQ 2861,
US-10-349-143-6795

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 218 TTCATTGCCAAAGAG 233
Db 5 TTCTTTGCCAAAGAG 20

RESULT 311
US-10-289-762-1803/c
; Sequence 1803, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1803
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1803

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
```

```
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 287 TTCACTACTGGAATTG 302
Db 19 TTCACTACGGGAATTG 4

RESULT 312
US-10-455-229-23/c
; Sequence 23, Application US/10455229
; Publication No. US20040016030A1
; GENERAL INFORMATION:
; APPLICANT: LOWE, BRENDA A.
; APPLICANT: CHOMET, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES
; TITLE OF INVENTION: WITH INCREASED TRANSFORMABILITY
; FILE REFERENCE: DEKM:195US
; CURRENT APPLICATION NUMBER: US/10/455,229
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,522
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-455-229-23

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 775 CCTTTTGGCTGGGGAT 790
Db 19 CCTTTTGGCTAGGGGAT 4

RESULT 313
US-10-293-864-44/c
; Sequence 44, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-44

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 812 GCTGAGCAGGCCTCT 827
Db 16 GCTGAGCAGGCCTCT 1

RESULT 314
US-10-233-864-45/c
; Sequence 45, Application US/10293864
; Publication No. US20040092465A1
```

; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-45

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 813 CTGAAGCAGGCGCTCTC 828
Db 20 CTGCAGCAGGCGCTCTC 5

RESULT 315
US-10-293-864-120
; Sequence 120, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 120
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-293-864-120

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 GCTGACGAGCGCTCTC 827
Db 5 GCTGCAGCAGGCGCTCTC 20

RESULT 316
US-10-293-864-121
; Sequence 121, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-293-864-121

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 813 CTGAAGCAGGCGCTCTC 828
Db 1 CTGCAGCAGGCGCTCTC 16

RESULT 317
US-10-688-706-2537
; Sequence 2537, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2537
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2537

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 553 TTAATATGCTGGGTTT 568
Db 5 TTAATAGCTGGGTTT 20

RESULT 318
US-10-688-706-2670
; Sequence 2670, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2670
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2670

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 554 TAATATGCTGGGTTT 569
Db 1 TAATAAGCTGGGTTT 16

RESULT 319
US-10-831-901A-4408
; Sequence 4408, Application US/10831901A
; Publication No. US2005010085A1

```
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4408
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4408

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      568 TTTTAATACCTTTATA 583
Db      1 TTTTAATTCCTTTATA 16

RESULT 320
US-10-831-901A-4409
; Sequence 4409, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4410

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      568 TTTTAATACCTTTATA 583
Db      1 TTTTAATTCCTTTATA 16

RESULT 320
US-10-831-901A-4409
; Sequence 4409, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4410
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4410

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      568 TTTTAATACCTTTATA 583
Db      1 TTTTAATTCCTTTATA 16
```

```
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4409

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      568 TTTTAATACCTTTATA 583
Db      2 TTTTAATTCCTTTATA 17

RESULT 321
US-10-831-901A-4410
; Sequence 4410, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4410
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4410

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      568 TTTTAATACCTTTATA 583
Db      2 TTTTAATTCCTTTATA 17
```

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```
Db      3 TTTTAATTCCTTTATA 18

RESULT 322
US-10-831-901A-4411
; Sequence 4411, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL000808US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4411
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4412
Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      568 TTTTAATACCTTTATA 583
      ||||| ||||| ||||| |||||
Db      5 TTTTAATTCCTTTATA 20

RESULT 324
US-11-008-747-297
; Sequence 297, Application US/11008747
; Publication No. US20050095710A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/11/008,747
; CURRENT FILING DATE: 2004-09-04
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 297
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-11-008-747-297
Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      343 GGCTGTGATCAAAATGG 358
      ||||| ||||| ||||| |||||
Db      1 GGCTGTGATCAAAAGG 16

RESULT 325
US-10-388-578-48
```



```

: Sequence 48, Application US/103988578
: Publication No. US2003022411A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Geron Corporation
: APPLICANT: Stanton, Lawrence
: APPLICANT: Ralph, Brandenberger
: APPLICANT: Joseph, Gold D.
: APPLICANT: John, Irving
: APPLICANT: Mandalam, Ramkumar
: APPLICANT: Mok, Michael
: APPLICANT: Shelton, Dawne
: TITLE OF INVENTION: Genes that are
: FILE REFERENCE: 135/001
: CURRENT APPLICATION NUMBER: US/10/3-13
: CURRENT FILING DATE: 2003-03-13
: NUMBER OF SEQ ID NOS: 139
: SOFTWARE: Custom
: SEQ ID NO 48
: LENGTH: 19
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-388-578-48

```

```
Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 827 TCATGACCCAGGAAGCCG 845
||| | ||||| |||
Db 1 TCATAAGCCAGGAAGCCG 19

```

RESULT 326
US-10-389-431-48
; Sequence 48, Application US/10389431
; Publication No. US20040180347A1
; GENERAL INFORMATION:
; APPLICANT: Genon Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; TITLE OF INVENTION: A Marker System
; TITLE OF INVENTION: Embryonic Stem
; FILE REFERENCE: 135/002
; CURRENT APPLICATION NUMBER: US/10/3
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-389-431-48

```

```
Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 827 TCATGACCCAGGAAGGCCG 845
|||||
Dd 1 TCATAAGCCAGGAAGGCCG 19

RESULT 327
US-10-858-500-599
; Sequence 599, Application US/10858500
; Publication No. US20050014257A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke

```

1  APPLICANT: Mark J. Graham
2  TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
3  FILE REFERENCE: BIO0014US
4  CURRENT APPLICATION NUMBER: US/10/858,500
5  CURRENT FILING DATE: 2004-06-01
6  PRIOR APPLICATION NUMBER: US 09/912,724
7  PRIOR FILING DATE: 2001-07-25
8  PRIOR APPLICATION NUMBER: US 60/475,272
9  PRIOR FILING DATE: 2003-06-02
10 PRIOR APPLICATION NUMBER: US 60/540,042
11 PRIOR FILING DATE: 2004-01-28
12 NUMBER OF SEQ ID NOS: 627
13 SEQ ID NO 599
14 LENGTH: 19
15 TYPE: DNA
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Antisense Oligonucleotide
19 US-10-858-500-599

```

Query Match	1.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 2.5e+02;		
Matches 16: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 56 CCCAGTTCGGGAGACATGG 74
|||||
Db 1 CCCATTTCAGGAGACCTGG 19

```

RESULT 328
US-10-478-633A-147
; Sequence 147, Application US/10478633A
; Publication No. US2005005900A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization m
; TITLE OF INVENTION: A acid amplificati
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 147
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed oligonuc
; OTHER INFORMATION: amplifying a porti
US-10-478-633A-147

```

Query Match	1.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%	Pred. No. 2.5e+02;		
Matches 16: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1064 CCAGTGGCTAAACCACTTA 1082
Db 1 CCAGAGGCTGAACCACTTA 19

RESULT 329
US-10-783-128-527
; Sequence-527, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: MGSwigen, James
; TITLE OF INVENTION: RNA Interference
; TITLE OF INVENTION: Expansion Disease
; FILE REFERENCE: 04-105 (400.146)

Fri Aug 19 11:00:02 2005

```

; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 527
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-527

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      804 CAGATAACGCTGAAGCAGG 822
Db      1 CAAATAAAGCUGAUGCAGG 19

RESULT 330
US-10-783-128-642
; Sequence 642, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repe
; TITLE OF INVENTION: Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; CURRENT APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 527
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-527

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      804 CAGATAACGCTGAAGCAGG 822
Db      1 CAAATAAAGCUGAUGCAGG 19

RESULT 330
US-10-783-128-642
; Sequence 642, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repe
; TITLE OF INVENTION: Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 527
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-527
```

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; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 642
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-642

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      194 CAGCCCATCTCCCATCC 212
Db      1 CAGCCCGUCCUCCUCAUCC 19

RESULT 331
US-10-783-128-1088
; Sequence 1088, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repe
; TITLE OF INVENTION: Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-1088

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.5e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      358 GGGAGCGCTGGCGCTGTG 376
Db      1 GGAAGUCUGCGCCUUGUG 19
```

```
RESULT 332
US-10-783-128-2279/c
; Sequence 2279, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repeat Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-783-128-2279

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 804 CAGATAACGCTGAGCAGG 822
Db 19 CAAATAAAGCTGATGACG 1

RESULT 333
US-10-783-128-2394/c
; Sequence 2394, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repeat Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-783-128-2279

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 804 CAGATAACGCTGAGCAGG 822
Db 19 CAAATAAAGCTGATGACG 1

RESULT 334
US-10-783-128-2840/c
; Sequence 2840, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repeat Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2840
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-783-128-2840

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 194 CACGCCATCTCCCCCATCC 212
Db 19 CACGCCGTCTCCCTCATCC 1
```

Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 358 GGGAGCGCTGGCCCTTG 376
 Db 19 GGAAGTCTGGCCCTTG 1

RESULT 335
 US-09-771-357-79
 ; Sequence 79, Application US/09771357
 ; Publication No. US200300174541
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: SUKUMAR, Saraswati
 ; APPLICANT: EVRON, Ella
 ; APPLICANT: DOOLEY, William
 ; APPLICANT: DAVIDSON, Nancy
 ; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
 ; FILE REFERENCE: JHU1630
 ; CURRENT APPLICATION NUMBER: US/09/771,357
 ; CURRENT FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 79
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR sense primer
 US-09-771-357-79

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTGAGGATTTATGCGCTTT 167
 Db 1 TTCGAGTTTATGCGCTTT 19

RESULT 336
 US-09-918-187-73
 ; Sequence 73, Application US/09918187
 ; Publication No. US20030083282A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosanne M. Crooke
 ; APPLICANT: Mark J. Graham
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-CoA DESATURASE EXPRESSION
 ; FILE REFERENCE: ISPH-0590
 ; CURRENT APPLICATION NUMBER: US/09/918,187
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 80
 ; SEQ ID NO 73
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-918-187-73

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 814 TGAAGCAGGCGCTCTCATGA 832
 Db 2 TCAAGCAGGCGCTCTCATGA 20

RESULT 337

US-10-054-225-12
 ; Sequence 12, Application US/10054225
 ; Publication No. US20020164623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saint Jude Children's Research Hospital
 ; APPLICANT: Tuomanen, Elaine
 ; APPLICANT: Atkinson, Robyn M
 ; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
 ; FILE REFERENCE: SJ-01-0022
 ; CURRENT APPLICATION NUMBER: US/10/054,225
 ; CURRENT FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: primer bind
 ; LOCATION: (1)..(20)
 ; OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
 US-10-054-225-12

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 ATTGAATTTCTTAGAACTC 507
 Db 1 ATTGAATTTCTTAGAACTC 19

RESULT 338
 US-10-024-450-12/c
 ; Sequence 12, Application US/10024450
 ; Publication No. US20030032606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huang, Shi
 ; APPLICANT: Chadwick, Robert B.
 ; TITLE OF INVENTION: Methods of Detecting and Treating
 ; TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
 ; FILE REFERENCE: P-LJ 5101
 ; CURRENT APPLICATION NUMBER: US/10/024,450
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: US 60/256,582
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic primer
 US-10-024-450-12

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 966 AGGACATTTTGATGAGATC 984
 Db 19 ACGACATTTTGCTGAGCTC 1

RESULT 339
 US-10-006-883A-73/c
 ; Sequence 73, Application US/10006883A
 ; Publication No. US20030119767A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION
 ; FILE REFERENCE: RTS-0337

APPLICANT: CHAMAILLARD, MATHIAS
TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 37991-0009

QY	Db	220	CATTGCCAAAGAGTCAAC	238	0
Db	2	CGTTTCCAGAAGTCAAC	20		
<p>RESULT 346</p> <p>US-10-300-683-333</p> <p>Sequence 333, Application US/10300683</p> <p>Publication No. US20030235834A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Dunlop, Charles L.M.</p> <p>APPLICANT: Weisel, James M.</p> <p>TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS</p> <p>FILE REFERENCE: CHARDON.010A</p> <p>CURRENT APPLICATION NUMBER: US/10/300,683</p> <p>CURRENT FILING DATE: 2002-11-19</p> <p>PRIOR APPLICATION NUMBER: 60/333,531</p> <p>PRIOR FILING DATE: 2001-11-19</p> <p>NUMBER OF SEQ ID NOS: 554</p> <p>SOFTWARE: FastSeq for Windows Version 4.0</p> <p>SEQ ID NO 333</p> <p>LENGTH: 20</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Diagnostic Oligonucleotide</p> <p>US-10-300-683-333</p>					
<p>Query Match 1.3%; Score 14.2; DB 1; Length 20;</p> <p>Best Local Similarity 84.2%; Pred. No. 2.7e+02;</p> <p>Mismatches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>					
QY	670	CTCAAATTATGTTACTTGT	688		
Db	1	CTCATACTTGTACTTGT	19		
<p>RESULT 347</p> <p>US-10-395-031-5/c</p> <p>Sequence 5, Application US/10395031</p> <p>Publication No. US20030235845A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: van Ommen, Garrit-Jan Boudewijn</p> <p>APPLICANT: van Deutekom, Judith Christina Theodora</p> <p>APPLICANT: Gen Dumen, Johannes Theodorus</p> <p>TITLE OF INVENTION: INDUCTION OF EXON SKIPPING IN EUKARYOTIC CELLS</p> <p>FILE REFERENCE: 2183-5910US (REN/P542580S10)</p> <p>CURRENT APPLICATION NUMBER: US/10/395,031</p> <p>CURRENT FILING DATE: 2003-03-21</p> <p>PRIOR APPLICATION NUMBER: PCT/NL01/00697</p> <p>PRIOR FILING DATE: 2001-09-21</p> <p>PRIOR APPLICATION NUMBER: EP 002063283.7</p> <p>PRIOR FILING DATE: 2000-09-21</p> <p>NUMBER OF SEQ ID NOS: 36</p> <p>SOFTWARE: PatentIn version 3.2</p> <p>SEQ ID NO 5</p> <p>LENGTH: 20</p> <p>TYPE: DNA</p> <p>ORGANISM: Mouse</p> <p>US-10-395-031-5</p>					
<p>Query Match 1.3%; Score 14.2; DB 1; Length 20;</p> <p>Best Local Similarity 84.2%; Pred. No. 2.7e+02;</p> <p>Mismatches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>					
QY	793	GCTTGGAGGAGCAGATAAC	811		
Db	19	GCTGGAAGAGCAGATAAC	1		
<p>RESULT 348</p> <p>US-10-349-143-9409/c</p> <p>Sequence 9409, Application US/10349143</p>					

; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement
US-10-349-143-9409

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 427 ATTGGAGAGGAGATGAT 445
| | | | |
Db 19 AGTTGGAGGGGAGATGAT 1

RESULT 349
US-10-188-470-69
; Sequence 69, Application US/10188470
; Publication No. US20040005707A1
; GENERAL INFORMATION:
; APPLICANT: Scott Cooper
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 5 EXPRESSION
; FILE REFERENCE: PTS-0024
; CURRENT APPLICATION NUMBER: US/10/188,470
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-470-69

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1029 GAGAAGTAAACATCACACC 1047
| | | | |
Db 1 GAGAAGGAACATCATGTC 19

RESULT 350
US-10-190-366-111/c
; Sequence 111, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
; FILE REFERENCE: PTS-0023
; CURRENT APPLICATION NUMBER: US/10/190,366
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 111
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-190-366-111

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 95 GCATTATCCTTCAGTGGG 113
| | | | |
Db 19 GCATTATCTTCAGAGGG 1

RESULT 351
US-10-190-366-308
; Sequence 308, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
; FILE REFERENCE: PTS-0023
; CURRENT APPLICATION NUMBER: US/10/190,366
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 308
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-190-366-308

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 95 GCATTATCCTTCAGTGGG 113
| | | | |
Db 2 GCATTATCTTCAGAGGG 20

RESULT 352
US-10-289-762-2125
; Sequence 2125, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2125

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;

Statistics	Conservative	Mismatches	Indels	Gaps
Mismatches	16	0	3	0

QY	940	AGAACTCTGAAGCCCCCACTC	958
QY	1	AGAACTCGGAACCCCCACGC	19

RESUIT 353

```

US-10-289-762-4121
; Sequence 4121, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-10-289-762-4121

```

1.3%: Score 14.2; DB 1; Length 20;

Query Match						
Best Local Similarity	84.2%	Pred. No.	2.7e+02;			
Matches	16:	Conservative	0;	Mismatches	3;	
Gaps	0;					

QY 771 GAAACCTTTTCTTGGGA 789
|||
1 CAGACCTTTTCTTGGGA 19

RESIT.T 354

```

US-10-289-762-5159
; Sequence 5159, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffalls, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; TITLE OF INVENTION:
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5159

```

1 3%: Score 14.2; DB 1; Length 20;

Query Match	1.00;	2.00;	
Best Local Similarity	84.2%;	Pred. No. 2.7e+02;	
Matches	16. Conservative	0; Mismatches	3; Indels
			0; Gaps

Qy 291 CTACTGGAATTGTTGTTTC 309

RESULT 355

```

RES001.330
US-10-289-762-5166
; Sequence 5166, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; TITLE OF INVENTION:
; FILE REFERENCE: 9710-003-999

```

```

; CURRENT APPLICATION NUMBER: US/10/289,762
;
; CURRENT FILING DATE: 2003-03-27
;
; NUMBER OF SEQ ID NOS: 6849
;
; SEQ ID NO 5166
;
; LENGTH: 20
;
; TYPE: DNA
;
; ORGANISM: Chlamydia pneumoniae
;
; US-10-289-762-5166

```

Query Match	1.3%	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%	Pred. No. 2.7e+02;		
Matches	16:	Conservative	0;	Mismatches 3:
				Indels

QY 291 CTACTGGAAATTGTTGTTTC 309
||| ||| ||| ||| ||| |||
nb 2 CTTCTGGAGTCTGTGTTTC 20

RESULT 356

```

US-10-289-762-6581
; Sequence 6581, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6581
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-10-289-762-6581

```

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 460 GTGGTAGCACTTTATCTG 478
|||
Db 2 GTGGTAGCACTATAACCTG 20

RESULT 357

```

US-10-317-500-76/c
; Sequence 76, Application US/10317500
; Publication No. US20040115637A1
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0380
; CURRENT APPLICATION NUMBER: US/10/317,500
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 276
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-500-76

```

```

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
                                0. Mismatches 3; Indels

```

Qy 266 TGTGGGAAC TGGCATATT 284
||| ||| ||| ||| ||| ||| |||
nb 20 TGTAGGTAA CCGGCATATT 2

RESULT 358

US-10-731-739-310/c

; Sequence 310, Application US/10731739

; Publication No. US20040176582A1

; GENERAL INFORMATION:

; APPLICANT: Carulli, John P.

; APPLICANT: Little, Randall D.

; APPLICANT: Recker, Robert R.

; APPLICANT: Johnson, Mark L.

; TITLE OF INVENTION: High bone mass gene of 11q13.3

; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/10/731,739

; PRIOR FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: US/09/544,398B

; PRIOR FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 09/229,319

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 60/071,449

; PRIOR FILING DATE: 1998-01-13

; PRIOR APPLICATION NUMBER: US 60/105,511

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 641

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 310

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-731-739-310

Query Match

; Sequence 310, Application US/10731739

; Best Local Similarity 84.2%; Score 14.2; DB 1; Length 20;

; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 882 AAGCAATGCGTCATTTC 400

; | | | | | | | | | | | | | | | | | |

Db 19 AATATTGGGCCACACAC 1

RESULT 359

US-10-424-041-105/c

; Sequence 105, Application US/10424041

; Publication No. US20040215006A1

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Thomas Condon

; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION

; FILE REFERENCE: BIOL0005US

; CURRENT APPLICATION NUMBER: US/10/424,041

; CURRENT FILING DATE: 2003-04-25

; NUMBER OF SEQ ID NOS: 184

; SEQ ID NO 105

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-10-424-041-105

Query Match

; Sequence 310, Application US/10680287A

; Best Local Similarity 84.2%; Score 14.2; DB 1; Length 20;

; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 382 AGGCAATGCGTCATTTC 400

; | | | | | | | | | | | | | | | | | |

Db 20 ATGCAATGCAAGCAATTC 2

RESULT 360

US-10-424-041-179

; Sequence 310, Application US/10680287A

; Publication No. US20040244069A1

; GENERAL INFORMATION:

; APPLICANT: Babij, Philip

; APPLICANT: Yaworsky, Paul

; Sequence 179, Application US/10424041

; Publication No. US20040215006A1

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Thomas Condon

; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION

; FILE REFERENCE: BIOL0005US

; CURRENT APPLICATION NUMBER: US/10/424,041

; CURRENT FILING DATE: 2003-04-25

; NUMBER OF SEQ ID NOS: 184

; SEQ ID NO 179

; LENGTH: 20

; TYPE: DNA

; ORGANISM: M. musculus

; FEATURE:

US-10-424-041-179

Query Match

; Sequence 310, Application US/10477238A

; Best Local Similarity 57.9%; Score 14.2; DB 1; Length 20;

; Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 382 AGGCAATGCGTCATTTC 400

; | | | | | | | | | | | | | | | | | |

Db 1 AUGCAUGCAAGCAUUUC 19

RESULT 361

US-10-477-238A-310/c

; Sequence 310, Application US/10477238A

; Publication No. US20040221326A1

; GENERAL INFORMATION:

; APPLICANT: Babij, Philip

; APPLICANT: Yaworsky, Paul

; APPLICANT: Bex, Frederick J. III

; APPLICANT: Bodine, Peter Van Nest

; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation

; FILE REFERENCE: 032796-212

; CURRENT APPLICATION NUMBER: US/10/477,238A

; CURRENT FILING DATE: 2003-11-10

; PRIOR APPLICATION NUMBER: US 60/290,071

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/291,311

; PRIOR FILING DATE: 2001-05-17

; PRIOR APPLICATION NUMBER: US 60/353,058

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: US 60/361,293

; PRIOR FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 812

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 310

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-477-238A-310

Query Match

; Sequence 310, Application US/10680287A

; Best Local Similarity 84.2%; Score 14.2; DB 1; Length 20;

; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 882 AAAAGTGTGGCCACACAC 900

; | | | | | | | | | | | | | | | | | |

Db 19 AATATTGGGCCACACAC 1

RESULT 362

US-10-680-287A-310/c

; Sequence 310, Application US/10680287A

; Publication No. US20040244069A1

; GENERAL INFORMATION:

; APPLICANT: Babij, Philip

; APPLICANT: Yaworsky, Paul

```

; APPLICANT: Bex, Frederick J. Iii
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-680-287A-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCACACAGAC 900
Db      19 AATATTGTGCCACACAC 1

RESULT 363
US-10-476-960-4
; Sequence 4, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
; FILE REFERENCE: RTSP-0392
; CURRENT APPLICATION NUMBER: US/10/476,960
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 09/851,520
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
; US-10-476-960-4

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      822 GCCTCTCATGACCCAGGAA 840
Db      1 GCCACTCCAGACCCAGGAA 19

RESULT 364
US-10-484-442-73
; Sequence 73, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL7COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH20695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-484-442-73

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      814 TGAAGCAGGCGCTCTCATGA 832
Db      2 TCAAGCAGGCGCATCTGATGA 20

RESULT 365
US-10-858-500-205
; Sequence 205, Application US/10858500
; Publication No. US20050014257A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: BIOL0014US
; CURRENT APPLICATION NUMBER: US/10/858,500
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 09/912,724
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/475,272
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/540,042
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 627
; SEQ ID NO 205
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-858-500-205

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      56 CCCAGTTGGGAGACATGG 74
Db      2 CCCATTTCAGGAGACTGG 20

RESULT 366
US-10-858-500-381/c
; Sequence 381, Application US/10858500
; Publication No. US20050014257A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: BIOL0014US
; CURRENT APPLICATION NUMBER: US/10/858,500
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 09/912,724
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/475,272
```

```
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/540,042
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 627
; SEQ ID NO 381
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-858-500-381

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 56 CCCAGTTCGGGAGACATGG 74
Db 19 CCCATTTCAGGACCTGG 1

RESULT 367
US-10-643-775-1061
; Sequence 1061, Application US/10643775
; Publication No. US20050026156A1
; GENERAL INFORMATION:
; APPLICANT: Lie, Oyatein
; APPLICANT: Slettan, Audun
; APPLICANT: Hoyum, Morten
; APPLICANT: Lingaas, Frode
; TITLE OF INVENTION: Verification of Food Origin Based on
; TITLE OF INVENTION: Nucleic Acid Pattern Recognition
; FILE REFERENCE: 66849-019
; CURRENT APPLICATION NUMBER: US/10/643,775
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US 60/404,200
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1061
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Oreochromis niloticus
US-10-643-775-1061

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 782 CTTGGGGATGCTTGGAG 800
Db 2 CTTGGGTTTGAGCTTGGAG 20

RESULT 368
US-10-619-253-73
; Sequence 73, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide

US-10-619-253-73
Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 814 TGAAGCAGGCTCTCATGA 832
Db 2 TCAAGCAGGCTCTCATGA 20

RESULT 369
US-10-477-173-310/c
; Sequence 310, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul
; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HEM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: US/10/477,173
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-173-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 882 AAAAGTGTGCCACACAC 900
Db 19 AATATTGTGCCACACAC 1

RESULT 370
US-10-831-901A-10393/c
; Sequence 10393, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
```

```

; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10393
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10393

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 407 ATTCAAGGTTTTCCTTA 425
||| ||| ||| ||| ||| ||| |||
Db 19 ATTAAAGGTTCTTTCCTTA 1

RESULT 371
US-10-831-901A-10394/c
; Sequence 10394, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOLO0008US)
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10394

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 407 ATTCAAGGTTTTCCTTA 425
||| ||| ||| ||| ||| ||| |||
Db 19 ATTAAAGGTTCTTTCCTTA 1

RESULT 372
US-10-831-901A-11295
; Sequence 11295, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOLO0008US)
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11295
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11295

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 407 ATTCAAGGTTTTCCTTA 425
||| ||| ||| ||| ||| ||| |||
Db 20 ATTAAAGGTTCTTTCCTTA 2

RESULT 373
US-10-831-901A-11296
; Sequence 11296, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOLO0008US)
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10394

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1014 AGAAGCATCATCAGAGA 1032
||| ||| ||| ||| ||| ||| |||
Db 1 AGCAGCATCATCATAACA 19

RESULT 373
US-10-831-901A-11296
; Sequence 11296, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOLO0008US)
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10394

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1014 AGAAGCATCATCAGAGA 1032
||| ||| ||| ||| ||| ||| |||
Db 1 AGCAGCATCATCATAACA 19
```

```
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11296
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11296

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1014 AGAAGCATCATCATAGAGA 1032
Db 2 AGCAGCATCATCATAAACA 20

RESULT 374
US-10-831-901A-12114
; Sequence 12114, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12115

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 596 TTTAAGAAAGACTTCATAA 614
Db 2 TTTGAGAACGACTTCAGAA 20

RESULT 376
US-10-831-901A-14584
; Sequence 14584, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12114

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 596 TTTAAGAAAGACTTCATAA 614
Db 1 TTTGAGAACGACTTCAGAA 19

RESULT 375
US-10-831-901A-12115
; Sequence 12115, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12115

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 596 TTTAAGAAAGACTTCATAA 614
Db 2 TTTGAGAACGACTTCAGAA 20

RESULT 376
US-10-831-901A-14584
; Sequence 14584, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
```

```

; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14584
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14584

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1006 AAAGTTTGAGAGCATCAT 1024
Db 1 ACAGTTTGAAGAACAT 19

RESULT 377
US-10-831-901A-14587
; Sequence 14587, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14587
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15628

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1004 TGAAGTTTGAGAGCATC 1022
Db 2 TGACAGTTTGAAGAACAC 20

RESULT 378
US-10-831-901A-15628
; Sequence 15628, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15628

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1017 AGCATCATCATGAGAGAT 1035
Db 1 AGAATCATCATGAGAGAT 19
```

```
RESULT 379
US-10-831-901A-26183/c
; Sequence 26183, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26183
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26183

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      318 GATTCCTCGTTATCTTCG 336
Db      19 GCTTCGGGTATCTTCG 1

RESULT 380
US-10-831-901A-26188/c
; Sequence 26188, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26188

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      318 GATTCCTCGTTATCTTCG 336
Db      19 GCTTCGGGTATCTTCG 1

RESULT 381
US-10-831-901A-26488/c
; Sequence 26488, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26488
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26488

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      322 TCGTGTATCTTCGTCGT 340
Db      20 TCGTGTATCTTCGTCGT 2
```

```
US-10-831-901A-26188/c
; Sequence 26188, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26188

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      322 TCGTGTATCTTCGTCGT 340
Db      20 TCGTGTATCTTCGTCGT 2

US-10-831-901A-26488/c
; Sequence 26488, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26488
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26488

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      322 TCGTGTATCTTCGTCGT 340
Db      20 TCGTGTATCTTCGTCGT 2
```

Fri Aug 19 11:00:02 2005

```

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: US10083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26897
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26897

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      699 ATGTAGTCACGGTCTCTC 717
      ||||| ||| ||| ||| |||
Db      2 ATGTAGCCACAGTGATCTC 20

RESULT 384
US-10-476-264-189/c
; Sequence 189, Application US/10476264
; Publication No. US20050123910A1
; GENERAL INFORMATION:
; APPLICANT: Cookson, William Osmond Charles Michael
; APPLICANT: Moffat, Miriam Fleur
; APPLICANT: Allen, Maxine
; APPLICANT: Lench, Nick
; TITLE OF INVENTION: Enzyme and SNP marker for disease
; FILE REFERENCE: 16721-002US1
; CURRENT APPLICATION NUMBER: US/10/476,264
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: PCT/GB02/01887
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: GB0110044.5
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: GB0110046.0
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: GB0124594.3
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: GB0124575.2
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 421
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 189
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-476-264-189

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      699 ATGTAGTCACGGTCTCTC 717
      ||||| ||| ||| ||| |||
Db      1 ATGTAGCCACAGTGATCTC 19

RESULT 383
US-10-831-901A-26897
; Sequence 26897, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: US10083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26896
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26896

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      699 ATGTAGTCACGGTCTCTC 717
      ||||| ||| ||| ||| |||
Db      1 ATGTAGCCACAGTGATCTC 19

RESULT 382
US-10-831-901A-26896
; Sequence 26896, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: US10083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26896
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26896

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      658 TAGATTATGTTACTCAAAAT 676
      ||||| ||||| |||
Db      19 TGGATTATGTTACTACAAAT 1

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: US10083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26896
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26896

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      658 TAGATTATGTTACTCAAAAT 676
      ||||| ||||| |||
Db      19 TGGATTATGTTACTACAAAT 1
```


Qy 472 TATTCTGATTACAGTGCAT 490
| | | | | | | | | | | | | | | |
Db 19 TGTTCGTGTTACAATGCAT 1

RESULT 385

US-10-834-377-310/c
; Sequence 310, Application US/10834377
; Publication No. US20050142617A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/10/834,377
; CURRENT FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US/09/543,771B
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-834-377-310

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 882 AAAAGTGTGGCCACAGAC 900
| | | | | | | | | | | | | | | |
Db 19 AATATTGTGGCCACACAC 1

RESULT 386

US-10-980-850-1
; Sequence 1, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer for GOS2 gene
US-10-980-850-1

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 798 GAGAGGCAGATAACGCTCA 816
| | | | | | | | | | | | | | | |
Db 1 GAGAGGAGGAGACGCTGA 19

RESULT 387

US-11-039-629-125/c
; Sequence 125, Application US/11039629
; Publication No. US20050164271A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0532US
; CURRENT APPLICATION NUMBER: US/11/039,629
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/538,173
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/550,191
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-11-039-629-125

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1075 ACCACTTAACCTCTCTGGG 1093
| | | | | | | | | | | | | | | |
Db 20 ACAACTTGACTTCTCTGGG 2

RESULT 388

US-10-774-721-43
; Sequence 43, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-43

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 CCGTGGCAGGAAGC 39
| | | | | | | | | | | | | | | |

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-706

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 10; Conservative 4; Mismatches 0;

QY 346 TGTGATCAAAATGGG 359
Db 2 UGUGAUCAAAUUGG 15

RESULT 391
US-10-349-143-5553
; Sequence 5553, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5553
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-5186 for SEQ 1619,
US-10-349-143-5553

Query Match 1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 200 ATCTCCCCCATCCC 213
Db 5 ATCTCCCCCATCCC 18

RESULT 392
US-10-719-993-55163
; Sequence 55163, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55163
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-55163

Query Match 1.3%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-706

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 10; Conservative 4; Mismatches 0;

QY 346 TGTGATCAAAATGGG 359
Db 2 UGUGAUCAAAUUGG 15

RESULT 389
US-09-504-231A-706
; Sequence 706, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 706
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-706

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 10; Conservative 4; Mismatches 0;

QY 346 TGTGATCAAAATGGG 359
Db 2 UGUGAUCAAAUUGG 15

RESULT 390
US-09-274-553D-706
; Sequence 706, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 706
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1060 CTTTCCAGTGCTA 1073
|||||
Db 1 CTTTCCAGTGCTA 14

RESULT 393

US-10-349-143-4185/c

; Sequence 156, Application US/09802669

; Patent No. US20020004490A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcussen, Eric G.

; APPLICANT: Wyatt, Jacqueline

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-545

; CURRENT APPLICATION NUMBER: US/09/802,669

; CURRENT FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: US 09/665,615

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 09/290,640

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 156

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-802-669-156

Query Match 1.3%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AGATGAGTTTATT 633
|||||
Db 18 AGATGAGTTTATT 5

RESULT 394

US-10-172-911-55

; Sequence 55, Application US/10172911

; Publication No. US2003023243A1

; GENERAL INFORMATION:

; APPLICANT: Lex M. Cowse

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN12 EXPRESSION

; FILE REFERENCE: PTS-0016

; CURRENT APPLICATION NUMBER: US/10/172,911

; CURRENT FILING DATE: 2002-06-17

; NUMBER OF SEQ ID NOS: 123

; SEQ ID NO 55

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-10-172-911-55

Query Match 1.3%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 345 CTGTGATCAATGG 358
|||||
Db 1 CTGTGATCAATGG 14

RESULT 395

US-10-349-143-5624

; Sequence 5624, Application US/10349143

; Publication No. US20040005584A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

US-10-349-143-4185/c

; Sequence 4185, Application US/10349143

; Publication No. US20040005584A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CP1

; CURRENT APPLICATION NUMBER: US/10/349,143

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US/09/422,978

; PRIOR FILING DATE: 1999-10-20

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 4185

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind

; LOCATION: 1..20

; OTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,

US-10-349-143-4185

Query Match 1.3%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAATA 575
|||||
Db 19 TGGGTTTTTAATA 6

RESULT 396

US-10-349-143-5624

; Sequence 5624, Application US/10349143

; Publication No. US20040005584A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CP1

; CURRENT APPLICATION NUMBER: US/10/349,143

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US/09/422,978

; PRIOR FILING DATE: 1999-10-20

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 5624

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind

; LOCATION: 1..20

; OTHER INFORMATION: upstream amplification primer 99-5681 for SEQ 1690,

US-10-349-143-5624

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 20;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 324 CTGTTATCTTGCT 337
Db 4 CIGTTATCTTGCT 17

RESULT 397
US-10-619-220-156/c
; Sequence 156, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-220-156
Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
Db 18 AGATGAGTTTATT 5

RESULT 398
US-10-831-901A-18964
; Sequence 18964, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18965
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18965
Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GCCTTTGGATTTC 324
Db 1 GCCTTTGGATTTC 14

RESULT 399
US-10-831-901A-18965
; Sequence 18965, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18965
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18965
Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GCCTTTGGATTTC 324
Db 2 GCCTTTGGATTTC 15
```

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RESULT 400
US-10-831-901A-18966
; Sequence 18966, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18966
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18966

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      311 GCCTTGGATTTC 324
Db      3 GCCTTGGATTTC 16

RESULT 401
US-10-831-901A-18967
; Sequence 18967, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18967
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18967

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      311 GCCTTGGATTTC 324
Db      3 GCCTTGGATTTC 16
```

```
RESULT 402
US-10-831-901A-18968
; Sequence 18968, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18968
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18968

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      311 GCCTTGGATTTC 324
Db      4 GCCTTGGATTTC 17

RESULT 403
US-10-831-901A-18969
; Sequence 18969, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18969
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18969

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      311 GCCTTGGATTTC 324
Db      4 GCCTTGGATTTC 17
```

```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GCCTTTGGATTCC 324
Db 5 GCCTTTGGATTCC 18

RESULT 403
US-10-831-901A-18969
; Sequence 18969, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: Acute Respiratory Syndrome (SARS)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18969
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18969

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GCCTTTGGATTCC 324
Db 6 GCCTTTGGATTCC 19

RESULT 404
US-10-831-901A-18970
; Sequence 18970, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank

```

```

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: Acute Respiratory Syndrome (SARS)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18970
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18970

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GCCTTTGGATTCC 324
Db 7 GCCTTTGGATTCC 20

RESULT 405
US-09-866-108-2563/c
; Sequence 2563, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: A60MICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2563

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 745 GCAGCTGCCACCTTATG 761
Db 17 GCAGCTGCCGCTTCTG 1

RESULT 406

US-09-866-108-2564/c
; Sequence 2564, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2564

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 744 GCAGCTGCCACCTTAT 760
Db 17 GCAGCTGCCGCTTCT 1

RESULT 407

US-09-866-108-6749
; Sequence 6749, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6749

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 836 AGGAGGCGGGGTGA 852
 Db 1 AGGAGGCGGTGAGGA 17
 RESULT 408
 US-09-780-533A-2567/c
 ; Sequence 2567, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haeblerli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00.878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09780,533A
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 2567
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-2567

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 413 GGGTTTTCCTTATTT 429
 Db 17 GAGTTTTCCTTATTT 1

RESULT 409
 US-09-848-754A-3616/c
 ; Sequence 3616, Application US/09848754A
 ; Publication No. US20030073207A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 ; FILE REFERENCE: MBH00-958-I (400/018)
 ; CURRENT APPLICATION NUMBER: US/09/848,754A
 ; CURRENT FILING DATE: 2001-05-03
 ; NUMBER OF SEQ ID NOS: 9645
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 3616
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-848-754A-3616

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 499 TTAGGCTCATATATC 515
 Db 17 TTAGGCTCATATATC 1

RESULT 410
 US-09-978-600-140/c
 ; Sequence 140, Application US/09978600
 ; Publication No. US20030087858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HERRNSTADT, CORINNA

; PARKER, WILLIAM D.
 ; DAVIS, ROBERT
 ; MILLER, SCOTT W.
 ; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
 ; Animal Models for Diseases Associated With Mitochondrial
 ; Defects
 ; NUMBER OF SEQUENCES: 206
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenyon & Kenyon
 ; STREET: 1025 Connecticut Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20036-5405
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/09/978,600
 ; FILING DATE: 15-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/413,740
 ; FILING DATE: 30-MAR-1995
 ; APPLICATION NUMBER: PCT/US95/04063
 ; FILING DATE: 30-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bonham, David B.
 ; REGISTRATION NUMBER: 34297
 ; REFERENCE/DOCKET NUMBER: 2105/7
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 429-1776
 ; TELEFAX: (202) 429-0796
 ; INFORMATION FOR SEQ ID NO: 140:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: YES
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
 US-09-978-600-140
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 562 TGGGTTTTTATACCT 578
 Db 17 TGGGTTTTTATACCT 1
 RESULT 411
 US-09-978-600-151/c
 ; Sequence 151, Application US/09978600
 ; Publication No. US20030087858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HERRNSTADT, CORINNA
 ; PARKER, WILLIAM D.
 ; DAVIS, ROBERT
 ; MILLER, SCOTT W.
 ; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
 ; Animal Models for Diseases Associated With Mitochondrial
 ; Defects
 ; NUMBER OF SEQUENCES: 206
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenyon & Kenyon
 ; STREET: 1025 Connecticut Avenue, N.W.
 ; CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 151:

US-09-978-600-151

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

RESULT 412

US-09-978-600-185/c
; Sequence 185, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; PARKER, WILLIAM D.
; DAVIS, ROBERT W.
; MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; Animal Models for Diseases Associated With Mitochondrial
; Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/978,600
; FILING DATE: 15-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 185:

US-09-978-600-185

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

RESULT 413

US-09-978-600-186/c
; Sequence 186, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; PARKER, WILLIAM D.
; DAVIS, ROBERT W.
; MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; Animal Models for Diseases Associated With Mitochondrial
; Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/978,600
; FILING DATE: 15-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-978-600-186

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTAATACCTT 579
|| ||||| ||||| |||||
Db 17 GGTTCCTTAATACCTT 1

RESULT 414
US-09-978-600-188/c
; Sequence 188, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; PARKER, WILLIAM D.
; DAVIS, ROBERT
; MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; Animal Models for Diseases Associated with Mitochondrial
; Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/978,600
; FILING DATE: 15-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0796
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-978-600-188

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTAATACCTT 579
|| ||||| ||||| |||||
Db 17 GGTTCCTTAATACCTT 1

RESULT 415
US-09-827-395A-217/c
; Sequence 217, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor C
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 217
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-217

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GGCTGCCCGGCGCTGG 31
|| ||||| ||||| |||||
Db 17 GCGCGCCCGGCGCTGG 1

RESULT 416
US-09-827-395A-888/c
; Sequence 888, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor C
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-888

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 AGGCTGCCCGGCGCGTG 30
| | | | | | | | | | | | | |
Db 17 AGGCGGCCCGGCGCGTG 1

RESULT 417

US-09-792-818-603
; Sequence 603, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 603
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-603

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 64.7%; Pred. No. 2.3e+02;

Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 105 TCAGTGGCGGCTATTGGA 121
: | | : | | | | : : | |
Db 1 UCAGUGGGCGUGUGGA 17

RESULT 418

US-10-060-756A-4243
; Sequence 4243, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 4243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4243

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 673 AAATTATGTTACTTGTT 689
| | | | | | | | | | | | | |
Db 1 AGATTATGTTCTTGTT 17

RESULT 419

US-10-339-782-270
; Sequence 270, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-0001100S
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-270

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 898 GACCAAGAGCCTCAACA 914
| | | | | | | | | | | | | |
Db 1 GATCAAGACCTCAACA 17

RESULT 420

US-10-240-046A-64
; Sequence 64, Application US/10240046A
; Publication No. US20030190639A1
; GENERAL INFORMATION:
; APPLICANT: HUGOT, JEAN-PIERRE
; APPLICANT: THOMAS, GILLES
; APPLICANT: ZOUALI, MOHAMED
; APPLICANT: LESAGE, SUZANNE
; APPLICANT: CHAMAILLARD, MATHIAS
; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE
; FILE REFERENCE: 37991-0009
; CURRENT APPLICATION NUMBER: US/10/240,046A
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: PCT/FR 01/00935
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: FR 00/03832
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-240-046A-64

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 197 GCCATCTCCCCCATCCC 213
| | | | | | | | | | | | | |
Db 1 GCCATCTCCCCCAAGCCC 17

US-10-430-882-888

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 AGGCTGCCGGCCGCGTG 30
||||| ||||| ||||| |||||
Db 17 AGGCGGCCAGGCGCGTG 1

RESULT 423

US-10-297-068-894

; Sequence 894, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 894
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-894

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 404 ACAATTCAAGGGTTTTT 420
||||| ||||| ||||| |||||
Db 1 ACAATTACAGGGTTTTT 17

RESULT 424

US-10-723-361-2563/c

; Sequence 2563, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

US-10-430-882-217/c

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GGCTGCCGGCCGCGTGG 31
||||| ||||| ||||| |||||
Db 17 GCGCGGCCAGGCGCGTGG 1

RESULT 422

US-10-430-882-888/c

; Sequence 888, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 217
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-217

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GGCTGCCGGCCGCGTGG 31
||||| ||||| ||||| |||||
Db 17 GCGCGGCCAGGCGCGTGG 1

RESULT 422

US-10-430-882-888/c

; Sequence 888, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2563

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      745 GCAGCTGCCACCTTATG 761
Db      17 GCAGCTGCCGCTTCTG 1

RESULT 425
US-10-723-361-2564/c
; Sequence 2564, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2564
```

```
Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      744 GCAGCTGCCACCTTAT 760
Db      17 GCAGCTGCCGCTTCT 1

RESULT 426
US-10-723-361-6749
; Sequence 6749, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 6749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6749

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      836 AGGAGCGCGGCTGGA 852
Db      1 AGGAGCGCGTGAGGA 17

RESULT 427
US-10-890-776A-4243
; Sequence 4243, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
```

Fri Aug 19 11:00:02 2005

RESULT 429
US-09-888-625-17
; Sequence 17, Application US/09888625
; Publication No. US20030064365A1
; GENERAL INFORMATION:
; Sequencing List
; APPLICANT: Kwangmyung Sungae Medical Foundation
; TITLE OF INVENTION: GAP VECTOR FOR E. COLI STOP CODON ASSAY AND METHOD FOR DETECTING
; FILE REFERENCE: Sungae-1
; CURRENT APPLICATION NUMBER: US/09/888,625
; CURRENT FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer BV-b5
US-09-888-625-17

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 CACATGAAAGTTTGAGA 1016
DB 1 CACATGCAAGTTTGAAA 17

RESULT 430
US-10-265-689-37/c
; Sequence 37, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RIQUIER, DANIEL
; APPLICANT: BOULLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-265-689-37

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 201 TCTCCCCCATCCCCCAT 217
DB 17 TCTCACCTTCCCCCAT 1

RESULT 428
US-09-468-147-6
; Sequence 6, Application US/09468147A
; Publication No. US20030049601A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlaunder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Deesai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushanwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/09/468,147A
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/173,141
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/061,199
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer C375
US-09-468-147-6

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 673 AAATTATGTTTACTTGT 689
DB 1 AGATTATGTTTCTGT 17

RESULT 428
US-09-468-147-6
; Sequence 6, Application US/09468147A
; Publication No. US20030049601A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlaunder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Deesai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushanwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/09/468,147A
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/173,141
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/061,199
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer C375
US-09-468-147-6

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1035 TAAACATCACACCCCAAC 1051
DB 2 TGAACATCAGCCCAAC 18

```
RESULT 431
US-10-319-745-6
; Sequence 6, Application US/10319745
; Publication No. US20030211467A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: HEPATITIS E VIRUS
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/10/319,745
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US/09/468,147A
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/173,141
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/061,199
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer C375
US-10-319-745-6

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1035 TAAACATCACACCCCAAC 1051
Db 2 TGAACATCACGCCCAAC 18
|||||

RESULT 432
US-10-108-260A-5064/c
; Sequence 5064, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5064
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-10-108-260A-5064

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 295 TGGATTGTTGTTCTG 311
Db 18 TGGATTGTTGTTCTG 2
|||||

RESULT 433
US-10-349-143-4732/c
; Sequence 4732, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4732
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798,
US-10-349-143-4732

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 905 AGCCTCAACATTTCCTA 921
Db 17 AGCCTCAGCATTCATA 1
|||||

RESULT 434
US-10-349-143-6041
; Sequence 6041, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6041
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-10-349-143-6041

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 942 AATCTGAAGCCCCACTC 958
```

```
Db      2 AATCTCAACCCCACTC 18
||||| ||| ||||| |||
RESULT 435
US-10-349-143-11352/c
; Sequence 11352, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSAT.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11352
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-4448 for SEQ 3487, in compleme
US-10-349-143-11352
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      204 CCCCCATCCCCCAATTC 220
||| ||||| ||| |||
Db      18 CCTCCATCCCCCACTC 2

RESULT 436
US-10-443-545-10
; Sequence 10, Application US/10443545
; Publication No. US20040038266A1
; GENERAL INFORMATION:
; APPLICANT: Neo Gen Screening, Inc.
; TITLE OF INVENTION: Advancing the Detection of Hearing Loss in Newborns through
; FILE REFERENCE: 2175
; CURRENT APPLICATION NUMBER: US/10/443,545
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: 60/370762
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-443-545-10
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      196 CGCCATCTCCCCATCC 212
| ||||| ||| |||
Db      1 CCCCATCTCCCCATCC 17
```

```
RESULT 437
US-10-486-319A-275
; Sequence 275, Application US/10486319A
; Publication No. US20050064410A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/486,319A
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 275
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for PGR
US-10-486-319A-275
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      616 TAGGAGATGAGTTTAT 632
||||| ||| |||
Db      2 TAGGAGATGAGATTTT 18

RESULT 438
US-10-486-319A-277/c
; Sequence 277, Application US/10486319A
; Publication No. US20050064410A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/486,319A
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 277
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for PGR
US-10-486-319A-277
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      616 TAGGAGATGAGTTTAT 632
||||| ||| |||
Db      17 TAGGAGATGAGATTTT 1

RESULT 439
US-10-352-179-63/c
; Sequence 63, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 63
```



```
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-63

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 414 GGTTTTCCTTATATT 430
Db 19 GGTTTTCCTTATATT 3

RESULT 440
US-10-444-795B-599/c
; Sequence 599, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 599
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - hTCPTP1.5
US-10-444-795B-599

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 343 GCCTGTGATCAATGGG 359
Db 18 GACTGTGATCATATGGG 2

RESULT 441
US-10-444-795B-600
; Sequence 600, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 600
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - hTCPTP1.5
US-10-444-795B-600

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 343 GCCTGTGATCAATGGG 359
| :|:|:|:|:|:|:|:|:|
```

```
Db 2 GACUGAUGAUCAUUGGG 18

RESULT 442
US-10-735-461-89
; Sequence 89, Application US/10735461
; Publication No. US20050014264A1
; GENERAL INFORMATION:
; APPLICANT: CZECH, Michael P.
; APPLICANT: ZHOU, Qionglin
; APPLICANT: JIANG, Zhen
; TITLE OF INVENTION: METHOD OF INTRODUCING siRNA INTO
; FILE REFERENCE: ADIPOCYTES
; CURRENT APPLICATION NUMBER: US/10/735,461
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/432427
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-735-461-89

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1097 TACCTGCTCATTTGTTT 1113
| | | | | | | | | | | | | | | |
Db 3 TACCACCTCATTTGTTT 19

RESULT 443
US-10-735-461-90
; Sequence 90, Application US/10735461
; Publication No. US20050014264A1
; GENERAL INFORMATION:
; APPLICANT: CZECH, Michael P.
; APPLICANT: ZHOU, Qionglin
; APPLICANT: JIANG, Zhen
; TITLE OF INVENTION: METHOD OF INTRODUCING siRNA INTO
; FILE REFERENCE: ADIPOCYTES
; CURRENT APPLICATION NUMBER: US/10/735,461
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/432427
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-735-461-90

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1097 TACCTGCTCATTTGTTT 1113
| | | | | | | | | | | | | | | |
Db 2 TACCACCTCATTTGTTT 18

RESULT 444
US-10-918-896-222/c
; Sequence 222, Application US/10918896
; Publication No. US20050164966A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
```

Fri Aug 19 11:00:02 2005

APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leo
APPLICANT: Chowira, Bharat
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
TITLE OF INVENTION: Growth Factor Receptor (IGF-1R) Gene Expression Using Short
TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/203 (MBHB03-195-B)
CURRENT APPLICATION NUMBER: US/10/918,896
CURRENT FILING DATE: 2004-08-16
PRIOR APPLICATION NUMBER: PCT/US03/05044
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720,448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-11-23
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 680
SOFTWARE: PatentIn version 3.3
SEQ ID NO 222
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-918-896-222

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 22 CGGGCCCTGGCAGGAG 38
Db 17 CGGCAGTGGCAGGGAG 1

RESULT 445
US-10-918-896-499
Sequence 499, Application US/10918896
Publication No. US20050164966A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Chowira, Bharat
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
TITLE OF INVENTION: Growth Factor Receptor (IGF-1R) Gene Expression Using Short
TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/203 (MBHB03-195-B)
CURRENT APPLICATION NUMBER: US/10/918,896
CURRENT FILING DATE: 2004-08-16
PRIOR APPLICATION NUMBER: PCT/US03/05044
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720,448

PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-11-23
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 680
SOFTWARE: PatentIn version 3.3
SEQ ID NO 499
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-918-896-499

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 22 CGGGCCCTGGCAGGAG 38
Db 3 CGGCAGUGGCAGGGAG 19

RESULT 446
US-10-923-329-124/c
Sequence 124, Application US/10923329
Publication No. US20050164968A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Richards, Ivan
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/225 (MBHB04-672)
CURRENT APPLICATION NUMBER: US/10/923,329
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: PCT/US04/13456
PRIOR FILING DATE: 2004-04-30
PRIOR APPLICATION NUMBER: US 10/780,447
PRIOR FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: US 60/292,217
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/362,016
PRIOR FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 60/363,883
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/311,865
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: US 10/727,780
PRIOR FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: US 60/543,480
PRIOR FILING DATE: 2004-02-10
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 514
SOFTWARE: PatentIn version 3.3
SEQ ID NO 124
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense

US-10-923-329-124

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 452 TGGGAGCAGTGGTAGCA 468
| | | | | | | | | | | | | | | | | | | | | |
Db 19 TGGGAGCAGAGGCAGCA 3

RESULT 447

US-10-923-329-320
; Sequence 320, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
; APPLICANT: Richards, Ivan
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
; FILE REFERENCE: 400/225 (MBH04-672)
; CURRENT APPLICATION NUMBER: US/10/923,329
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 320
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-923-329-320

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 452 TGGGAGCAGTGGTAGCA 468
: | | | | | | | | | | | | | | | | | | | | | |
Db 1 UGGGAGCAGAGGCAGCA 17

RESULT 448

US-09-916-466-24/c
; Sequence 24, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Relate

; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-916-466-24

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 380 GCAGGCAATGCAGTC 394
| | | | | | | | | | | | | | | | | | | | | |
Db 15 GCAGGCAAGCAGTC 1

RESULT 449

US-10-277-494-24/c
; Sequence 24, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-277-494-24

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 380 GCAGGCAATGCAGTC 394
| | | | | | | | | | | | | | | | | | | | | |
Db 15 GCAGGCAAGCAGTC 1

RESULT 450

US-10-339-674-1179/c
; Sequence 1179, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1179
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1357006)...(1357020)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-339-674-1179

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1034 GTAAACATCACACCC 1048
DB 15 GTAAACAGCACACCC 1

RESULT 451
US-10-339-674-3197/c
; Sequence 3197, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 3197
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (4276408)...(4276422)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4240
US-10-339-674-3197

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1034 GTAAACATCACACCC 1048
DB 15 GTAAACAGCACACCC 1

RESULT 452
US-10-342-450-3/c
; Sequence 3, Application US/10342450
; Publication No. US20040091880A1
; GENERAL INFORMATION:
; APPLICANT: Wiebusch, Heiko
; APPLICANT: Schmitt-John, Thomas
; APPLICANT: Weidner, Jurgen
; TITLE OF INVENTION: A Method For Direct Genetic Analysis of
; TARGET CELLS BY USING FLUORESCENCE PROBES
; FILE REFERENCE: 3515.1000-000
; CURRENT APPLICATION NUMBER: US/10/342,450
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/EP01/08202
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: EP 00115268.5
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-342-450-3

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 GAAGCAGCGCGGCC 56
DB 15 GAAGCAGCGCGGCC 1

RESULT 453
US-10-255-120-466

; Sequence 466, Application US/10255120
; Publication No. US20040091865A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori, strain J99 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/255,120
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 903
; SOFTWARE: Proprietary
; SEQ ID NO 466
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Helicobacter pylori, strain J99 complete genome.
; FEATURE:
; LOCATION: (821578)...(821593)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 703,
US-10-255-120-466

Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTTACCTGGGA 456
DB 1 TGGTTTTCAGCTGGGA 15

RESULT 454
US-10-255-120-890
; Sequence 890, Application US/10255120
; Publication No. US20040091865A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori, strain J99 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/255,120
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 903
; SOFTWARE: Proprietary
; SEQ ID NO 890
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Helicobacter pylori, strain J99 complete genome.
; FEATURE:
; LOCATION: (1618564)...(1618579)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 135,
US-10-255-120-890

Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTTACCTGGGA 456
DB 1 TGGTTTTCAGCTGGGA 15

RESULT 455
US-09-866-108-2567/c
; Sequence 2567, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2567

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCACCT 1

RESULT 456
US-09-866-108-6287
; Sequence 6287, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6287

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGGCCGTGGCAGG 35
Db 3 CCGGGCCGTGGCAGG 17

RESULT 457
US-09-866-108-6288
; Sequence 6288, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

Fri Aug 19 11:00:02 2005

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 6288
; TYPE: DNA
; LENGTH: 17
; ORGANISM: Homo sapiens
US-09-866-108-6288

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
        ||||| |||||
Db       2 CCGGGCCGTGGCAGG 16

RESULT 458
US-09-866-108-6289
; Sequence 6289, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
```

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; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 6289
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6289

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
        ||||| |||||
Db       1 CCGGGCCGTGGCAGG 15

RESULT 459
US-09-780-533A-818
; Sequence 818, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION: Pharmaceuticals, Inc.
; APPLICANT: Ribozyme
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 818
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-818

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      49 CCGCGGCCCGCCAGTTC 63
        ||||| |||||
Db       2 CCGCGGCCCGCCAGUC 16

RESULT 460
US-09-780-533A-819
; Sequence 819, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION: Pharmaceuticals, Inc.
; APPLICANT: Ribozyme
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 819
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

US-09-780-533A-819

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 49 CCGGGCCCCCAGTTC 63
:|||||:|
Db 1 CCGGGCCCCCAGUC 15

RESULT 461

US-09-780-533A-2566/c
; Sequence 2566, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00_878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2566
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2566

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 415 GTTTTCCTTATTT 429
:|||||:|
Db 16 GTTTTCCTTATTT 2

RESULT 462

US-09-877-478-949
; Sequence 949, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1995-05-04

; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-949

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 570 TTAATACCTTTATAT 584
:|||||:|
Db 1 UUAAGCCUUUAU 15

RESULT 463

US-09-877-478-1483
; Sequence 1483, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1483

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 569 TTTAATACCTTTATA 583
:|||||:|
Db 3 UUAAGCCUUUAU 17

RESULT 464

US-10-060-756A-4244
; Sequence 4244, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

```
Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative      8; Mismatches 1; Indels 0; Gaps 0;
```



```
QY 570 TTAATACCTTTATAT 584
      ::||: ||::||:|
Db 1 UUAAGCCUUUAU 15

RESULT 468
US-10-342-902-1483
; Sequence 1483, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-1483

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATA 583
      ::||: ||::||:|
Db 3 UUAAGCCUUUAU 17

RESULT 469
US-10-138-674-4443/c
; Sequence 4443, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4443

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATA 583
      ::||: ||::||:|
Db 3 UUAAGCCUUUAU 17

RESULT 469
US-10-138-674-4443/c
; Sequence 4443, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4443
```

```
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCAGCA 640
      ||||| |||||
Db 15 GTTTATGCTCAGCA 1

RESULT 470
US-10-138-674-9117/c
; Sequence 9117, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9117
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-9117

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 817 AGCAGGCTTCATG 831
      ||||| |||||
Db 15 AGCAGAGCTTCATG 1

RESULT 471
US-10-287-949A-4443/c
; Sequence 4443, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4443

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCAGCA 640
      ||||| |||||
Db 15 GTTTATGCTCAGCA 1
```

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; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-949

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches      6; Conservative      8; Mismatches      1; Indels      0; Gaps      0;

QY      570 TTAATACCTTTATAT 584
DB      1 UUAAGCCUUUAU 15

RESULT 474
US-10-669-841-1483
; Sequence 1483, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-1483

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches      6; Conservative      8; Mismatches      1; Indels      0; Gaps      0;

QY      569 TTTAATACCTTTATA 583
DB      3 UUUAAUGCCUUUAU 17

```

RESULT 475

US-10-723-361-2567/c
; Sequence 2567, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2567

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCGCT 1

RESULT 476

US-10-723-361-6287
; Sequence 6287, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6287

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGCGCTGGCAGG 35
Db 3 CCGGCGCTGGCAGG 17

RESULT 477

US-10-723-361-6288
; Sequence 6288, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.

Fri Aug 19 11:00:02 2005

```
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 6288
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6288

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
    ||||| |||||
DB 2 CCGGGCTGTGGCAGG 16

RESULT 478
US-10-723-361-6289
; Sequence 6289, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PH0105
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 6289
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6289

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
    ||||| |||||
DB 1 CCGGGCTGTGGCAGG 15

RESULT 479
US-10-712-633-348/c
```

```
; Sequence 348, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-348

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCTCAGCA 640
    ||||| |||||
DB 15 GTTTATGCTCAGCA 1

RESULT 480
US-10-712-633-4385/c
; Sequence 4385, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
```

```
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4385
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-4385

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      817 AGCAGGCTCTCATG 831
Db      15 AGCAGACCTCTCATG 1

RESULT 481
US-10-494-343-812/c
; Sequence 812, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 812
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-812

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      393 TCATTTTCCTTACAA 407
Db      17 TCATTTTCCTTTCAA 3

RESULT 482
US-10-494-343-813/c
; Sequence 813, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 813
```

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-813

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      393 TCATTTTCCTTACAA 407
Db      16 TCATTTTCCTTTCAA 2

RESULT 483
US-10-494-343-814/c
; Sequence 814, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 814
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-814

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      393 TCATTTTCCTTACAA 407
Db      15 TCATTTTCCTTTCAA 1

RESULT 484
US-10-890-776A-4244
; Sequence 4244, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
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Fri Aug 19 11:00:02 2005

```
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4244
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4244

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 675 ATTATGTTTCTTGT 689
Db 2 ATTATGTTTCTTGT 16

RESULT 485
US-10-890-776A-4245
; Sequence 4245, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4245
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4245

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 675 ATTATGTTTCTTGT 689
Db 1 ATTATGTTTCTTGT 15

RESULT 486
US-10-704-513-258/c
; Sequence 258, Application US/10704513
; Publication No. US20050170500A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: KAMMERER, STEFAN M.
```

```
; APPLICANT: BRAUN, ANDREAS
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS
; FILE REFERENCE: SEQ-4062-UT
; CURRENT APPLICATION NUMBER: US/10/704,513
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 60/489,703
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 60/424,475
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 774
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
US-10-704-513-258

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 702 TAGTCACGGTGCTCT 716
Db 16 TAGTCACGGTGCTCT 2

RESULT 487
US-09-969-373-3260
; Sequence 3260, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3260
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3260

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 994 TGTATGCACATGAAA 1008
Db 1 TGTATGCACATGAAA 15

RESULT 488
US-09-816-814-2
; Sequence 2, Application US/09816814
; Publication No. US20030027136A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
```

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-816-814-2

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      277 GGCATATTTCTTCAC 231
Db      1 GGCATGTTTCTTCAC 15

RESULT 489
US-10-138-316-43
; Sequence 43, Application US/10138316
; Publication No. US20030054380A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-162
; CURRENT APPLICATION NUMBER: US/10/138,316
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-138-316-43

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      48 GCGCGGCGCCCGAGTT 62
Db      2 GCGCGGCGCCCGAGTT 16

RESULT 490
US-10-128-560-139/c
; Sequence 139, Application US/10128560
; Publication No. US20030134272A1
; GENERAL INFORMATION:
; APPLICANT: Universiteit Gent
; TITLE OF INVENTION: Improved mutation analysis of the NF1 Gene
; FILE REFERENCE: UG-005-PCT
; CURRENT APPLICATION NUMBER: US/10/128,560
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 09/9870216.1
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: EP 99870216.1
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: EP 00870122.9
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: UG 60/211,929
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 195
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-560-139/c

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      416 TTTTTCCTTATATTT 430
Db      18 TTTTTCCTTATAGTT 4

RESULT 491
US-10-128-560-195/c
; Sequence 195, Application US/10128560
; Publication No. US20030134272A1
; GENERAL INFORMATION:
; APPLICANT: Universiteit Gent
; TITLE OF INVENTION: Improved mutation analysis of the NF1 Gene
; FILE REFERENCE: UG-005-PCT
; CURRENT APPLICATION NUMBER: US/10/128,560
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 99870216.1
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: EP 00870122.9
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: UG 60/211,929
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 195
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-560-195/c

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      416 TTTTTCCTTATATTT 430
Db      18 TTTTTCCTTATAGTT 4

RESULT 492
US-10-368-643-43
; Sequence 43, Application US/10368643
; Publication No. US20030170708A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLOT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-163
; CURRENT APPLICATION NUMBER: US/10/368,643
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/597,731
; PRIOR FILING DATE: 2000-06-19
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; PRIOR APPLICATION NUMBER: US 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: US 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: US 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: US 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: US 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-368-643-43

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      48  GCGCGCGCCCGCAGTT 62
          ||||| |||||
Db       2  GCGCGCGCCCGCAGTT 16

RESULT 493
US-10-349-143-5495/c
; Sequence 5495, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-21
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-11-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5495
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-4677 for SEQ 1561,
US-10-349-143-5495

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1060 CTTTCCAGTGGCTAA 1074
          ||| |||||
Db       18  CTTACCAGTGGCTAA 4

RESULT 494
US-10-349-143-5744
; Sequence 5744, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel

```

```

; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-21
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-11-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5744
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6557 for SEQ 1810,
US-10-349-143-5744

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      612  TAAGTAGGAGATGAG 626
          ||||| |||||
Db       3  TAAGTAAGAGATGAG 17

RESULT 495
US-10-764-238-81
; Sequence 81, Application US/10764238
; Publication No. US20040219616A1
; GENERAL INFORMATION:
; APPLICANT: Eirx Therapeutics Ltd.
; APPLICANT: Seery, Liam
; APPLICANT: Hayes, Ian
; APPLICANT: Murphy, Finbarr
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
; FILE REFERENCE: 8912/2012
; CURRENT APPLICATION NUMBER: US/10/764,238
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/457,533
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: UK 0301566.5
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: QPCR Reverse Primer (Bcl2)
US-10-764-238-81

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      199  CATCTCCCGCATCCC 213
          ||||| |||||
Db       3  CATCTCCCGCATCCC 17

RESULT 496
US-10-861-520-43
; Sequence 43, Application US/10861520

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; Publication No. US20040233038A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-167
; CURRENT APPLICATION NUMBER: US/10/861,520
; CURRENT FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: 10/138,316
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-861-520-43

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      48  GCCGCGGCCCCAGTT 62
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Db      2  GCCGCGGCCCCAGTT 16

RESULT 497
US-10-911-678-43
; Sequence 43, Application US/10911678
; Publication No. US2005003439A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-169
; CURRENT APPLICATION NUMBER: US/10/911,678
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: 10/138,316
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-911-678-43

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      48  GCCGCGGCCCCAGTT 62
        ||||| |||||
Db      2  GCCGCGGCCCCAGTT 16

RESULT 497
US-10-911-678-43
; Sequence 43, Application US/10911678
; Publication No. US2005003439A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-169
; CURRENT APPLICATION NUMBER: US/10/911,678
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: 10/138,316
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-911-678-43

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      199 CATCTCCCGCATCCC 213
        ||||| |||||
Db      3  CATCTCCCGCATCCC 17

RESULT 499
US-09-901-484A-372/c
; Sequence 372, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T111XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
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; PRIORITY APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-901-484A-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 500
US-09-853-526-372/c
; Sequence 372, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18C1P
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIORITY APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-853-526-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 501
US-10-349-143-4387/c
; Sequence 4387, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
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; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIORITY APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4387
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453,
US-10-349-143-4387

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 502
US-10-349-143-11326
; Sequence 11326, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11326
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-4233 for SEQ 3461, in compleme
US-10-349-143-11326

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 CATTTCCTTACAAT 408
Db 4 CATTTCCTTACAAT 18

RESULT 503
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US-10-746-167-80/C
; Sequence 80, Application US/10746167
; Publication No. US20040185530A1
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
; FILE REFERENCE: 1794.0030004
; CURRENT APPLICATION NUMBER: US/10/746.167
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/09/818,780
; PRIOR FILING DATE: 2001-03-28

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Qy 415 GTTTTCCCTATTT 429
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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1779
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1547
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-522-1547

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 958 CTGGACCCAGGACAT 972
Db 15 CTGGACTCAGGACAT 1

RESULT 510

US-10-864-044-66/c
; Sequence 66, Application US/10864044
; Publication No. US20050171040A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 04-466-B (400/161)
; CURRENT APPLICATION NUMBER: US/10/864,044
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 10/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-864-044-66

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 370 CCTTGTGTGGCAGG 384
Db 18 CCTTGTGTGGCAGG 4

RESULT 511

US-10-864-044-166
; Sequence 166, Application US/10864044
; Publication No. US20050171040A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 04-466-B (400/161)
; CURRENT APPLICATION NUMBER: US/10/864,044
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 10/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-864-044-166

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 370 CCTTGTGTGGCAGG 384
Db 2 CCUGUUUGGCAGG 16

Search completed: August 19, 2005, 10:59:40
Job time : 13 secs

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:54:17 ; Search time 6 Seconds
(without alignments)

2.738 Million cell updates/sec

Title: US-10-774-721-21

Perfect score: 1114

Sequence: 1 gctcggcttggcaggtgc.....gttaccgtcattgttta 1114

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 422 seqs, 7374 residues

Total number of hits satisfying chosen parameters: 844

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 471 summaries

Database : isdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	1.7	19	1	US-08-803-346-51
2	18.8	1.7	25	1	US-09-396-196G-107033
3	18.6	1.7	25	1	US-09-396-196G-125800
4	18	1.6	18	1	US-08-803-346-50
5	18	1.6	18	1	US-08-780-562-30
6	18	1.6	18	1	US-08-780-562-31
7	17.6	1.6	25	1	US-09-396-196G-20048
8	16.2	1.5	21	1	US-08-222-177A-296
9	16.2	1.5	21	1	US-08-117-952-600
10	15.8	1.4	20	1	US-08-836-261A-72
11	15.8	1.4	21	1	US-09-816-814-7
12	15.8	1.4	22	1	US-09-792-024-382
13	15.4	1.4	18	1	US-09-422-978-11660
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15	15.4	1.4	20	1	PCT-US94-06311A-65
16	15.4	1.4	20	1	US-08-486-408-14
17	15.4	1.4	20	1	US-08-975-570-14
18	15.2	1.4	20	1	US-09-428-584-11
19	15.2	1.4	20	1	US-09-198-452A-6064
20	15.2	1.4	20	1	US-09-980-052-219
21	15.2	1.4	21	1	US-09-657-472-690
22	14.8	1.3	20	1	US-09-280-799-152
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24	14.8	1.3	20	1	US-08-875-847B-9
25	14.8	1.3	20	1	US-09-378-842-9
26	14.8	1.3	20	1	US-09-858-152B-9
27	14.8	1.3	21	1	US-09-667-472-1733
28	14.4	1.3	17	1	US-09-866-108A-2565
29	14.4	1.3	17	1	US-09-866-108A-2566
30	14.4	1.3	19	1	US-09-544-398B-588
31	14.4	1.3	19	1	US-09-696-791-3308
32	14.4	1.3	19	1	US-09-543-771B-588
33	14.4	1.3	20	1	US-09-422-978-6795

C 34	14.4	1.3	20	1	US-09-198-452A-1803	Sequence 1803, Ap
C 35	14.4	1.3	20	1	US-09-953-318-37	Sequence 37, Appl
C 36	14.4	1.3	20	1	US-09-917-963-91	Sequence 91, Appl
C 37	14.2	1.3	20	1	US-08-105-483-336	Sequence 336, Appl
C 38	14.2	1.3	20	1	US-08-389-067-9	Sequence 9, Appl
C 39	14.2	1.3	20	1	US-08-709-209-336	Sequence 336, Appl
C 40	14.2	1.3	20	1	US-08-458-101-336	Sequence 336, Appl
C 41	14.2	1.3	20	1	US-08-478-178A-86	Sequence 86, Appl
C 42	14.2	1.3	20	1	US-08-488-177-86	Sequence 86, Appl
C 43	14.2	1.3	20	1	US-08-634-350-24	Sequence 24, Appl
C 44	14.2	1.3	20	1	US-08-481-072A-86	Sequence 86, Appl
C 45	14.2	1.3	20	1	US-08-664-336-86	Sequence 86, Appl
C 46	14.2	1.3	20	1	US-08-481-066A-86	Sequence 86, Appl
C 47	14.2	1.3	20	1	US-08-578-615A-94	Sequence 94, Appl
C 48	14.2	1.3	20	1	US-09-392-580-12	Sequence 12, Appl
C 49	14.2	1.3	20	1	US-09-43-699-36	Sequence 36, Appl
C 50	14.2	1.3	20	1	US-08-829-637A-86	Sequence 86, Appl
C 51	14.2	1.3	20	1	US-09-851-520-4	Sequence 4, Appl
C 52	14.2	1.3	20	1	US-09-792-594-57	Sequence 57, Appl
C 53	14.2	1.3	20	1	US-09-668-313A-208	Sequence 208, App
C 54	14.2	1.3	20	1	US-09-422-978-9409	Sequence 9409, Ap
C 55	14.2	1.3	20	1	US-10-025-139-86	Sequence 86, Appl
C 56	14.2	1.3	20	1	US-09-198-452A-2125	Sequence 2125, Ap
C 57	14.2	1.3	20	1	US-09-198-452A-4121	Sequence 4121, Ap
C 58	14.2	1.3	20	1	US-09-198-452A-5159	Sequence 5159, Ap
C 59	14.2	1.3	20	1	US-09-198-452A-5166	Sequence 5166, Ap
C 60	14.2	1.3	20	1	US-09-198-452A-6581	Sequence 6581, Ap
C 61	14.2	1.3	20	1	US-10-054-225-12	Sequence 12, Appl
C 62	14.2	1.3	20	1	US-09-771-357-79	Sequence 79, Appl
C 63	14.2	1.3	20	1	US-09-543-398B-310	Sequence 310, Appl
C 64	14.2	1.3	20	1	US-09-543-771B-310	Sequence 310, Appl
C 65	14.2	1.3	20	1	US-10-059-579A-79	Sequence 79, Appl
C 66	14.2	1.3	20	1	PCT-US94-07770-94	Sequence 94, Appl
C 67	14	1.3	15	1	US-08-319-492B-460	Sequence 460, Appl
C 68	14	1.3	18	1	US-09-422-978-5553	Sequence 5553, Ap
C 69	14	1.3	20	1	US-09-422-978-4185	Sequence 4185, Ap
C 70	14	1.3	20	1	US-09-422-978-5624	Sequence 5624, Ap
C 71	14	1.3	20	1	US-09-665-615B-156	Sequence 156, Appl
C 72	14	1.3	20	1	US-10-172-911-55	Sequence 55, Appl
C 73	13.8	1.2	17	1	US-08-219-842-12	Sequence 12, Appl
C 74	13.8	1.2	17	1	US-08-451-096-12	Sequence 12, Appl
C 75	13.8	1.2	17	1	US-08-810-599-64	Sequence 64, Appl
C 76	13.8	1.2	17	1	US-08-413-740A-140	Sequence 140, Appl
C 77	13.8	1.2	17	1	US-08-413-740A-151	Sequence 151, Appl
C 78	13.8	1.2	17	1	US-08-413-740A-185	Sequence 185, Appl
C 79	13.8	1.2	17	1	US-08-413-740A-186	Sequence 186, Appl
C 80	13.8	1.2	17	1	US-08-413-740A-188	Sequence 188, Appl
C 81	13.8	1.2	17	1	US-09-866-108A-2563	Sequence 2563, Ap
C 82	13.8	1.2	17	1	US-09-866-108A-2564	Sequence 2564, Ap
C 83	13.8	1.2	17	1	US-09-866-108A-6749	Sequence 6749, Ap
C 84	13.8	1.2	17	1	PCT-US95-04063-140	Sequence 140, Appl
C 85	13.8	1.2	17	1	PCT-US95-04063-151	Sequence 151, Appl
C 86	13.8	1.2	17	1	PCT-US95-04063-185	Sequence 185, Appl
C 87	13.8	1.2	17	1	PCT-US95-04063-186	Sequence 186, Appl
C 88	13.8	1.2	17	1	PCT-US95-04063-188	Sequence 188, Appl
C 89	13.8	1.2	18	1	US-08-219-842-23	Sequence 23, Appl
C 90	13.8	1.2	18	1	US-08-451-096-23	Sequence 23, Appl
C 91	13.8	1.2	18	1	US-08-634-350-23	Sequence 23, Appl
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C 93	13.8	1.2	18	1	US-09-422-978-6041	Sequence 6041, Ap
C 94	13.8	1.2	18	1	US-09-422-978-11352	Sequence 11352, A
C 95	13.8	1.2	19	1	US-09-696-791-649	Sequence 649, Appl
C 96	13.8	1.2	19	1	US-09-696-791-1039	Sequence 1039, Ap
C 97	13.4	1.2	16	1	US-08-311-760A-354	Sequence 354, Appl
C 98	13.4	1.2	16	1	US-08-774-310-354	Sequence 354, Appl
C 99	13.4	1.2	17	1	US-08-373-144A-1915	Sequence 1915, Ap
C 100	13.4	1.2	17	1	US-08-435-628-1915	Sequence 1915, Ap
C 101	13.4	1.2	17	1	US-09-371-772B-4443	Sequence 4443, Ap
C 102	13.4	1.2	17	1	US-09-866-108A-2567	Sequence 2567, Ap
C 103	13.4	1.2	17	1	US-09-866-108A-6287	Sequence 6287, Ap
C 104	13.4	1.2	17	1	US-09-866-108A-6288	Sequence 6288, Ap
C 105	13.4	1.2	17	1	US-09-866-108A-6289	Sequence 6289, Ap
C 106	13.4	1.2	18	1	US-09-135-021-41	Sequence 41, Appl

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107	13.4	1.2	18	1	US-09-135-020-43	Sequence 43, Appl	C 180	12.8	1.1	17	US-09-866-108A-7017
108	13.4	1.2	18	1	US-09-135-010A-43	Sequence 43, Appl	C 181	12.8	1.1	17	US-09-866-108A-7967
109	13.4	1.2	18	1	US-09-444-871-43	Sequence 43, Appl	C 182	12.8	1.1	17	US-09-866-108A-7968
110	13.4	1.2	18	1	US-09-662-402A-6	Sequence 6, Appl	C 183	12.8	1.1	17	US-09-866-108A-8291
111	13.4	1.2	18	1	US-09-597-735-43	Sequence 43, Appl	C 184	12.8	1.1	17	US-09-866-108A-8292
112	13.4	1.2	18	1	US-09-444-235-43	Sequence 43, Appl	C 185	12.8	1.1	17	US-09-866-108A-8292
113	13.4	1.2	18	1	US-09-597-732-43	Sequence 43, Appl	C 186	12.8	1.1	17	US-09-720-435A-351
114	13.4	1.2	18	1	US-09-422-978-5495	Sequence 5495, Ap	C 187	12.8	1.1	17	US-09-902-563-40
115	13.4	1.2	18	1	US-09-422-978-5744	Sequence 5744, Ap	C 188	12.8	1.1	17	US-09-093-972C-731
116	13.4	1.2	18	1	US-09-597-731-43	Sequence 43, Appl	C 189	12.8	1.1	17	US-09-093-972C-749
117	13.4	1.2	18	1	US-09-816-814-2	Sequence 2, Appl	C 190	12.8	1.1	18	US-08-403-634-21
118	13.4	1.2	19	1	US-09-338-907-372	Sequence 372, App	C 191	12.8	1.1	18	US-08-468-580-34
119	13.4	1.2	19	1	US-09-218-207-372	Sequence 372, App	C 192	12.8	1.1	18	US-08-816-693A-25
120	13.4	1.2	19	1	US-09-228-302-23	Sequence 23, Appl	C 193	12.8	1.1	18	US-09-212-771-42
121	13.4	1.2	19	1	US-09-422-978-4387	Sequence 4387, Ap	C 194	12.8	1.1	18	US-09-213-768-39
122	13.4	1.2	19	1	US-09-422-978-11326	Sequence 11326, A	C 195	12.8	1.1	18	US-09-161-244-74
123	13.4	1.2	19	1	US-09-818-780-80	Sequence 80, Appl	C 196	12.8	1.1	18	US-09-255-888-35
124	13.4	1.2	19	1	US-09-696-791-3671	Sequence 3671, Ap	C 197	12.8	1.1	18	US-08-757-024-711
125	13.2	1.2	18	1	US-08-02-547-12	Sequence 12, Appl	C 198	12.8	1.1	18	US-08-757-024-730
126	13.2	1.2	18	1	US-08-800-751-34	Sequence 34, Appl	C 199	12.8	1.1	18	US-08-757-024-748
127	13.2	1.2	18	1	US-08-712-357-12	Sequence 12, Appl	C 200	12.8	1.1	18	US-08-885-291-25
128	13.2	1.2	18	1	US-08-525-849C-3	Sequence 3, Appl	C 201	12.8	1.1	18	US-08-913-441B-21
129	13.2	1.2	18	1	US-08-749-495A-3	Sequence 3, Appl	C 202	12.8	1.1	18	US-08-643-212-56
130	13.2	1.2	18	1	US-08-990-818-34	Sequence 34, Appl	C 203	12.8	1.1	18	US-09-496-672-25
131	13.2	1.2	18	1	US-09-205-204-37	Sequence 37, Appl	C 204	12.8	1.1	18	US-09-167-109-184
132	13.2	1.2	18	1	US-09-169-078-3	Sequence 3, Appl	C 205	12.8	1.1	18	US-09-506-768-2
133	13.2	1.2	18	1	US-08-434-511-2	Sequence 2, Appl	C 206	12.8	1.1	18	US-09-475-947A-340
134	13.2	1.2	18	1	US-09-229-150-2	Sequence 2, Appl	C 207	12.8	1.1	18	US-09-422-978-5124
135	13.2	1.2	18	1	US-09-182-145-131	Sequence 131, App	C 208	12.8	1.1	18	US-09-422-978-7460
136	13.2	1.2	18	1	US-09-422-978-5708	Sequence 5708, Ap	C 209	12.8	1.1	18	US-09-696-791-4204
137	13.2	1.2	18	1	US-09-422-978-9959	Sequence 9959, Ap	C 210	12.8	1.1	18	US-09-856-662-80
138	13.2	1.2	18	1	US-09-533-494A-29	Sequence 29, Appl	C 211	12.8	1.1	18	US-09-720-435A-349

C 253	12.4	1.1	16	1	US-09-479-005A-12	Sequence 12, Appl	C 326	12.2	1.1	17	1	US-08-373-124A-458	Sequence 458, App
C 254	12.4	1.1	16	1	US-09-410-416-19	Sequence 19, Appl	327	12.2	1.1	17	1	US-08-373-124A-504	Sequence 504, App
C 255	12.4	1.1	17	1	US-07-696-793A-19	Sequence 19, Appl	328	12.2	1.1	17	1	US-08-373-124A-716	Sequence 716, App
C 256	12.4	1.1	17	1	US-07-696-793A-20	Sequence 20, Appl	C 329	12.2	1.1	17	1	US-08-373-124A-1341	Sequence 1341, Ap
C 257	12.4	1.1	17	1	US-07-977-694-19	Sequence 19, Appl	330	12.2	1.1	17	1	US-08-373-124A-1559	Sequence 1559, Ap
C 258	12.4	1.1	17	1	US-07-977-694-20	Sequence 20, Appl	331	12.2	1.1	17	1	US-08-373-124A-2393	Sequence 2393, Ap
C 259	12.4	1.1	17	1	US-08-098-726-46	Sequence 46, Appl	332	12.2	1.1	17	1	US-08-373-124A-2437	Sequence 2437, Ap
C 260	12.4	1.1	17	1	US-08-098-043-43	Sequence 43, Appl	333	12.2	1.1	17	1	US-08-373-124A-2563	Sequence 2563, Ap
C 261	12.4	1.1	17	1	US-08-093-577-39	Sequence 39, Appl	C 334	12.2	1.1	17	1	US-08-200-232-5	Sequence 5, Appl
C 262	12.4	1.1	17	1	US-08-390-850-601	Sequence 601, App	C 335	12.2	1.1	17	1	US-08-435-634-479	Sequence 479, App
C 263	12.4	1.1	17	1	US-08-373-124A-572	Sequence 572, App	C 336	12.2	1.1	17	1	US-08-435-634-480	Sequence 480, App
C 264	12.4	1.1	17	1	US-08-373-124A-1611	Sequence 1611, Ap	C 337	12.2	1.1	17	1	US-07-936-421-22	Sequence 22, Appl
C 265	12.4	1.1	17	1	US-08-373-124A-1917	Sequence 1917, Ap	C 338	12.2	1.1	17	1	US-08-435-628-456	Sequence 456, App
C 266	12.4	1.1	17	1	US-08-434-411-55	Sequence 55, Appl	C 339	12.2	1.1	17	1	US-08-435-628-458	Sequence 458, App
C 267	12.4	1.1	17	1	US-08-096-623A-51	Sequence 51, Appl	C 340	12.2	1.1	17	1	US-08-435-628-504	Sequence 504, App
C 268	12.4	1.1	17	1	US-08-434-402-55	Sequence 55, Appl	341	12.2	1.1	17	1	US-08-435-628-716	Sequence 716, App
C 269	12.4	1.1	17	1	US-08-435-628-601	Sequence 601, Appl	C 342	12.2	1.1	17	1	US-08-435-628-1341	Sequence 1341, Ap
C 270	12.4	1.1	17	1	US-08-783-288-55	Sequence 55, Appl	C 343	12.2	1.1	17	1	US-08-435-628-1559	Sequence 1559, Ap
C 271	12.4	1.1	17	1	US-08-435-628-572	Sequence 572, App	C 344	12.2	1.1	17	1	US-08-435-628-2393	Sequence 2393, Ap
C 272	12.4	1.1	17	1	US-08-435-628-1611	Sequence 1611, Ap	C 345	12.2	1.1	17	1	US-08-435-628-2437	Sequence 2437, Ap
C 273	12.4	1.1	17	1	US-08-435-628-1917	Sequence 1917, Ap	C 346	12.2	1.1	17	1	US-08-435-628-2563	Sequence 2563, Ap
C 274	12.4	1.1	17	1	US-08-313-185-35	Sequence 35, Appl	C 347	12.2	1.1	17	1	US-08-985-162-157	Sequence 157, App
C 275	12.4	1.1	17	1	US-08-890-640-55	Sequence 55, Appl	C 348	12.2	1.1	17	1	US-08-985-162-283	Sequence 283, App
C 276	12.4	1.1	17	1	US-09-082-614A-35	Sequence 35, Appl	C 349	12.2	1.1	17	1	US-08-985-162-337	Sequence 337, App
C 277	12.4	1.1	17	1	US-09-306-595C-27	Sequence 27, Appl	C 350	12.2	1.1	17	1	US-08-985-162-631	Sequence 631, App
C 278	12.4	1.1	17	1	US-08-584-040-2568	Sequence 2568, Ap	351	12.2	1.1	17	1	US-08-985-162-653	Sequence 653, App
C 279	12.4	1.1	17	1	US-08-584-040-3886	Sequence 3886, Ap	C 352	12.2	1.1	17	1	US-08-985-162-654	Sequence 654, App
C 280	12.4	1.1	17	1	US-09-634-918-3	Sequence 1, Appl	C 353	12.2	1.1	17	1	US-08-988-706-45	Sequence 45, Appl
C 281	12.4	1.1	17	1	US-09-634-918-3	Sequence 3, Appl	C 354	12.2	1.1	17	1	US-09-192-104-7	Sequence 7, Appl
C 282	12.4	1.1	17	1	US-09-474-432B-475	Sequence 475, App	355	12.2	1.1	17	1	US-09-275-680-7	Sequence 7, Appl
C 283	12.4	1.1	17	1	US-09-474-432B-667	Sequence 667, App	C 356	12.2	1.1	17	1	US-09-324-867-24	Sequence 24, Appl
C 284	12.4	1.1	17	1	US-09-371-772B-1092	Sequence 1092, Ap	C 357	12.2	1.1	17	1	US-09-543-446-7	Sequence 7, Appl
C 285	12.4	1.1	17	1	US-09-371-772B-1653	Sequence 1653, Ap	C 358	12.2	1.1	17	1	US-08-584-040-1689	Sequence 1689, Ap
C 286	12.4	1.1	17	1	US-09-371-772B-5446	Sequence 5446, Ap	C 359	12.2	1.1	17	1	US-08-584-040-1739	Sequence 1739, Ap
C 287	12.4	1.1	17	1	US-09-371-772B-6259	Sequence 6259, Ap	C 360	12.2	1.1	17	1	US-08-584-040-2165	Sequence 2165, Ap
C 288	12.4	1.1	17	1	US-09-371-772B-6260	Sequence 6260, Ap	C 361	12.2	1.1	17	1	US-08-584-040-2167	Sequence 2167, Ap
C 289	12.4	1.1	17	1	US-09-925-388-27	Sequence 27, Appl	C 362	12.2	1.1	17	1	US-08-584-040-4021	Sequence 4021, Ap
C 290	12.4	1.1	17	1	US-09-476-387-474	Sequence 474, App	C 363	12.2	1.1	17	1	US-08-584-040-5664	Sequence 5664, Ap
C 291	12.4	1.1	17	1	US-09-476-387-666	Sequence 666, App	C 364	12.2	1.1	17	1	US-08-584-040-5710	Sequence 5710, Ap
C 292	12.4	1.1	17	1	US-09-827-998-513	Sequence 513, App	C 365	12.2	1.1	17	1	US-08-584-040-7398	Sequence 7398, Ap
C 293	12.4	1.1	17	1	US-09-827-998-514	Sequence 514, App	C 366	12.2	1.1	17	1	US-08-584-040-8014	Sequence 8014, Ap
C 294	12.4	1.1	17	1	US-09-866-108A-1694	Sequence 1694, Ap	C 367	12.2	1.1	17	1	US-08-679-645-677	Sequence 677, App
C 295	12.4	1.1	17	1	US-09-866-108A-1695	Sequence 1695, Ap	C 368	12.2	1.1	17	1	US-08-679-645-790	Sequence 790, App
C 296	12.4	1.1	17	1	US-09-866-108A-1696	Sequence 1696, Ap	C 369	12.2	1.1	17	1	US-09-371-772B-234	Sequence 234, App
C 297	12.4	1.1	17	1	US-09-866-108A-1697	Sequence 1697, Ap	C 370	12.2	1.1	17	1	US-09-371-772B-284	Sequence 284, App
C 298	12.4	1.1	17	1	US-09-866-108A-2568	Sequence 2568, Ap	C 371	12.2	1.1	17	1	US-09-371-772B-710	Sequence 710, App
C 299	12.4	1.1	17	1	US-09-866-108A-6286	Sequence 6286, Ap	C 372	12.2	1.1	17	1	US-09-371-772B-712	Sequence 712, App
C 300	12.4	1.1	17	1	US-09-866-108A-6290	Sequence 6290, Ap	C 373	12.2	1.1	17	1	US-09-371-772B-1788	Sequence 1788, Ap
C 301	12.4	1.1	17	1	US-09-866-108A-6310	Sequence 6310, Ap	C 374	12.2	1.1	17	1	US-09-371-772B-2553	Sequence 2553, Ap
C 302	12.4	1.1	17	1	US-09-866-108A-6311	Sequence 6311, Ap	C 375	12.2	1.1	17	1	US-09-371-772B-2594	Sequence 2594, Ap
C 303	12.4	1.1	17	1	US-09-866-108A-7015	Sequence 7015, Ap	C 376	12.2	1.1	17	1	US-09-371-772B-3206	Sequence 3206, Ap
C 304	12.4	1.1	17	1	US-09-866-108A-7016	Sequence 7016, Ap	C 377	12.2	1.1	17	1	US-09-371-772B-3797	Sequence 3797, Ap
C 305	12.4	1.1	17	1	US-09-866-108A-7019	Sequence 7019, Ap	C 378	12.2	1.1	17	1	US-09-371-772B-4538	Sequence 4538, Ap
C 306	12.4	1.1	17	1	US-09-866-108A-7020	Sequence 7020, Ap	C 379	12.2	1.1	17	1	US-09-371-772B-4854	Sequence 4854, Ap
C 307	12.4	1.1	17	1	US-09-866-108A-7789	Sequence 7789, Ap	C 380	12.2	1.1	17	1	US-09-371-772B-6139	Sequence 6139, Ap
C 308	12.4	1.1	17	1	US-09-866-108A-7790	Sequence 7790, Ap	C 381	12.2	1.1	17	1	US-09-401-063-157	Sequence 157, App
C 309	12.4	1.1	17	1	US-09-866-108A-7791	Sequence 7791, Ap	C 382	12.2	1.1	17	1	US-09-401-063-283	Sequence 283, App
C 310	12.4	1.1	17	1	US-09-866-108A-7792	Sequence 7792, Ap	C 383	12.2	1.1	17	1	US-09-401-063-337	Sequence 337, App
C 311	12.4	1.1	17	1	US-09-866-108A-9275	Sequence 9275, Ap	C 384	12.2	1.1	17	1	US-09-401-063-631	Sequence 631, App
C 312	12.4	1.1	17	1	US-09-866-108A-9276	Sequence 9276, Ap	C 385	12.2	1.1	17	1	US-09-401-063-653	Sequence 653, App
C 313	12.4	1.1	17	1	US-09-866-108A-9277	Sequence 9277, Ap	C 386	12.2	1.1	17	1	US-09-401-063-654	Sequence 654, App
C 314	12.4	1.1	17	1	US-09-866-108A-9278	Sequence 9278, Ap	C 387	12.2	1.1	17	1	US-09-827-998-333	Sequence 333, App
C 315	12.4	1.1	17	1	US-09-404-912-589	Sequence 589, App	C 388	12.2	1.1	17	1	US-09-827-998-1795	Sequence 1795, Ap
C 316	12.4	1.1	17	1	US-09-155-885A-14	Sequence 14, Appl	C 389	12.2	1.1	17	1	US-09-957-189-7	Sequence 7, Appl
C 317	12.4	1.1	17	1	US-09-155-885A-33	Sequence 33, Appl	C 390	12.2	1.1	17	1	US-09-866-108A-400	Sequence 400, App
C 318	12.4	1.1	17	1	US-09-685-664B-1092	Sequence 1092, Ap	C 391	12.2	1.1	17	1	US-09-866-108A-401	Sequence 401, App
C 319	12.4	1.1	17	1	US-09-685-664B-1653	Sequence 1653, Ap	C 392	12.2	1.1	17	1	US-09-866-108A-402	Sequence 402, App
C 320	12.4	1.1	17	1	US-09-993-192A-5	Sequence 5, Appl	C 393	12.2	1.1	17	1	US-09-866-108A-437	Sequence 437, App
C 321	12.4	1.1	17	1	5194592-80	Patent No. 5194592	C 394	12.2	1.1	17	1	US-09-866-108A-733	Sequence 733, App
C 322	12.4	1.1	17	1	5194592-80	Patent No. 5194592	C 395	12.2	1.1	17	1	US-09-866-108A-1071	Sequence 1071, Ap
C 323	12.2	1.1	17	1	US-08-390-850-479	Sequence 479, App	C 396	12.2	1.1	17	1	US-09-866-108A-1072	Sequence 1072, Ap
C 324	12.2	1.1	17	1	US-08-390-850-480	Sequence 480, App	C 397	12.2	1.1	17	1	US-09-866-108A-1487	Sequence 1487, Ap
C 325	12.2	1.1	17	1	US-08-373-124A-456	Sequence 456, App	C 398	12.2	1.1	17	1	US-09-866-108A-6438	Sequence 6438, Ap

ALIGNMENTS

RESULT 1

US-08-803-346-51

Sequence 51, Application US/08803346

Patent No. 6281346

GENERAL INFORMATION:

APPLICANT: HESS, JOHN W.

APPLICANT: CASKEY, C. THOMAS

APPLICANT: LIU, QINGYUN

APPLICANT: PHILLIPS, MICHAEL SEAN

TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES

TITLE OF INVENTION: ENCODING THEM

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.

STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/803,346

FILING DATE: 20-FEB-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: GIESSEY, JOANNE M

REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 19642Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3046

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-803-346-51

Query Match 1.7%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 19; Conservative 0; Mismatches 0; Indels

QY 90 TCGTGGCATATTCCTTCAG 108

DB 1 TCGTGGCATATTCCTTCAG 19

RESULT 2

US-09-396-1966G-107033/c

Sequence 107033, Application US/093961966G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1999-09-15
 ; APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 107033
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-09-396-196G-107033

Query Match 1.7%; Score 18.8; DB 1; Length 25;
 Best Local Similarity 90.9%; Pred. No. 13;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTTTATTCTCAGCAATAGAC 647
 |||||
 DB 25 GTTTATTCTCAGCCAGAGAC 4

RESULT 3
 US-09-396-196G-125800
 ; Sequence 125800, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affimetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 125800
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-09-396-196G-125800

Query Match 1.7%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 14;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 864 GTTGATGCCATGCTATTAAGTG 888
 |||||
 DB 1 GCTGTACTCATGCTGTTAAAGTG 25

RESULT 4
 US-08-803-346-50
 ; Sequence 50, Application US/08803346
 ; Patent No. 6281346
 ; GENERAL INFORMATION:
 ; APPLICANT: HESS, JOHN W.
 ; APPLICANT: CASKEY, C. THOMAS
 ; APPLICANT: LIU, QINGYUN
 ; APPLICANT: PHILLIPS, MICHAEL SEAN
 ; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
 ; TITLE OF INVENTION: ENCODING THEM
 ; NUMBER OF SEQUENCES: 77
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
 ; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/803,346
 ; FILING DATE: 20-FEB-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GIESSER, JOANNE M
 ; REGISTRATION NUMBER: 32,838
 ; REFERENCE/DOCKET NUMBER: 19642Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 732-594-3046
 ; TELEFAX: 732-594-4720
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 US-08-803-346-50

Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 CTTATGCTGGGATGTGCC 148
 |||||
 DB 1 CTTATGCTGGGATGTGCC 18

RESULT 5
 US-08-780-562-30/c
 ; Sequence 30, Application US/08780562
 ; Patent No. 6541604
 ; GENERAL INFORMATION:
 ; APPLICANT: Matthews, William
 ; APPLICANT: Bennett, Brian
 ; TITLE OF INVENTION: WSX RECEPTOR
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/780,562
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/585005
 ; FILING DATE: 01/08/97
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/
 ; FILING DATE: 01/08/97
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0986R1
 ; TELECOMMUNICATION INFORMATION:

1 GCTGGGATGTCCTTAGA 18

RESULT 7

US-09-396-196G-20048/c

; Sequence 20048, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20048

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-20048

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 23;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 957 TCTGGACCCAGGACATTTTGATGA 980

|||||

Db 25 TCTTGACCCCAAGACACTTTGGTGA 2

RESULT 8

US-08-222-177A-296

; Sequence 296, Application US/08222177A

; Patent No. 5582979

; GENERAL INFORMATION:

; APPLICANT: Weber, James L.

; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

; TITLE OF INVENTION: (dC-da)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME

; NUMBER OF SEQUENCES: 460

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dewitt Ross & Stevens, S.C.

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: USA

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,177A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/341,562

; FILING DATE: 21-APR-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Sara, Charles S.

; REGISTRATION NUMBER: 30,492

; REFERENCE/DOCKET NUMBER: 09865.601

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 831-2100

; TELEFAX: (608) 831-2106

; TELEX:

; INFORMATION FOR SEQ ID NO: 296:

; SEQUENCE CHARACTERISTICS:

1.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153

|||||

Db 18 GCTGGGATGTCCTTAGA 1

RESULT 6

US-08-780-562-31

; Sequence 31, Application US/08780562

; Patent No. 6541604

; GENERAL INFORMATION:

; APPLICANT: Matthews, William

; APPLICANT: Bennett, Brian

; TITLE OF INVENTION: WSX RECEPTOR

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/780,562

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/585005

; FILING DATE: 01/08/97

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/

; FILING DATE: 01/08/97

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0986R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

US-08-780-562-30

Query Match 1.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153

|||||

Db 18 GCTGGGATGTCCTTAGA 1

RESULT 6

US-08-780-562-31

; Sequence 31, Application US/08780562

; Patent No. 6541604

; GENERAL INFORMATION:

; APPLICANT: Matthews, William

; APPLICANT: Bennett, Brian

; TITLE OF INVENTION: WSX RECEPTOR

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/780,562

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/585005

; FILING DATE: 01/08/97

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/

; FILING DATE: 01/08/97

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0986R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

US-08-780-562-31

Query Match 1.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153

|||||

Db 18 GCTGGGATGTCCTTAGA 1

```

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
; US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 9
US-08-117-952-600
; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-600

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
; US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 9
US-08-117-952-600
; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-600

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
; US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 9
US-08-117-952-600
; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-600

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
; US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 9
US-08-117-952-600
; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-600

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
; US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 9
US-08-117-952-600
; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-600

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0
```



```

; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-584-11

Query Match          1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 TCGGAGACATGCGGCGT 81
      ||||| ||||| |||||
Db 20 TCGGGCAACATGCGGGTGT 1

RESULT 19
US-09-198-452A-6064/c
; Sequence 6064, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6819
; SEQ ID NO 6064
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6064

Query Match          1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 459 AGTGGTAGCACTTATCTG 478
      || ||||| ||||| |||||
Db 20 AGCGGTAGCAGTTCTCTG 1

RESULT 20
US-09-980-052-219
; Sequence 219, Application US/09980052
; Patent No. 6670130
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joong; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 219

```

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
US-09-980-052-219

Query Match          1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 998 TCCACATGAAGTTTGAGAA 1017
      ||||| ||||| ||||| |||||
Db 1 TGCACAACAACACTTTGAGAA 20

RESULT 21
US-09-657-472-690/c
; Sequence 690, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-690

Query Match          1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 733 GCAGTCTGTAGCGAGCTGC 752
      ||||| ||||| ||||| |||||
Db 20 GCAGTCATTTAGCGAGCTGC 1

RESULT 22
US-09-280-799-152
; Sequence 152, Application US/09280799
; Patent No. 6136603
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karrias, James G
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA

```

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/115
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-06331A-65

Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1077 CACTTAACCTCTCTGGG 1093
Db 18 CCCTTAACCTCTCTGGG 2

RESULT 16
US-08-486-408-14/c
Sequence 14, Application US/08486408
Patent No. 5716846
GENERAL INFORMATION:
APPLICANT: Brown, Steven Joel
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
TITLE OF INVENTION: mRNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,408
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1009
TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-486-408-14

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CAGGAAGCGGAGCAG 48
Db 18 CAGGAAGCGGAGCAG 2

RESULT 17
US-08-975-570-14/c
Sequence 14, Application US/08975570
Patent No. 5945336
GENERAL INFORMATION:
APPLICANT: Brown, Steven Joel
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
TITLE OF INVENTION: mRNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,570
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,408
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1009
TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-570-14

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CAGGAAGCGGAGCAG 48
Db 18 CAGGAAGCGGAGCAG 2

RESULT 18
US-09-428-594-11/c
Sequence 11, Application US/09428584
Patent No. 6136604
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF METHIONINE AMINOPEPTIDASE 2 EXPRESSION
FILE REFERENCE: RIS-0114
CURRENT APPLICATION NUMBER: US/09/428,584
CURRENT FILING DATE: 1999-10-27

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 US-09-280-799-152

Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 77;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCAG 1067
 |||||

Db 2 ACTTCCTTACCTTTCCTG 19
 |||||

RESULT 23

US-09-277-020-16
 Sequence 16, Application US/09277020
 Patent No. 6210892
 GENERAL INFORMATION:
 APPLICANT: Bennett, C. Frank
 TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
 TITLE OF INVENTION: of mRNA Processing.
 FILE REFERENCE: ISPH-0339
 CURRENT APPLICATION NUMBER: US/09/277,020
 CURRENT FILING DATE: 1999-03-26
 EARLIER APPLICATION NUMBER: 09/167,921
 EARLIER FILING DATE: 1998-10-07
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 16
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 US-09-277-020-16

Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 77;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCAG 1067
 |||||

Db 2 ACTTCCTTACCTTTCCTG 19
 |||||

RESULT 24

US-08-875-847B-9/C
 Sequence 9, Application US/08875847B
 Patent No. 6255105
 GENERAL INFORMATION:
 APPLICANT: The Government of the United
 APPLICANT: States of America as represented by the
 APPLICANT: Secretary, Department of Health and Human
 APPLICANT: Services; Callahan, Robert; Marchetti,
 APPLICANT: Antonio; Buttitta, Fiama; Smith, Gilbert H.
 TITLE OF INVENTION: Nucleotide And Deduced
 TITLE OF INVENTION: Amino Acid Sequences Of A New Tumor Gene,
 TITLE OF INVENTION: Int6, And the Use Of Reagents Derived From
 TITLE OF INVENTION: These Sequences In Diagnostic Assays,
 TITLE OF INVENTION: Vaccines, Immunotherapy And Gene Therapy
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS WORD 97
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,847B
 FILING DATE: 09-FEB-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/385,998
 FILING DATE: 09-FEB-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: William S. Feiler
 REGISTRATION NUMBER: 26,728
 REFERENCE/DOCKET NUMBER: 2026-4179PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-875-847B-9

Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 77;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 CTTATTAGAAATGCAGAA 943
 |||||

Db 20 CTAATTAAAAATGCAGAA 3
 |||||

RESULT 25

US-09-378-842-9/C
 Sequence 9, Application US/09378842
 Patent No. 6342392
 GENERAL INFORMATION:
 APPLICANT: The Government of the United
 APPLICANT: States of America as represented by the
 APPLICANT: Secretary, Department of Health and Human
 APPLICANT: Services; Callahan, Robert; Marchetti,
 APPLICANT: Antonio; Buttitta, Fiama; Smith, Gilbert H.
 TITLE OF INVENTION: Nucleotide And Deduced
 TITLE OF INVENTION: Amino Acid Sequences Of A New Tumor Gene,
 TITLE OF INVENTION: Int6, And the Use Of Reagents Derived From
 TITLE OF INVENTION: These Sequences In Diagnostic Assays,
 TITLE OF INVENTION: Vaccines, Immunotherapy And Gene Therapy
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS WORD 97
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/378,842
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,847
 FILING DATE: 09-FEB-1996
 APPLICATION NUMBER: 08/385,998
 FILING DATE: 09-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: William S. Feiler

Fri Aug 19 10:59:59 2005

```

;
;   REGISTRATION NUMBER: 26,728
;   REFERENCE/DOCKET NUMBER: 2026-4179PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 758-4800
;   TELEFAX: (212) 751-6849
;   TELEX: 421792
;   INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-09-378-842-9

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      926 CTTATTAGAAATGCAGAA 943
      ||||| ||||| |||||
Db      20 CTAATTAAATGCAGAA 3

RESULT 26
US-09-858-152B-9/c
; Sequence 9, Application US/09858152B
; Patent No. 6737251
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Marchetti, Antonio
; APPLICANT: Buttitta, Fianna
; APPLICANT: Smith, Gilbert H.
; APPLICANT: Callahan, Robert
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6
; FILE REFERENCE: 4239-59122
; CURRENT APPLICATION NUMBER: US/09/858,152B
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/858,152
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
;
US-09-858-152B-9

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      926 CTTATTAGAAATGCAGAA 943
      ||||| ||||| |||||
Db      20 CTAATTAAATGCAGAA 3

RESULT 27
US-09-657-472-1733/c
; Sequence 1733, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
;

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;
;   CURRENT APPLICATION NUMBER: US/09/657,472
;   CURRENT FILING DATE: 2000-09-07
;   PRIOR APPLICATION NUMBER: US 60/153,357
;   PRIOR FILING DATE: 1999-09-10
;   PRIOR APPLICATION NUMBER: US 60/220,947
;   PRIOR FILING DATE: 2000-07-26
;   PRIOR APPLICATION NUMBER: US 60/225,724
;   PRIOR FILING DATE: 2000-08-16
;   NUMBER OF SEQ ID NOS: 2551
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 1733
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;
US-09-657-472-1733

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 CTGGCTTGGCAGGCTGCC 22
      ||||| ||||| |||||
Db      21 CTGCTGGGGYAGGCTGTCC 2

RESULT 28
US-09-866-108A-2565/c
; Sequence 2565, Application US/09866108A
; Patent No. 6886188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6886188
; SEQ ID NO 2565
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-866-108A-2565

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 89;

```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCTT 758
|||||
Db 17 AGGCAGCTGCCACCTT 2

RESULT 29

US-09-866-108A-2566/c
; Sequence 2566, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: A6MICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: A6mica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 2566

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-2566

Query Match 1.3%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 89;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCTT 758
|||||
Db 16 AGGCAGCTGCCACCTT 1

RESULT 30

US-09-544-398B-588

; Sequence 588, Application US/09544398B

; Patent No. 6770461

; GENERAL INFORMATION:

; APPLICANT: Carulli, John P.

; APPLICANT: Little, Randall D.

; APPLICANT: Recker, Robert R.

; APPLICANT: Johnson, Mark L.

; TITLE OF INVENTION: High bone mass gene of 11q13.3

; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/09/544,398B

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 09/229,319

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 60/071,449

; PRIOR FILING DATE: 1998-01-13

; PRIOR APPLICATION NUMBER: US 60/105,511

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 641

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 588

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-544-398B-588

Query Match 1.3%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 91;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TGGAAATTCCTTCTTCT 310
|||||
Db 1 TGGAAATTCCTTCTTCT 16

RESULT 31

US-09-696-791-3308/c

; Sequence 3308, Application US/09696791

; Patent No. 6770633

; GENERAL INFORMATION:

; APPLICANT: Robbins, Joan M.

; APPLICANT: Tritz, Richard

; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 480124.407

; CURRENT APPLICATION NUMBER: US/09/696,791

; CURRENT FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 4523

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3308

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Cyclin B1 ribozyme binding site

US-09-696-791-3308

Query Match 1.3%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 91;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 791 GTGCTTGGAGAGGCAG 806
|||||
Db 19 GGGCTTGGAGAGGCAG 4

RESULT 32

US-09-543-771B-588

; Sequence 588, Application US/09543771B

; Patent No. 6780609

; GENERAL INFORMATION:

; APPLICANT: Carulli, John P.

; APPLICANT: Little, Randall D.

; APPLICANT: Recker, Robert R.

; APPLICANT: Johnson, Mark L.

; TITLE OF INVENTION: High bone mass gene of 11q13.3

; FILE REFERENCE: 032796-014

; CURRENT APPLICATION NUMBER: US/09/543,771B

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 09/229,319

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 60/071,449

; PRIOR FILING DATE: 1998-01-13

188.188

Fri Aug 19 10:59:59 2005

```
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1803

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 287 TTCACACTGGAATTG 302
    |||||
Db 19 TTCACACTGGAATTG 4

RESULT 35
US-09-953-318-37
; Sequence 37, Application US/09953318
; Patent No. 6710174
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-318-37

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCTCAGCAA 641
    |||||
Db 4 GTTTTATTCTCAGCAA 19

RESULT 36
US-09-917-963-91/c
; Sequence 91, Application US/09917963
; Patent No. 6767739
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0591
; CURRENT APPLICATION NUMBER: US/09/917,963
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 137
; SEQ ID NO 91
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-917-963-91

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 130 TCTTATGCTGGCATGT 145
    |||||
Db 18 TCTTATGCTGGCATGT 3

RESULT 37
```

US-08-105-483-336
; Sequence 336, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,483
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-105-483-336

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 394 CATTTTCCTTCAATTCAA 412
||| ||||| ||||| |||||
Db 1 CATGTCTCTTCAAGTCAA 19

RESULT 38
US-08-389-067-9/c
; Sequence 9, Application US/08389067
; Patent No. 5714312
; GENERAL INFORMATION:
; APPLICANT: NUNO BARDOSA NOLASCO, Gustavo
; APPLICANT: DE BLAS BEORLEGUI, Carmen
; APPLICANT: BORJA TOME, Maria Jose
; APPLICANT: PONS ASCASO, Fernando
; APPLICANT: TORRES PASCUAL, Vicente
; TITLE OF INVENTION: PROCEDURE FOR THE DETECTION AND
; TITLE OF INVENTION: IDENTIFICATION OF VIRAL AND SUBVIRAL PATHOGENS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-8403
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,067
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,729
; FILING DATE: 02-JUN-1993
; APPLICATION NUMBER: ES 9201232
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: EA-1849 (613-54)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-389-067-9

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 857 TCTTTGTGTTGTAGTCCAT 875
||||| ||||| ||||| |||||
Db 19 TCTTTGTGTTGTAGTCCAT 1

RESULT 39
US-08-709-209-336
; Sequence 336, Application US/08709209
; Patent No. 5762938
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,209
; FILING DATE: 21-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,483
; FILING DATE: 12-AUG-1993
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400

iss.res

Fri Aug 19 10:59:59 2005

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-709-209-336
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 394 CATTTTCCTTACAATCAA 412
Db 1 CATGTTCTTTCAAGTCAA 19

RESULT 41
US-08-478-178A-86/c
; Sequence 86, Application US/08478178A
; Patent No. 5882927
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5882927ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA: US/08/478,178A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
;
US-08-478-178A-86
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATCATTTAGCT 452
Db 19 AGAGGAGAGGATTTGGCT 1

RESULT 42
US-08-488-177-86/c
; Sequence 86, Application US/08488177
; Patent No. 5885970
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5885970ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-488-177-86

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGGATGATTTAGCT 452
Db 19 AGAGGAGGATTTGGCT 1

RESULT 43
US-08-634-350-24/c
; Sequence 24, Application US/08634350
; Patent No. 5911982
; GENERAL INFORMATION:
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: H2-1 VIRUS PERSISTENCE-ASSOCIATED
; TITLE OF INVENTION: GENE 1(pag1) PROMOTER, USES
; TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING SAME OR PRODUCTS
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,350
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

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; NAME: Lawrence, William F.
; REGISTRATION NUMBER: 28,029
; REFERENCE/DOCKET NUMBER: 516450-2008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-634-350-24

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 566 TTTTAAATACCTTTATAT 584
Db 19 TTGTTTAAATACCTTTGTTT 1

RESULT 44
US-08-481-072A-86/c
; Sequence 86, Application US/08481072A
; Patent No. 5916807
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5916807ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,072A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-481-072A-86

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Kinase C

QY	DB	AGAGAGAGATGATTTAGCT 452	AGAGAGAGATTTGGCT 1	QY	DB	AGAGAGAGATGATTTAGCT 452	AGAGAGAGATTTGGCT 1
434	19	AGAGAGAGATGATTTAGCT 452	AGAGAGAGATTTGGCT 1	434	19	AGAGAGAGATGATTTAGCT 452	AGAGAGAGATTTGGCT 1
<p>STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA COUNTRY: USA ZIP: 19103</p> <p>COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/481.066A FILING DATE: herewith CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: 852,852 FILING DATE: March 16, 1992 ATTORNEY/AGENT INFORMATION: NAME: Rebecca Ralph Gaumond REGISTRATION NUMBER: 35,152 REFERENCE/DOCKET NUMBER: ISIS-1154 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100 TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 86: LENGTH: 20 SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ANTI-SENSE: yes</p> <p>US-08-481-066A-86</p>							
<p>Query Match 1.3%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 1e+02; 3; Indels 0; Gaps 0; Matches 16; Conservative</p>							
QY	DB	434	AGAGAGAGATGATTTAGCT 452	QY	DB	434	AGAGAGAGATGATTTAGCT 452
			19				19
<p>US-08-578-615A-94/c Sequence 94, Application US/08578615A Patent No. 6015892</p> <p>GENERAL INFORMATION: APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C NUMBER OF SEQUENCES: 122 CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA COUNTRY: USA ZIP: 19103</p> <p>COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS SOFTWARE: WORDPERFECT 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/578.615A FILING DATE: 11-JAN-1996 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: 852,852 FILING DATE: 16-MAR-1992 APPLICATION NUMBER: 08/089,996 FILING DATE: 09-JUL-1993 APPLICATION NUMBER: 08/199,779 FILING DATE: 22-FEB-1994</p>							
<p>US-08-664-336-86/c Sequence 86, Application US/08664336 Patent No. 5922686</p> <p>GENERAL INFORMATION: APPLICANT: Nicholas Dean, C. Frank Bennett TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C NUMBER OF SEQUENCES: 121 CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock Washburn Kurtz ADDRESSEE: Mackiewicz & No. 5922686ris STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA COUNTRY: USA ZIP: 19103</p> <p>COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS SOFTWARE: WORDPERFECT 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/664.336 FILING DATE: herewith CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: 852,852 FILING DATE: March 16, 1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 089,996 FILING DATE: July 9, 1993 ATTORNEY/AGENT INFORMATION: NAME: Paul K. Legaard REGISTRATION NUMBER: 38,534 REFERENCE/DOCKET NUMBER: ISIS-2345 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100 TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 86: LENGTH: 20 SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ANTI-SENSE: yes</p> <p>US-08-664-336-86</p>							
<p>Query Match 1.3%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 1e+02; 3; Indels 0; Gaps 0; Matches 16; Conservative</p>							
QY	DB	434	AGAGAGAGATGATTTAGCT 452	QY	DB	434	AGAGAGAGATGATTTAGCT 452
			19				19
<p>US-08-481-066A-86/c Sequence 86, Application US/08481066A Patent No. 5959096</p> <p>GENERAL INFORMATION: APPLICANT: Nicholas Dean, C. Frank Bennett TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C NUMBER OF SEQUENCES: 121 CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock Washburn Kurtz ADDRESSEE: Mackiewicz & No. 5959096ris</p>							


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1568
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
; US-08-578-615A-94

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 ACAGGAGATGATTTAGCT 452
DB 19 ACAGGAAGAGGATTTGGCT 1

RESULT 48
US-09-392-580-12/c
; Sequence 12, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-580-12

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 426 TATTTGGAAGAGGAGATGA 444
DB 20 TATTTCAAGAGAGATGA 2

RESULT 49
US-09-433-699-36/c
; Sequence 36; Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; FILE REFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433,699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-433-699-36
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 800 GAGGAGATACGCTGAAG 818
DB 19 GAGGAAGATGACTCTGAAG 1

RESULT 50
US-08-829-637A-86/c
; Sequence 86, Application US/08829637A
; Patent No. 6339066
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Phillip Dan Cook
; APPLICANT: Nicholas Dean
; APPLICANT: Glenn Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES WHICH HAVE
; TITLE OF INVENTION: PHOSPHOROTHOIATE LINKAGES OF HIGH CHIRAL PURITY AND
; TITLE OF INVENTION: WHICH MODULATE al, all, , k, n, AND ISOFORMS OF
; TITLE OF INVENTION: PROTEIN KINASE C
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Caldwell (28,937) Woodcock
; ADDRESSEE: Washburn Kurtz Mackiewicz & No. 6339066ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,637A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,066
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,129
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,851
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,569
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/089,996
; FILING DATE: 09-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/058,023
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,007
; FILING DATE: 16-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,760
; FILING DATE: 15-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,852
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00243
; FILING DATE: 11-JAN-1991
; PRIOR APPLICATION DATA:
```


Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 427 ATTTGGAGAGGAGATGAT 445
 DB 19 AGTTGGAGGGGAGATGAT 1

RESULT 55
 US-10-025-139-86/c
 ; Sequence 86, Application US/10025139
 ; Patent No. 6537973
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Holmlund, Jon T.
 ; APPLICANT: Dorr, F. Andrew
 ; TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
 ; FILE REFERENCE: ISIS4954
 ; CURRENT APPLICATION NUMBER: US/10/025,139
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: US 08/829,637
 ; PRIOR FILING DATE: 1997-03-31
 ; PRIOR APPLICATION NUMBER: US 08/478,178
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: US 08/089,996
 ; PRIOR FILING DATE: 1993-07-09
 ; PRIOR APPLICATION NUMBER: US 07/852,852
 ; PRIOR FILING DATE: 1992-03-16
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 86
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-025-139-86

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTAGCT 452
 DB 19 AGAGAGAGGATTTGGCT 1

RESULT 56
 US-09-198-452A-2125
 ; Sequence 2125, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 2125
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-2125

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 AGAATCTGAAGCCCACTC 958
 DB 1 AGAATCGAAACCCCAAGC 19

RESULT 57
 US-09-198-452A-4121
 ; Sequence 4121, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 4121
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-4121

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 771 GAAACCTTTCTGGGGA 789
 DB 1 GAGACCTTTTCTTTGGGA 19

RESULT 58
 US-09-198-452A-5159
 ; Sequence 5159, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 5159
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-5159

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAATTTGTTTC 309
 DB 2 CTCTGGAGTCTGTTTC 20

RESULT 59
 US-09-198-452A-5166
 ; Sequence 5166, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24

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```
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5166

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      291 CTACTGGAATGTTGTTTC 309
Db      2 CTCCTGAGTCGTTGTTTC 20

RESULT 60
US-09-198-452A-6581
; Sequence 6581, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6581
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6581

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      460 GTGGTAGCAGCTTTATTCG 478
Db      2 GTGGTAGCACTATACCTG 20

RESULT 61
US-10-054-225-12
; Sequence 12, Application US/10054225
; Patent No. 6623931
; GENERAL INFORMATION:
; APPLICANT: Saint Jude Children's Research Hospital
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Atkinson, Robyn M
; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
; FILE REFERENCE: SJ-01-0022
; CURRENT APPLICATION NUMBER: US/10/054,225
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(20)
; OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
US-10-054-225-12

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      489 ATTGAATTTCTTAGAATC 507
Db      489 ATTGAATTTCTTAGAATC 507

; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5166

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      291 CTACTGGAATGTTGTTTC 309
Db      2 CTCCTGAGTCGTTGTTTC 20

RESULT 62
US-09-771-357-79
; Sequence 79, Application US/09771357
; Patent No. 6756200
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William
; APPLICANT: DAVIDSON, Nancy
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630
; CURRENT APPLICATION NUMBER: US/09/771,357
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-09-771-357-79

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      149 TTGAGGATTATGCGTTT 167
Db      1 TTGGAAGTTTATGCGTTT 19

RESULT 63
US-09-544-398B-310/c
; Sequence 310, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGCGCCACACAC 900
Db      19 AATATTGTGCGCCACACAC 1
```

```
RESULT 64
US-09-543-771B-310/c
; Sequence 310, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-310

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
Db 19 AATATTGGCCACACAC 1

RESULT 65
US-10-059-579A-79
; Sequence 79, Application US/10059579A
; Patent No. 6835541
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: FACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-10-059-579A-79

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGGCGTTT 167
Db 1 TTGGAAGTTTATGGCGTTT 19

RESULT 66
PCT-US94-07770-94/c
; Sequence 94, Application PC/TUS9407770
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett and
; APPLICANT: Russell T. Boggs
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07770
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; APPLICATION NUMBER: 08/089,996
; FILING DATE: July 9, 1993
; APPLICATION NUMBER: 08/199,779
; FILING DATE: February 22, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
PCT-US94-07770-94

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTAGCT 452
Db 19 AGAGAAGAGAGATTTGGCT 1

RESULT 67
US-08-319-492B-460
; Sequence 460, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James G.
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

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Fri Aug 19 10:59:59 2005

STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,492B
 FILING DATE: October 7, 1994
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Wardburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/276
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 460:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-319-492B-460

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1e+02;
 Matches 6; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 QY 123 TGACTTTTCTTATG 136
 Db 1 UGACUUUUUUUAUG 14

RESULT 68
 US-09-422-978-5553
 ; Sequence 5553, Application US/09422978
 ; Patent No. 6537751
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 ; FILE REFERENCE: GENSET.020CP1
 ; CURRENT APPLICATION NUMBER: US/09/422,978
 ; CURRENT FILING DATE: 1999-10-20
 ; EARLIER APPLICATION NUMBER: US 09/298,850
 ; EARLIER FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,732
 ; EARLIER FILING DATE: 1998-11-23
 ; EARLIER APPLICATION NUMBER: US 60/082,614
 ; EARLIER FILING DATE: 1998-04-21
 ; NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 5553
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1..18

; OTHER INFORMATION: upstream amplification primer 99-5186 for SEQ 1619,
 US-09-422-978-5553

Query Match 1.3%; Score 14; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ATCTCCCCCATCC 213
 Db 5 ATCTCCCCCATCC 18

RESULT 69
 US-09-422-978-4185/c
 ; Sequence 4185, Application US/09422978
 ; Patent No. 6537751
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 ; FILE REFERENCE: GENSET.020CP1
 ; CURRENT APPLICATION NUMBER: US/09/422,978
 ; CURRENT FILING DATE: 1999-10-20
 ; EARLIER APPLICATION NUMBER: US 09/298,850
 ; EARLIER FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,732
 ; EARLIER FILING DATE: 1998-11-23
 ; EARLIER APPLICATION NUMBER: US 60/082,614
 ; EARLIER FILING DATE: 1998-04-21
 ; NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 4185
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1..20
 ; OTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,
 US-09-422-978-4185

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAATA 575
 Db 19 TGGGTTTTTAATA 6

RESULT 70
 US-09-422-978-5624
 ; Sequence 5624, Application US/09422978
 ; Patent No. 6537751
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 ; FILE REFERENCE: GENSET.020CP1
 ; CURRENT APPLICATION NUMBER: US/09/422,978
 ; CURRENT FILING DATE: 1999-10-20
 ; EARLIER APPLICATION NUMBER: US 09/298,850
 ; EARLIER FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,732
 ; EARLIER FILING DATE: 1998-11-23
 ; EARLIER APPLICATION NUMBER: US 60/082,614
 ; EARLIER FILING DATE: 1998-04-21
 ; NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 5624
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens

```
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-5681 for SEQ 1690,
US-09-422-978-5624

Query Match          1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTGTATTCTTGCT 337
Db 4 CTGTATTCTTGCT 17

RESULT 71
US-09-665-615B-156/c
; Sequence 156, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Ras Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-665-615B-156

Query Match          1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
Db 18 AGATGAGTTTATT 5

RESULT 72
US-10-172-911-55
; Sequence 55, Application US/10172911
; Patent No. 6743909
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTFN12 EXPRESSION
; FILE REFERENCE: PTS-0016
; CURRENT APPLICATION NUMBER: US/10/172,911
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-172-911-55

Query Match          1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 CTGTATCAATGG 358
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Db 1 CTGTATCAATGG 14

RESULT 73
US-08-219-842-12/c
; Sequence 12, Application US/08219842
; Patent No. 5565323
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,842
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-219-842-12

Query Match          1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTTAACT 578
Db 17 TGGTTTTTCTTAATACCT 1

RESULT 74
US-08-451-096-12/c
; Sequence 12, Application US/08451096
; Patent No. 5760205
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,096
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,842
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-451-096-12

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```

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 562 TGGGTTTTTTTAATACCT 578
   ||| ||| ||| ||| ||| |||
DB 17 TGGTTTTTCTAATACCT 1

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```

RESULT 75
US-08-810-599-64/c
; Sequence 64, Application US/08810599
; Patent No. 5976798
; GENERAL INFORMATION:
; APPLICANT: PARKER, W. Davis
; APPLICANT: HERRNSTADT, Corinna
; APPLICANT: GHOSH, Soumitra S.
; APPLICANT: FAHY, Eoin
; TITLE OF INVENTION: Methods for Detecting Mitochondrial Mutations
; TITLE OF INVENTION: Diagnostic for Alzheimer's Disease and Methods for Determining
; TITLE OF INVENTION: of Mitochondrial Nucleic Acid
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,599
; FILING DATE: Concurrent Herewith
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/757,438
; FILING DATE: 27 No. 5976798 1996
; APPLICATION NUMBER: US 08/614,072
; FILING DATE: 12 Mar 1996
; APPLICATION NUMBER: US 08/536,036
; FILING DATE: 29 Sep 1995
; APPLICATION NUMBER: US 08/414,969
; FILING DATE: 31 Mar 1995
; APPLICATION NUMBER: US 08/413,740

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; FILING DATE: 30 Mar 1995
; APPLICATION NUMBER: US 08/410,658
; FILING DATE: 24 MARCH 1995
; APPLICATION NUMBER: US 08/397,808
; FILING DATE: 3 Mar 1995
; APPLICATION NUMBER: US 08/219,842
; FILING DATE: 30 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 2105/17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHEICAL: No
; ANTI-SENSE: No
;
; US-08-810-599-64

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Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 562 TGGGTTTTTTTAATACCT 578
   ||| ||| ||| ||| ||| |||
DB 17 TGGTTTTTCTAATACCT 1

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RESULT 76
US-08-413-740A-140/c
; Sequence 140, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7

```


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TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial

TITLE OF INVENTION: Defects

NUMBER OF SEQUENCES: 206

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20036-5405

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/413,740A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04063

FILING DATE: 30-MAR-1995

APPLICATION NUMBER: 08/413,740

FILING DATE: 30-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bonham, David B.

REGISTRATION NUMBER: 34297

REFERENCE/DOCKET NUMBER: 2105/7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-1776

TELEFAX: (202) 429-0796

INFORMATION FOR SEQ ID NO: 188:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-413-740A-188

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 563 GGGTTTTTTTAATACCTT 579

Db 17 GGGTTTTTTTAATACCTT 1

RESULT 81

US-09-866-108A-2563/c

Sequence 2563, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharron G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AECMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

TITLE OF INVENTION: Diagnosis, Therapy and Cellular and

TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial

TITLE OF INVENTION: Defects

NUMBER OF SEQUENCES: 206

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20036-5405

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/413,740A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04063

FILING DATE: 30-MAR-1995

APPLICATION NUMBER: 08/413,740

FILING DATE: 30-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bonham, David B.

REGISTRATION NUMBER: 34297

REFERENCE/DOCKET NUMBER: 2105/7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-1776

TELEFAX: (202) 429-0796

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-413-740A-186

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 563 GGGTTTTTTTAATACCTT 579

Db 17 GGGTTTTTTTAATACCTT 1

RESULT 80

US-08-413-740A-188/c

Sequence 188, Application US/08413740A

Patent No. 6171859

GENERAL INFORMATION:

APPLICANT: HERRNSTADT, CORINNA

APPLICANT: PARKER, WILLIAM D.

APPLICANT: DAVIS, ROBERT

APPLICANT: MILLER, SCOTT W.

TITLE OF INVENTION: Diagnosis, Therapy and Cellular and

```

; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2563

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATG 761
Db      17 GCAGCTGCCGCTTCTG 1

RESULT 82
US-09-866-108A-2564/c
; Sequence 2564, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2564
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2564/c

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATG 761
Db      17 GCAGCTGCCGCTTCTG 1

RESULT 83
US-09-866-108A-6749
; Sequence 6749, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6749

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      836 AGGAAGCGCGGTGGA 852
Db      1 AGGAAGCGCGGTGGA 17

RESULT 84
PCT-US95-04063-140/c

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; Patent No. 6686188
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2564

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      744 GCAGCTGCCACCTTAT 760
Db      17 GCAGCTGCCGCTTCT 1

RESULT 83
US-09-866-108A-6749
; Sequence 6749, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6749

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      836 AGGAAGCGCGGTGGA 852
Db      1 AGGAAGCGCGGTGGA 17

RESULT 84
PCT-US95-04063-140/c

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Fri Aug 19 10:59:59 2005

; Sequence 140, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US95-04063-140

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAACT 578
Db 17 TGGTTTTCTAACT 1

RESULT 85
PCT-US95-04063-151/c
; Sequence 151, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US95-04063-140

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAACT 578
Db 17 TGGTTTTCTAACT 1

RESULT 85
PCT-US95-04063-151/c
; Sequence 151, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US95-04063-151

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAACT 578
Db 17 TGGTTTTCTAACT 1

RESULT 86
PCT-US95-04063-185/c
; Sequence 185, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

```
;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-185
```

```
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 562 TGGTTTCTTAATACCT 578
Db 17 TGGTTTCTTAATACCT 1
```

RESULT 87

```
PCT-US95-04063-186/c
; Sequence 186, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-186
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```
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 563 GGGTTTCTTAATACCTT 579
Db 17 GGGTTTCTTAATACCTT 1
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RESULT 88

```
PCT-US95-04063-188/c
; Sequence 188, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-188
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```
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 563 GGGTTTCTTAATACCTT 579
Db 17 GGGTTTCTTAATACCTT 1
```

RESULT 89

```
US-08-219-842-23/c
; Sequence 23, Application US/08219842
; Patent No. 5565323
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,842
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(1, "")
OTHER INFORMATION: /note= "N = fluorescein"
US-08-219-842-23

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAAATACCT 578
DB 18 TGGTTTTTCTAATACCT 2

RESULT 91
US-08-634-350-23/c
Sequence 23, Application US/08634350
Patent No. 5911982
GENERAL INFORMATION:
APPLICANT: Chao, Yu-Chan
TITLE OF INVENTION: H2-1 VIRUS PERSISTENCE-ASSOCIATED
TITLE OF INVENTION: GENE 1(pag1) PROMOTER, USES
TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
TITLE OF INVENTION: CONTAINING SAME OR PRODUCTS
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,350
FILING DATE: 18-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 516450-2008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-634-350-23

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 566 TTTTAAATACCTTTAT 582
DB 17 TTGTTTAATACCTTTGT 1

RESULT 92
```

```
US-09-422-978-4732/c
; Sequence 4732, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US 09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-04-21
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4732
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798,
US-09-422-978-4732
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 905 AGCCTCAACATTTCCTA 921
Db 17 AGCCTCAGCAATTCATA 1
RESULT 93
US-09-422-978-6041
; Sequence 6041, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US 09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-04-21
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6041
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-09-422-978-6041
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 942 ATCTGAAGCCCCCACTC 958
Db 2 AATCTCAACCCCCCACTC 18
US-09-422-978-11352/c
; Sequence 11352, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US 09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-04-21
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11352
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-4448 for SEQ 3487, in compler
US-09-422-978-11352
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 CCCCATCCCCCATTC 220
Db 18 CCTCCATCCCCCATCTC 2
RESULT 95
US-09-696-791-649/c
; Sequence 649, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US 09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 649
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk6 ribozyme binding site
US-09-696-791-649
Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 603 AAGACTTCATAAGTAGG 619
Db 19 AACACTTCAGAAGTAGG 3
RESULT 96
US-09-696-791-1039/c
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ISS.RES

Fri Aug 19 10:59:59 2005

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-760A-354

Query Match      1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      448 TAGCTGGGACGAGTG 462
DB      16 TAGCTGGGACGAGTG 2

RESULT 98
US-08-774-310-354/c
; Sequence 354, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,760
; FILING DATE: September 23, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 354:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-310-354

Query Match      1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      448 TAGCTGGGACGAGTG 462
DB      16 TAGCTGGGACGAGTG 2

US-08-311-760A-354/c
; Sequence 354, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 354:

```


Db 16 TAGCTGGGAACAGTG 2

RESULT 99

US-08-373-124A-1915/c
; Sequence 1915, Application US/08373124A

; Patent No. 5646042

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Draper, Kenneth

; APPLICANT: McSwiggen, James

; APPLICANT: Jarvis, Thale

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

; NUMBER OF SEQUENCES: 2627

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/373,124A

; FILING DATE: January 13, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/245,466

; FILING DATE: May 18, 1994

; APPLICATION NUMBER: 08/192,943

; FILING DATE: February 7, 1994

; APPLICATION NUMBER: 07/987,132

; FILING DATE: December 7, 1992

; APPLICATION NUMBER: 07/936,422

; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/035

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 1915:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-373-124A-1915

Query Match

Best Local Similarity 1.2%; Score 13.4; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 274 ACTGGCATATTTCTT 288

Db 16 ACTGGCATATTTCTT 2

RESULT 100

US-08-435-628-1915/c

; Sequence 1915, Application US/08435628

; Patent No. 5817796

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435,628

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/373,124

; FILING DATE: January 13, 1995

; APPLICATION NUMBER: 08/245,466

; FILING DATE: May 18, 1994

; APPLICATION NUMBER: 08/192,943

; FILING DATE: February 7, 1994

; APPLICATION NUMBER: 07/987,132

; FILING DATE: December 7, 1992

; APPLICATION NUMBER: 07/936,422

; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/035

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 1915:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-435-628-1915

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 274 ACTGGCATATTTCTT 288

Db 16 ACTGGCATATTTCTT 2

RESULT 101

US-09-371-772B-4443/c

; Sequence 4443, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

iss.res

Fri Aug 19 10:59:59 2005

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FILE REFERENCE: MEH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4443
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-4443

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;

Qy      626 GTTTTATCTCAGCA 640
Db      15 GTTTTATGCTCAGCA 1

RESULT 102
US-09-866-108A-2567/c
; Sequence 2567, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2567

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;

Qy      626 GTTTTATCTCAGCA 640
Db      15 GTTTTATGCTCAGCA 1

RESULT 103
US-09-866-108A-6287
; Sequence 6287, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6287

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;

Qy      21 CCGGGCGGTGCGCAGG 35
Db      3 CCGGGCGGTGCGCAGG 17

RESULT 104
US-09-866-108A-6288
; Sequence 6288, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

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; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: AEWICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6288
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6288

Query Match      1.2%   Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21  CCGGCGCCGTGGCAGG 35
Db      21  CCGGCGCCGTGGCAGG 16

RESULT 105
US-09-866-108A-6289
; Sequence 6289, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: AEWICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6289
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6289

Query Match      1.2%   Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21  CCGGCGCCGTGGCAGG 35
Db      21  CCGGCGCCGTGGCAGG 15

RESULT 106
US-09-135-021-41
; Sequence 41, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 41
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-021-41

Query Match      1.2%   Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      48  GCGGCGCCGCCAGTT 62
Db      2   GCGGCGCCGCCAGTT 16

RESULT 107
US-09-135-020-43
; Sequence 43, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068

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; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-135-020-43

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
Db 2 GCCGCGGCCCCAGTT 16

RESULT 108
US-09-135-010A-43
; Sequence 43, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-135-010A-43

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
Db 2 GCCGCGGCCCCAGTT 16

RESULT 109
US-09-444-871-43
; Sequence 43, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor

```

```

; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-444-871-43

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
Db 2 GCCGCGGCCCCAGTT 16

RESULT 110
US-09-662-402A-6
; Sequence 6, Application US/09662402A
; Patent No. 6420117
; GENERAL INFORMATION:
; APPLICANT: Wessler, Susan R
; APPLICANT: Casa, Alexandra M
; TITLE OF INVENTION: MINIATURE INVERTED REPEAT TRANSPOSABLE ELEMENTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 235,00230101
; CURRENT APPLICATION NUMBER: US/09/662,402A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/153,812
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer
; US-09-662-402A-6

Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 909 TCACACATTTCCTAGA 923
Db 1 TCACAGTTTCCTAGA 15

RESULT 111
US-09-597-735-43
; Sequence 43, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.

```

; APPLICANT: Sanguinetti, Michael C.
 ; APPLICANT: Curran, Mark E.
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Splawski, Igor
 ; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
 ; FILE REFERENCE: 2323-133
 ; CURRENT APPLICATION NUMBER: US/09/597,735
 ; CURRENT FILING DATE: 2000-06-19
 ; EARLIER APPLICATION NUMBER: 09/135,010
 ; EARLIER FILING DATE: 1998-08-17
 ; EARLIER APPLICATION NUMBER: 60/094,477
 ; EARLIER FILING DATE: 1998-07-29
 ; EARLIER APPLICATION NUMBER: 08/921,068
 ; EARLIER FILING DATE: 1997-08-29
 ; EARLIER APPLICATION NUMBER: 08/739,383
 ; EARLIER FILING DATE: 1996-10-29
 ; EARLIER APPLICATION NUMBER: 60/019,014
 ; EARLIER FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 43
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-597-735-43

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGCAGTT 62
 Db 2 GCCGCGGCCCGCAGTT 16

RESULT 112
 US-09-444-295-43
 ; Sequence 43, Application US/09444295
 ; Patent No. 6432644
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating, Mark T.
 ; APPLICANT: Sanguinetti, Michael C.
 ; APPLICANT: Splawski, Igor
 ; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
 ; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
 ; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
 ; FILE REFERENCE: 2323-131
 ; CURRENT APPLICATION NUMBER: US/09/444,295
 ; CURRENT FILING DATE: 1999-11-22
 ; PRIOR APPLICATION NUMBER: 09/135,020
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 08/921,068
 ; PRIOR FILING DATE: 1997-08-29
 ; PRIOR APPLICATION NUMBER: 08/739,383
 ; PRIOR FILING DATE: 1996-10-29
 ; PRIOR APPLICATION NUMBER: 60/019,014
 ; PRIOR FILING DATE: 1995-12-22
 ; PRIOR APPLICATION NUMBER: 60/094,477
 ; PRIOR FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 43
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-444-295-43

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGCAGTT 62
 Db 2 GCCGCGGCCCGCAGTT 16

RESULT 113
 US-09-597-732-43
 ; Sequence 43, Application US/09597732
 ; Patent No. 6451534
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating, Mark T.
 ; APPLICANT: Sanguinetti, Michael C.
 ; APPLICANT: Curran, Mark E.
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Splawski, Igor
 ; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
 ; FILE REFERENCE: 2323-133
 ; CURRENT APPLICATION NUMBER: US/09/597,732
 ; CURRENT FILING DATE: 2000-06-19
 ; PRIOR APPLICATION NUMBER: 09/135,010
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/094,477
 ; PRIOR FILING DATE: 1998-07-29
 ; PRIOR APPLICATION NUMBER: 08/921,068
 ; PRIOR FILING DATE: 1997-08-29
 ; PRIOR APPLICATION NUMBER: 08/739,383
 ; PRIOR FILING DATE: 1996-10-29
 ; PRIOR APPLICATION NUMBER: 60/019,014
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 43
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-597-732-43

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGCAGTT 62
 Db 2 GCCGCGGCCCGCAGTT 16

RESULT 114
 US-09-422-978-5495/c
 ; Sequence 5495, Application US/09422978
 ; Patent No. 6537751
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 ; FILE REFERENCE: GENSET.020CPI
 ; CURRENT APPLICATION NUMBER: US/09/422,978
 ; CURRENT FILING DATE: 1999-10-20
 ; EARLIER APPLICATION NUMBER: US 09/298,850
 ; EARLIER FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,732
 ; EARLIER FILING DATE: 1998-11-23
 ; EARLIER APPLICATION NUMBER: US 60/082,614
 ; EARLIER FILING DATE: 1998-04-21
 ; NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 5495
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE: primer_bind
 ; NAME/KEY: primer_bind

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; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-4677 for SEQ 1561,
US-09-422-978-5495

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1060 CTTTCCAGTGGCTAA 1074
Db       18 CTTACCAAGTGGCTAA 4

RESULT 115
US-09-422-978-5744
; Sequence 5744, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5744
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6557 for SEQ 1810,
US-09-422-978-5744

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      612 TAAGTAGGAGATGAG 626
Db       3 TAAGTAGGAGATGAG 17

RESULT 116
US-09-597-731-43
; Sequence 43, Application US/09597731
; Patent No. 6582913
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,731
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29

; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-4677 for SEQ 1561,
US-09-422-978-5495

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1060 CTTTCCAGTGGCTAA 1074
Db       18 CTTACCAAGTGGCTAA 4

RESULT 117
US-09-816-814-2
; Sequence 2, Application US/09816814
; Patent No. 6818406
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-816-814-2

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      277 GGCATATTTCTTCAC 291
Db       1 GGCATGTTTCTTCAC 15

RESULT 118
US-09-338-907-372/C
; Sequence 372, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CPICP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA

```

```
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-338-907-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 119
US-09-218-207-372/c
; Sequence 372, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CPI
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-218-207-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 120
US-09-228-302-23
; Sequence 23, Application US/09228302
; Patent No. 6399370
; GENERAL INFORMATION:
; APPLICANT: WILSON, James M
; APPLICANT: GOLDMAN, Mitchell
; APPLICANT: BALS, Robert
; APPLICANT: STOLZENBERG, Ethan D
; APPLICANT: ANDERSON, Mark
; APPLICANT: ZASLOFF, Michael
; APPLICANT: KARI, Prasad
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE OF DEFENSIN
; FILE REFERENCE: 209596.0161/16U2
; CURRENT APPLICATION NUMBER: US/09/228,302
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/023,424
; PRIOR FILING DATE: 1998-08-22
; PRIOR APPLICATION NUMBER: US 60/027,334
```

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; PRIOR FILING DATE: 1996-10-01
; PRIOR APPLICATION NUMBER: US 08/915,011
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Forward Primer
US-09-228-302-23

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 954 CACTCTGGACCCAGG 968
Db 3 CACTCTGGACCCCTGG 17

RESULT 121
US-09-422-978-4387/c
; Sequence 4387, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4387
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453,
US-09-422-978-4387

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 122
US-09-422-978-11326
; Sequence 11326, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
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; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11326
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-4233 for SEQ 3461, in compleme
US-09-422-978-11326

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 394 CATTTCCTTACCAAT 408
Db 4 CATTGCCTTACCAAT 18

RESULT 123
US-09-818-780-80/c
; Sequence 80, Application US/09818780
; Patent No. 6677146
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
; FILE REFERENCE: 1794.0030004
; CURRENT APPLICATION NUMBER: US/09/818,780
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,736
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse/antisense ATG primer #P133-A1237
US-09-818-780-80

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 835 CAGGAAGCGCGGGT 849
Db 15 CTGGAAGCGCGGGT 1

RESULT 124
US-09-696-791-3671
; Sequence 3671, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3671
; LENGTH: 19
; TYPE: DNA

```

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3671

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 238 CTATGACTCAGATGC 252
Db 2 CTATCACTCAGATGC 16

RESULT 125
US-08-802-547-12/c
; Sequence 12, Application US/08802547
; Patent No. 5780611
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
; TITLE OF INVENTION: COLLAGEN GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,547
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 24129-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816-474-9050
; TELEFAX: 816-474-9057
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; POSITION IN GENOME:
; UNITS: bp
US-08-802-547-12

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 202 CTCCTCCATCCCCCATTT 219
Db 18 CTCCTCCCTCTCTCCCTTT 1

RESULT 126
US-08-800-751-34/c

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; Sequence 34, Application US/08800751
; Patent No. 5807730
; GENERAL INFORMATION:
; APPLICANT: ITO, Kiyoshi
; APPLICANT: YAMAKI, Toshifumi
; APPLICANT: ARII, Teruo
; APPLICANT: TSUROOKA, Miyuki
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,751
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-027004
; FILING DATE: 14-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 028022-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; US-08-800-751-34

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 CTGCGCGGCGCGTGGCAG 34
Db 18 CTGCTGTCGCGCGGCGAG 1

RESULT 127
US-08-712-357-12/c
; Sequence 12, Application US/08712357
; Patent No. 5808027
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT
; EXPRESSION OF COLLAGEN GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.

; Sequence 34, Application US/08800751
; Patent No. 5807730
; GENERAL INFORMATION:
; APPLICANT: ITO, Kiyoshi
; APPLICANT: YAMAKI, Toshifumi
; APPLICANT: ARII, Teruo
; APPLICANT: TSUROOKA, Miyuki
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,751
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-027004
; FILING DATE: 14-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 028022-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; US-08-800-751-34

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 CTGCGCGGCGCGTGGCAG 34
Db 18 CTGCTGTCGCGCGGCGAG 1

RESULT 128
US-08-525-849C-3
; Sequence 3, Application US/08525849C
; Patent No. 5866411
; GENERAL INFORMATION:
; APPLICANT: Pederson, Finn S
; APPLICANT: Lund, Anders H
; APPLICANT: Lovmand, Jette
; APPLICANT: Jorgensen, Poul
; APPLICANT: Duch, Mogens
; TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
; VECTOR FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
; TRANSFECTED WITH SAID VECTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Building, 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,849C
; FILING DATE: 08-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: BNRIAS 100
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-0030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: trna
US-08-525-849C-3
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 192 TCCACGCCATCTCCCCCA 209
Db 1 UCCCGCGCAUCCACCACCA 18

RESULT 129
US-08-749-495A-3
; Sequence 3, Application US/08749495A
; Patent No. 5886166
; GENERAL INFORMATION:
; APPLICANT: Pederson, Finn S
; APPLICANT: Lund, Anders H
; APPLICANT: Lovmand, Jette
; APPLICANT: Jorgensen, Poul
; APPLICANT: Duch, Mogens
; TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
; TITLE OF INVENTION: SYSTEM FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
; TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Building, 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,495A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,849
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: ENRIAS 100
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-0030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: trna
US-08-749-495A-3
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-0030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: trna
US-08-525-849C-3
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 192 TCCACGCCATCTCCCCCA 209
Db 1 UCCCGCGCAUCCACCACCA 18

RESULT 130
US-08-990-818-34/c
; Sequence 34, Application US/08990818
; Patent No. 5910432
; GENERAL INFORMATION:
; APPLICANT: ITO, Kiyoshi
; APPLICANT: YAMAKI, Toshifumi
; APPLICANT: ARII, Teruo
; APPLICANT: TSURUOKA, Miyuki
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,818
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/800,751
; FILING DATE:
; APPLICATION NUMBER: JP 8-027004
; FILING DATE: 14-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 028022-007
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-990-818-34
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 17 CTGCCCCGGCGCGTGGCAG 34
Db 18 CTGCTCGTGGCGGGGCGAG 1

RESULT 131
US-09-205-204-37/c
; Sequence 37, Application US/09205204
; Patent No. 5958772
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann

```

APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRESSION
FILE REFERENCE: RTS-0020
CURRENT APPLICATION NUMBER: US/09/205,204
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 37
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-204-37

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 TTGATGAGATCCAAAGGA 991
DB 18 TTGATGAGATTCAGGTA 1

RESULT 132
US-09-163-078-3
Sequence 3, Application US/09169078
Patent No. 6037172
GENERAL INFORMATION:
APPLICANT: Pedersen, Finn S
APPLICANT: Lund, Anders H
APPLICANT: Lovmand, Jette
APPLICANT: Jorgensen, Poul
APPLICANT: Duch, Mogens
TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
TITLE OF INVENTION: SYSTEM FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Building, 310 East Michigan
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,078
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,849
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: BNRIS 100
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: tRNA

US-09-163-078-3

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 192 TCCAGCCCATCTCCCCCA 209
DB 1 UCCCGCAUCCUCCACCA 18

RESULT 133
US-08-434-511-2/c
Sequence 2, Application US/08434511
Patent No. 6057114
GENERAL INFORMATION:
APPLICANT: Akong, Anthony
APPLICANT: Harpold, Michael
APPLICANT: Velicelebi, Gonul
APPLICANT: Brust, Paul
TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY
TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,511
FILING DATE: 04-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,985
FILING DATE: 20-JUN-1994
APPLICATION NUMBER: PCT/US92/11090
FILING DATE: 18-DEC-1992
APPLICATION NUMBER: 07/812,254
FILING DATE: 20-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9738
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-434-511-2

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 695 GTTCATGTAGTCACGGTG 712
DB 18 GTTCATGAATTCAGGTG 1

Fri Aug 19 10:59:59 2005

RESULT 134
US-09-169-248-3
; Sequence 3, Application US/09169248
; Patent No. 6107478
; GENERAL INFORMATION:
; APPLICANT: Pederson, Finn S
; APPLICANT: Lund, Anders H
; APPLICANT: Lovmand, Jette
; APPLICANT: Jorgensen, Poul
; APPLICANT: Duch, Mogens
; TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
; TITLE OF INVENTION: SYSTEM FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
; TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Building, 310 East Michigan
; STREET: Avenue
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09169,248
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,849
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: BNR1AS 100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: tRNA
; US-09-169-248-3
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 192 TCCACGCCATCTCCCCCA 209
Db 1 UCCCCGGCAUCCACCA 18
RESULT 135
US-08-229-150-2/c
; Sequence 2, Application US/08229150
; Patent No. 6127133
; GENERAL INFORMATION:
; APPLICANT: Akong, Michael A.
; APPLICANT: Harpold, Michael M.
; APPLICANT: Velicelc, G.
; APPLICANT: Brust, Paul
; TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY METHOD FOR DETECTING CELL
; TITLE OF INVENTION: PROTEIN FUNCTION USING SAME
; FILE REFERENCE: 24735-51505B
; CURRENT APPLICATION NUMBER: US/08/229,150

CURRENT FILING DATE: 1994-04-18
; EARLIER APPLICATION NUMBER: 07/812,254
; EARLIER FILING DATE: 1991-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for screening of products having
; OTHER INFORMATION: EcoRI site adjacent to initiation codon of human
; OTHER INFORMATION: HM1 coding region
US-08-229-150-2
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 695 GTTCATGTAGTCACGGTG 712
Db 18 GTTCATGAATTCAGGTG 1
RESULT 136
US-09-182-145-131
; Sequence 131, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 131
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-18
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-131
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 897 AGACCAAGAGCCTCAACA 914
Db 1 AGTCCAAAGAGTCTCAGCA 18
RESULT 137
US-09-422-978-5708

```

; Sequence 5708, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5708
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6298 for SEQ 1774,
US-09-422-978-5708

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred.No.1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      871   TCCATGCTATTAAAAGTG 888
Db       |          |||||         |
        1   TCCATGCTTTACCAGTG 18

RESULT 138
US-09-422-978-9959
; Sequence 9959, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9959
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-8478 for SEQ 2094, in complene
US-09-422-978-9959

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred.No.1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      209   ATCCCCCATTTTCATTGCC 226
Db       |          |||||         |
        1   ATCCCCCTCTTTCATTTC 18

```

;; TITLE OF INVENTION: AND EVALUATING THE INTRACELLULAR TRANSDUCTION
;; TITLE OF INVENTION: OF AN EXTRACELLULAR SIGNAL
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fitch Even Tabin & Flannery
;; STREET: 135 So. LaSalle Street, Suite 900
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60603
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/05625
;; FILING DATE: 19910807
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/563,751
;; FILING DATE: 07-AUG-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 1838-51826
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-552-1311
;; TELEFAX: 619-552-0095
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 7..12
;; OTHER INFORMATION: /function="EcoRI restriction
;; OTHER INFORMATION: recognition sequence"
;; OTHER INFORMATION: /label= EcoRI
;; PCT-US91-05625-4
;;
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;;
QY 695 GTTCATGTAATCAAGGTG 712
| | | | | | | | | | | | | | | | | | | | | |
Db 18 GTTCATGTAATCAAGGTG 1
| | | | | | | | | | | | | | | | | | | | | |
;;
RESULT 142
US-09-158-980-16/c
; Patent No. 5401629
; APPLICANT: HAROLD, MICHAEL M.; BRUST, PAUL
; TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS USEFUL
; FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/563,751
; FILING DATE: 07-AUG-1990
; SEQ ID NO:3:
; LENGTH: 18
5401629-3
;;
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 695 GTTCATGTAATCAAGGTG 712
| | | | | | | | | | | | | | | | | | | | | |

Db 18 GTTCATGTAATCAAGGTG 1
| | | | | | | | | | | | | | | | | | | | | |
;;
RESULT 143
US-08-657-884-16/c
; Sequence 16, Application US/08657884
; Patent No. 5858981
; GENERAL INFORMATION:
; APPLICANT: SCHREIBER, ALAN D.
; APPLICANT: PARK, JONG-GU
; TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/657,884
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 555-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-657-884-16
;;
Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 67 AGACATGGCGGC 79
| | | | | | | | | | | | | | | | | | | | | |
Db 16 AGACATGGCGGC 4
| | | | | | | | | | | | | | | | | | | | | |
;;
RESULT 144
US-09-158-980-16/c
; Sequence 16, Application US/09158980
; Patent No. 6242427
; GENERAL INFORMATION:
; APPLICANT: SCHREIBER, ALAN D.
; APPLICANT: PARK, JONG-GU
; TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,980
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/657,884
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 555-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-158-980-16

Query Match      1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 AGACATGGCGGC 79
Db      16 AGACATGGCGGC 4

RESULT 145
US-09-811-492-16/c
; Sequence 16, Application US/09811492
; Patent No. 6638764
; GENERAL INFORMATION:
; APPLICANT: SCHREIBER, ALAN D.
; PARK, JONG-GU
; TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/811,492
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/657,884
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 555-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-811-492-16

Query Match      1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 AGACATGGCGGC 79
Db      16 AGACATGGCGGC 4

RESULT 146
US-09-014-065-4/c
; Sequence 4, Application US/09014065
; Patent No. 6033854
; GENERAL INFORMATION:
; APPLICANT: Kurnit, David M.
; APPLICANT: Chiang, Pei-Wen
; APPLICANT: Wang, Chang-Ning J.
; TITLE OF INVENTION: METHOD FOR DETERMINING THE COPY NUMBER OF A NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 06498/004001
; CURRENT APPLICATION NUMBER: US/09/014,065
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 08/434,474
; EARLIER FILING DATE: 1995-05-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-014-065-4

Query Match      1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      746 CAGCTGCCACCTT 758
Db      13 CAGCTGCCACCTT 1

RESULT 147
US-07-988-194A-6
; Sequence 6, Application US/07988194A
; Patent No. 5359046
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Weiss, Arthur
; APPLICANT: Irving, Brian A.
; APPLICANT: Roberts, Margo R.
; APPLICANT: Zeebo, Krisztina
; TITLE OF INVENTION: Chimeric Chains for Receptor
; TITLE OF INVENTION: Associated Signal Transduction Pathways
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton &
; ADDRESSEE: Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,194A

```

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Fri Aug 19 10:59:59 2005

FILING DATE: December 9, 1992
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55107-1 CELL-0051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-988-194A-6
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 59 AGTTCGGGACATGG 74
Db 1 AGTTGGGACACGGG 16
RESULT 148
US-08-757-024-750
Sequence 750, Application US/08757024
Patent No. 6025339
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 750:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-750
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 64 GGGACATGGCGGC 79

Db 1 GGGCGCATGGCGGC 16
RESULT 149
US-08-582-776C-35/c
Sequence 35, Application US/08582776C
Patent No. 6077510
GENERAL INFORMATION:
APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Kliche, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Stitz, Lothar
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017-2576
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT
SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,776C
FILING DATE: 04-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,822
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,831
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A.
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/892-9200
TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-582-776C-35
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 22 CGGGCGGTGGCAGGAA 37
Db 16 CGGCGGTGGCAGGAA 1
RESULT 150
US-08-611-587-16/c
Sequence 16, Application US/08611587
Patent No. 6150091
GENERAL INFORMATION:

APPLICANT: PANDOLFO, MASSIMO
APPLICANT: MONTERMINI, LAURA
APPLICANT: MOLTO, MARIA D.
APPLICANT: Koenig, Michael
APPLICANT: Campuzano, Victoria
APPLICANT: Coesse, Mireille
TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
STREET: Fulbright & Jaworski L.L.P. Patent Dept.
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 03-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Brashears-Macatee, Sarah J.
REGISTRATION NUMBER: 38,087
REFERENCE/DOCKET NUMBER: D-5901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5620
TELEFAX: 713-651-5246
TELEX: 76-2829
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
POSITION IN GENOME:
UNITS: bp
US-08-611-587-16
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 39 CCGGAAGCAGCGCGG 54
Db 16 CCGGAACAGCGCGG 1
RESULT 151
US-08-479-737-6
Sequence 6, Application US/08479737
Patent No. 6319494
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J
Weiss, Arthur
Irving, Brian A
Roberts, Margo R
Zeebo, Krisztina
TITLE OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR ASSOCIATED
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: CELL GENESYS, INC.
STREET: 322 Lakeside Drive
CITY: Foster City
STATE: California

COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,405
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralyn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: Cell 5.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-9600
TELEFAX: (415) 358-0803
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-479-737-6
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 59 AGTTCGGGAGACATGG 74
Db 1 AGTTGGGAGACATGG 16
RESULT 152
US-08-475-442A-6
Sequence 6, Application US/08475442A
Patent No. 6407221
GENERAL INFORMATION:
APPLICANT: CAPON, DANIEL J
APPLICANT: WEISS, ARTHUR
APPLICANT: IRVING, BRIAN A
APPLICANT: ROBERTS, MARGO R
APPLICANT: ZEEBO, KRISZTINA
TITLE OF INVENTION: CHIMERIC CHAINS FOR
RECEPTOR-ASSOCIATED SIGNAL TRANSDUCTION PATHWAYS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,442A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,405
FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:

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```

; APPLICATION NUMBER: US 07/988,194
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,643
; FILING DATE: 14-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09431
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUPEN, KAREN I
; REGISTRATION NUMBER: 34,647
; REFERENCE/DOCKET NUMBER: CELLS.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)358-9600x131
; TELEFAX: (415)349-7392
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-475-442A-6

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AGTTGGGAGACATGG 74
Db 1 AGTTGGGAGACAGGG 16

RESULT 153
US-09-093-972C-750
; Sequence 750, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: Nvce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/093,972C
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 750:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 750:
US-09-093-972C-750

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 GGGAGACATGGCGGC 79
Db 1 GGGCGCATGGCGGC 16

RESULT 154
US-09-716-319-2
; Sequence 2, Application US/09716319
; Patent No. RE38028
; GENERAL INFORMATION:
; APPLICANT: BRIGGS, ROBERT E.
; TATUM, FRED M.
; TITLE OF INVENTION: MOLECULAR GENETIC CONSTRUCTION OF
; VACCINE STRAINS OF PASTEURELLACEAE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER AND WITCOFF, LTD.
; STREET: 1001 G STREET, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/716,319
; APPLICATION NUMBER: US/09/716,319
; FILING DATE: 21-No. RE38028-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,234
; FILING DATE: 19-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 0295.56516
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508 9100
; TELEFAX: 202 508 9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pasteurella haemolytica
; STRAIN: serotype 1/pd70
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-716-319-2
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Fri Aug 19 10:59:59 2005

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; APPLICATION NUMBER: US 07/988,194
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,643
; FILING DATE: 14-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09431
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUPEN, KAREN I
; REGISTRATION NUMBER: 34,647
; REFERENCE/DOCKET NUMBER: CELLS.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)358-9600x131
; TELEFAX: (415)349-7392
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-475-442A-6

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 GGGAGACATGGCGGC 79
Db 1 GGGCGCATGGCGGC 16

RESULT 154
US-09-716-319-2
; Sequence 2, Application US/09716319
; Patent No. RE38028
; GENERAL INFORMATION:
; APPLICANT: BRIGGS, ROBERT E.
; TATUM, FRED M.
; TITLE OF INVENTION: MOLECULAR GENETIC CONSTRUCTION OF
; VACCINE STRAINS OF PASTEURELLACEAE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER AND WITCOFF, LTD.
; STREET: 1001 G STREET, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/716,319
; APPLICATION NUMBER: US/09/716,319
; FILING DATE: 21-No. RE38028-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,234
; FILING DATE: 19-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 0295.56516
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508 9100
; TELEFAX: 202 508 9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pasteurella haemolytica
; STRAIN: serotype 1/pd70
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-716-319-2
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Query Match 1.1%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CCTGTTATCTTGCTC 338
 ||||| |||||
 Db 2 CCTGTTTTCCTGCTC 17

RESULT 155

US-08-390-850-478/c
 ; Sequence 478, Application US/08390850
 ; Patent No. 5612215

; GENERAL INFORMATION:
 ; APPLICANT: Draper, Kenneth G.
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Gustofson, John
 ; APPLICANT: Stinchcomb, Dan T.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
 ; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
 ; NUMBER OF SEQUENCES: 1151
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/390,850
 ; FILING DATE: February 17, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/354,920
 ; FILING DATE: December 13, 1994
 ; APPLICATION NUMBER: 08/152,487
 ; FILING DATE: No. 5612215ember 12, 1993
 ; APPLICATION NUMBER: 07/989,848
 ; FILING DATE: December 7, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 211/084
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 478:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-390-850-478

Query Match 1.1%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 904 GAGCCTCAACATTTC 919
 ||||| |||||
 Db 16 GAGCCAAAACATTTC 1

RESULT 156

US-08-435-634-478/c

; Sequence 478, Application US/08435634
 ; Patent No. 5731295

; GENERAL INFORMATION:
 ; APPLICANT: Draper, Kenneth G.
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Gustofson, John
 ; APPLICANT: Stinchcomb, Dan T.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
 ; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
 ; NUMBER OF SEQUENCES: 1151
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,634
 ; FILING DATE: 05-MAY-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/390,850
 ; FILING DATE: February 17, 1995
 ; APPLICATION NUMBER: 08/354,920
 ; FILING DATE: December 13, 1994
 ; APPLICATION NUMBER: 08/152,487
 ; FILING DATE: No. 5731295ember 12, 1993
 ; APPLICATION NUMBER: 07/989,848
 ; FILING DATE: December 7, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 211/084
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 478:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-435-634-478

Query Match 1.1%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 904 GAGCCTCAACATTTC 919
 ||||| |||||
 Db 16 GAGCCAAAACATTTC 1

RESULT 157

US-08-758-306-65/c
 ; Sequence 85, Application US/08758306
 ; Patent No. 5807743

; GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: McSwiggen, James A.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: TREATMENT OF DISEASES
 ; TITLE OF INVENTION: ASSOCIATED WITH

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 631:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-758-306-631

Query Match 1.1%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 AAACACTTAACCTCT 1088
 |||||
 Db 17 AAAGCACTGAACCTCT 2

RESULT 160
 US-08-770-234-2
 ; Sequence 2, Application US/08770234
 ; Patent No. 5840556

GENERAL INFORMATION:
 APPLICANT: BRIGGS, ROBERT E.
 APPLICANT: TATUM, FRED M.
 TITLE OF INVENTION: MOLECULAR GENETIC CONSTRUCTION OF
 TITLE OF INVENTION: VACCINE STRAINS OF PASTEURELLACEAE
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER AND WITCOFF, LTD.
 STREET: 1001 G STREET, NW
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20001

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 19-DEC-1996
 APPLICATION NUMBER: US/08/770,234
 CLASSIFICATION: A24
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 0295.56516
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 508 9100
 TELEFAX: 202 508 9299

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pasteurella haemolytica
 STRAIN: serotype 1/pd70
 US-08-770-234-2

Query Match 1.1%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CCTGTATTCTTGCTC 338

Db 2 CCTGTTTCTGCTC 17
 |||||

RESULT 161
 US-08-757-024-731
 ; Sequence 731, Application US/08757024
 ; Patent No. 6025339
 ; GENERAL INFORMATION:
 APPLICANT: NYCE, Jonathan W.
 TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
 NUMBER OF SEQUENCES: 952
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BELL, SELTZER, PARK & GIBSON
 STREET: P.O. Drawer 34009
 CITY: Charlotte
 STATE: No. 6025339th Carolina
 COUNTRY: USA
 ZIP: 28234

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 26-NOV-1996
 APPLICATION NUMBER: US/08/757,024
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Sibley, Kenneth D.
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5218-41
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-881-3140
 TELEFAX: 919-881-3175
 TELEX: 575102

INFORMATION FOR SEQ ID NO: 731:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-757-024-731

Query Match 1.1%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGGCGGC 79
 |||||
 Db 2 GGGCGCATGGCGGC 17

RESULT 162
 US-08-757-024-749
 ; Sequence 749, Application US/08757024
 ; Patent No. 6025339
 ; GENERAL INFORMATION:
 APPLICANT: NYCE, Jonathan W.
 TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
 NUMBER OF SEQUENCES: 952
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BELL, SELTZER, PARK & GIBSON
 STREET: P.O. Drawer 34009
 CITY: Charlotte
 STATE: No. 6025339th Carolina
 COUNTRY: USA
 ZIP: 28234

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

iss.res

Fri Aug 19 10:59:59 2005

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;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 749:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-757-024-749
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGCGGGC 79
DB 1 GGGCGGATGCGGGC 16

RESULT 163
US-09-442-143A-40/c
; Sequence 40, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-442-143A-40
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 202 CTCCTCCATCCCTCCAT 217
DB 16 CTCCTCAATGCCCAT 1

RESULT 164
US-09-474-432B-368
; Sequence 368, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleo
; FILE REFERENCE: MBH800-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-368
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 359 GGAGCTGCGGCTTG 374
DB 359 GGAGCTGCGGCTTG 374
```

```

; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleo
; FILE REFERENCE: MBH800-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 368
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-368
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.8e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCAGGCTGCGGGCC 27
DB 2 GCCGCGCAGCGGCC 17

RESULT 165
US-09-474-432B-578
; Sequence 578, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleo
; FILE REFERENCE: MBH800-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-578
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 359 GGAGCTGCGGCTTG 374
DB 359 GGAGCTGCGGCTTG 374
```

Db 2 GGAGCGGGCGCCUUG 17

RESULT 166

US-09-474-432B-579
; Sequence 579, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/084,727
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 301,511
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 579
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-579

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.8e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 361 AGCTCGCGGCCTGTG 376
||| |||||:|:
DB 1 AGCUGGCGCCUUG 16

RESULT 167

US-09-371-772B-6170/c
; Sequence 6170, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6170
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6170

Query Match 1.1%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 288 TCACCTACTGGAATTGT 303
||||| |||||
DB 17 TCACCTTTTGGAAATTGT 2

RESULT 168

US-09-371-772B-6171/c
; Sequence 6171, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6171
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6171

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 288 TCACCTACTGGAATTGT 303
||||| |||||
DB 16 TCACCTTTTGGAAATTGT 1

RESULT 169

US-09-589-560B-3/c
; Sequence 3, Application US/09589560B
; Patent No. 6605451
; GENERAL INFORMATION:
; APPLICANT: Marmaro, Jeffery M.
; APPLICANT: Gerdes, John C.
; TITLE OF INVENTION: Methods and Devices for Multiplexing Amplification Reactions
; FILE REFERENCE: XTR005
; CURRENT APPLICATION NUMBER: US/09/589,560B
; CURRENT FILING DATE: 2000-08-06
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-589-560B-3

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 340 TGTGGCTCTGATCAAA 355
||||| |||||
DB 17 TGTGGCTCTGATTTAA 2

RESULT 170

```

US-09-476-387-367
; Sequence 367, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Beigelman, Leo
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MEHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 367
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-367

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.8e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCAGGCTGCCGGGCC 27
DB 2 GCCGGCUGACGGGCC 17

RESULT 171
US-09-476-387-577
; Sequence 577, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MEHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
; LENGTH: 17
; TYPE: RNA

```


; SEQ ID NO 515
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-515

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 310 TGCCTTTGGAATTCCT 325
DB 17 TTCCTTTGGAATTCCT 2

RESULT 174

US-09-827-998-516/c
; Sequence 516, Application US/09827998
; Patent No. 6656700

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORE-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 516

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-827-998-516

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 310 TGCCTTTGGAATTCCT 325
DB 16 TTCCTTTGGAATTCCT 1

RESULT 175

US-09-866-108A-2562/c
; Sequence 2562, Application US/09866108A
; Patent No. 6686188

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2562

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-2562

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 746 CAGCTGCCACCTTATG 761
DB 17 CAGCTGCCACCTTATG 2

RESULT 176

US-09-866-108A-6308/c

; Sequence 6308, Application US/09866108A

; Patent No. 6686188

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 6308

; LENGTH: 17

; TYPE: DNA

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Fri Aug 19 10:59:59 2005

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; ORGANISM: Homo sapiens
US-09-866-108A-6308

Query Match          1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTCCTT 150
Db 17 TGCTGGGAGGTGCCCT 2

RESULT 177
US-09-866-108A-6309/c
; Sequence 6309, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6309
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6309

Query Match          1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTCCTT 150
Db 16 TGCTGGGAGGTGCCCT 1

RESULT 178
US-09-866-108A-6748
; Sequence 6748, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
```

```
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6748
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6748

Query Match          1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 836 AGGAGGCGCGGTGG 851
Db 2 AGGAGGCGCGGTGGAGG 17

RESULT 179
US-09-866-108A-6750
; Sequence 6750, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6750
; TYPE: DNA
; LENGTH: 17
; ORGANISM: Homo sapiens
US-09-866-108A-6750

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      837 GGAAGCGCGGGTGA 852
Db      1 GGAAGCGCGGTGAGGA 16

RESULT 180
US-09-866-108A-7017/c
; Sequence 7017, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7017
; LENGTH: 17

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7017

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACCTT 758
Db      17 AAGCAGCTGCCACCAT 2

RESULT 181
US-09-866-108A-7018/c
; Sequence 7018, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7018
; TYPE: DNA
; LENGTH: 17
; ORGANISM: Homo sapiens
US-09-866-108A-7018

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACCTT 758
Db      16 AAGCAGCTGCCACCAT 1

RESULT 182
US-09-866-108A-7967/c
; Sequence 7967, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:

```

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Fri Aug 19 10:59:59 2005

```
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7967
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7967

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      313 CTTTGGATTTCCTGTT 328
DB      17 CTCGTGATTTCTGTT 2

RESULT 183
US-09-866-108A-7968/c
; Sequence 7968, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7968
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7968

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      313 CTTTGGATTTCCTGTT 328
DB      16 CTCGTGATTTCTGTT 1

RESULT 184
US-09-866-108A-8291/c
; Sequence 8291, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8291
```

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; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8291

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 475 TCTGATTACAGTGCAT 490
Db 17 TCTGACACAGTGCAT 2

RESULT 185
US-09-866-108A-8292/c
; Sequence 8292, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecmica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8292
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8292

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 475 TCTGATTACAGTGCAT 490
Db 16 TCTGACACAGTGCAT 1

RESULT 186
US-09-720-435A-351/c
; Sequence 351, Application US/09720435A
; Patent No. 6803187
```

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; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease
; FILE REFERENCE: 11362.0030.PCUS00 INNS:030
; CURRENT APPLICATION NUMBER: US/09/720,435A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/EP99/04317
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 98870143.9
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 351
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Aids-associated retrovirus
US-09-720-435A-351

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 370 CCTTGCTGTGGCAGGC 385
Db 17 CCTTATGTGACAGGC 2

RESULT 187
US-09-902-563-40/c
; Sequence 40, Application US/09902563
; Patent No. 6805863
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-902-563-40

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 202 CTCCTCCCATCCCCCAT 217
Db 16 CTCCTCCCATGCCCAT 1

RESULT 188
US-09-093-972C-731
; Sequence 731, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
```

iss.res

Fri Aug 19 10:59:59 2005

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; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/093,972C
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 731:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 731:
US-09-093-972C-731

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGGCGGC 79
Db 2 GGGCGCATGGCGGC 17

RESULT 189
US-09-093-972C-749
; Sequence 749, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998

```

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 749:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 749:
US-09-093-972C-749

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGGCGGC 79
Db 1 GGGCGCATGGCGGC 16

RESULT 190
US-08-403-634-21
; Sequence 21, Application US/08403634
; Patent No. 5674748
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; TITLE OF INVENTION: NOVEL HUMAN CYCLIN-DEPENDENT
; KINASE-LIKE PROTEINS AND METHODS
; TITLE OF INVENTION: OF USING THE SAME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 5674748ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,634
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,575
; FILING DATE: 08-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100

```

TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-403-634-21

Query Match 1.1%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 792 TCCTTGAGAGGAGCAGA 807
 Db 2 TCCTTGAGAGGAGCAGA 17

RESULT 191
 US-08-468-580-34
 Sequence 34, Application US/08468580
 Patent No. 5824642
 GENERAL INFORMATION:
 APPLICANT: Attie, Kenneth
 APPLICANT: Carlsson, Lena
 APPLICANT: Gesundheit, Neil
 APPLICANT: Goddard, Audrey
 TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,580
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/410452
 FILING DATE: 24-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/224982
 FILING DATE: 07-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: P0884P1C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-468-580-34

Query Match 1.1%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1080 TTAACCTCTCTGGGTG 1095

Db 1 TTAACCTCTGTGGCTG 16
 RESULT 192
 US-08-816-693A-25/C
 Sequence 25, Application US/08816693A
 Patent No. 5874241
 GENERAL INFORMATION:
 APPLICANT: Takahashi, Joseph S
 APPLICANT: Turek, Fred W
 APPLICANT: Pinto, Lawrence H
 TITLE OF INVENTION: Clock Gene and Gene Product
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/816,693A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5874241thrup, Thomas E
 REGISTRATION NUMBER: 33,268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-816-693A-25

Query Match 1.1%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1048 CAACTTCCTTATCTTT 1063
 Db 16 CAACTACCTTATCTGT 1

RESULT 193
 US-09-212-771-42/c
 Sequence 42, Application US/09212771
 Patent No. 5958773
 GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
 APPLICANT: Lex M. Cowser
 TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
 FILE REFERENCE: RTS-0034
 CURRENT APPLICATION NUMBER: US/09/212,771
 CURRENT FILING DATE: 1998-12-16
 NUMBER OF SEQ ID NOS: 47
 SEQ ID NO 42
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 US-09-212-771-42

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Fri Aug 19 10:59:59 2005

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; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD4 EXPRESSION
; FILE REFERENCE: RTS-0041
; CURRENT APPLICATION NUMBER: US/09/255,888
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-888-35

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      661 ATTATGTTACTCAAAAT 676
      ||||| ||||| |||||
Db      16 ATTATGTTCTTCAAAAT 1

RESULT 194
US-09-213-768-39/c
; Sequence 39, Application US/09213768
; Patent No. 5985664
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-213-768-39

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      282 ATTCTTCTACTACTGG 297
      ||| ||||| |||||
Db      16 ATTACTTCACTCCTGG 1

RESULT 195
US-09-161-244-74
; Sequence 74, Application US/09161244
; Patent No. 6004814
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION
; FILE REFERENCE: RTS-0007
; CURRENT APPLICATION NUMBER: US/09/161,244
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-161-244-74

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      216 ATTTCATTGCCAAAAG 231
      ||| ||||| |||||
Db      1 ATCTCAGTGCACAAAAG 16

RESULT 196
US-09-255-888-35/c
; Sequence 35, Application US/09255888
; Patent No. 6013787
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD4 EXPRESSION
; FILE REFERENCE: RTS-0041
; CURRENT APPLICATION NUMBER: US/09/255,888
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-888-35

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      64 GGGAGACATGGCGGCG 79
      ||| ||||| |||||
Db      3 GGGCGGCATGGCGGCG 18

RESULT 197
US-08-757-024-711
; Sequence 711, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 711:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-711

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      64 GGGAGACATGGCGGCG 79
      ||| ||||| |||||
Db      3 GGGCGGCATGGCGGCG 18
```


RESULT 198
US-08-757-024-730
; Sequence 730, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 730:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-730

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGGACATGGCGGC 79
Db 2 GGGGCGCATGGCGGC 17

RESULT 199
US-08-757-024-748
; Sequence 748, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024

; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 748:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-748

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGGACATGGCGGC 79
Db 1 GGGGCGCATGGCGGC 16

RESULT 200
US-08-885-291-25/c
; Sequence 25, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-885-291-25

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1048 CAACTTCCTTATCTTT 1063
Db 16 CAACTACCTTATCTGT 1

RESULT 201
US-08-913-441B-21
; Sequence 21, Application US/08913441B
; Patent No. 6162612
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; TITLE OF INVENTION: No. 6162612el Human Cyclin-Dependent Kinase-Like Proteins and
; TITLE OF INVENTION: Methods of Using The Same
; FILE REFERENCE: 8321-76 CII
; CURRENT APPLICATION NUMBER: US/08/913,441B
; CURRENT FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 08/403,634
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/US96/03557

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DB      1  TTAACCTCTGTGGCTG 16
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|||||

RESULT 203
US-09-496-672-25/c
; Sequence 25, Application US/09496672
; Patent No. 6291429
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/09/496,672
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/885,291
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 08/816,693
; PRIOR FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-496-672-25

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1048  CAACTTCCTTATCTTT 1063
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|||||

DB      16  CAACTACCTTATCTGT 1

RESULT 204
US-09-496-694B-116
; Sequence 116, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 116
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-116

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      953  CCACCTCTGGACCCAGG 968
|||||
|||||
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|||||

DB      1  CCACCTCTGGACCCAGG 16

RESULT 205

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US-09-167-109-184
; Sequence 184, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:

APPLICANT: Baker, Brenda F.
APPLICANT: Cowsert, Lex M.
APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION

; FILE REFERENCE: ISPH-0321

; CURRENT APPLICATION NUMBER: US/09/167,109

; CURRENT FILING DATE: 1998-10-06

; NUMBER OF SEQ ID NOS: 228

; SEQ ID NO 184

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antisense sequence

US-09-167-109-184

Query Match 1.1%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 267 GTCGGGAAGTGGCATA 282

DB 2 GTAGGGAAGTGGCATA 17

RESULT 206

US-09-506-768-2

; Sequence 2, Application US/09506768

; Patent No. 6448059

; GENERAL INFORMATION:

APPLICANT: Hou, Ya-Ming

; TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities

; FILE REFERENCE: JEPF-0229

; CURRENT APPLICATION NUMBER: US/09/506,768

; CURRENT FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: US 60/026,094

; PRIOR FILING DATE: 1996-09-13

; PRIOR APPLICATION NUMBER: US 08/928,362

; PRIOR FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 18

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Yeast D stem-loop

US-09-506-768-2

Query Match 1.1%; Score 12.8; DB 1; Length 18;

Best Local Similarity 75.0%; Pred. No. 1.8e+02;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 454 GCAGCAGTGGTAGCAC 469

DB 2 GCGCGAGUGGAGCGC 17

RESULT 207

US-09-475-947A-340

; Sequence 340, Application US/09475947A

; Patent No. 6472154

; GENERAL INFORMATION:

APPLICANT: Garner, Harold R.

APPLICANT: Wren, Jonathan D.

APPLICANT: Minna, John D.

; TITLE OF INVENTION: Polymorphic Repeats in Human Genes

; FILE REFERENCE: UTSD0667

; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 340

; LENGTH: 18

; TYPE: DNA

; ORGANISM: human

US-09-475-947A-340

Query Match

Best Local Similarity 1.1%; Score 12.8; DB 1; Length 18;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 45 GCAGCCGCGCCCCAG 60

DB 1 GCAGCAGCAGCCCCAG 16

RESULT 208

US-09-422-978-5124/c

; Sequence 5124, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 5124

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

NAME/KEY: primer bind

LOCATION: 1..18

; OTHER INFORMATION: upstream amplification primer 99-21079 for SEQ 1190,

US-09-422-978-5124

Query Match

Best Local Similarity 1.1%; Score 12.8; DB 1; Length 18;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AGTTCGGGAGACATGG 74

DB 16 AGTTCGGAACATGG 1

RESULT 209

US-09-422-978-7460/c

; Sequence 7460, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

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; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7460
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-49 for SEQ 3526,
; US-09-422-978-7460

Query Match          1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 308 TCTGCTTTGGATTTC 323
Db 17 TCTGACTGTGGATTTC 2

RESULT 210
US-09-696-791-4204/c
; Sequence 4204, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Hammerhead ribozyme recognition site for cdc 2 kinase
; US-09-696-791-4204

Query Match          1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 424 TATATTTGGAAGGGA 439
Db 17 TATATTTGGATGACGA 2

RESULT 211
US-09-856-662-80/c
; Sequence 80, Application US/09856662
; Patent No. 6790616
; GENERAL INFORMATION:
; APPLICANT: MORIBE, Toyoki et al.
; TITLE OF INVENTION: Method for typing HLA class 1 genes
; FILE REFERENCE: 0032-0261P
; CURRENT APPLICATION NUMBER: US/09/856,662
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: JP P1998-335151
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA probe 134-g

```

```

US-09-856-662-80

Query Match          1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 811 CGCTGAAGCAGGCTCTC 828
Db 18 CGATGAAGCGGGCTCYC 1

RESULT 212
US-09-720-435A-349/c
; Sequence 349, Application US/09720435A
; Patent No. 6803187
; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease
; TITLE OF INVENTION: gene
; FILE REFERENCE: 11362.0030.PCUS00 INNS:030
; CURRENT APPLICATION NUMBER: US/09/720,435A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/EP99/04317
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 98870143.9
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 349
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Aids-associated retrovirus
; US-09-720-435A-349

Query Match          1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 370 CCTTGTTGGCAGGC 385
Db 18 CCTATGTTGACAGGC 3

RESULT 213
US-09-571-985C-21
; Sequence 21, Application US/09571985C
; Patent No. 6822080
; GENERAL INFORMATION:
; APPLICANT: Antonio Giordano
; TITLE OF INVENTION: No. 6822080el Human Cyclin-Dependent Kinase-Like
; TITLE OF INVENTION: Proteins and Methods of Using Same
; FILE REFERENCE: 8321-76 D11
; CURRENT APPLICATION NUMBER: US/09/571,985C
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 08/913,441
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 08/403,634
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/US96/03557
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-571-985C-21

Query Match          1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 792 TCCTTGGAGAGCACA 807
 Db 2 TCCTTGGAGAGCACA 17

RESULT 214
 US-09-093-972C-711
 ; Sequence 711, Application US/09093972C
 ; Patent No. 6825174
 ; GENERAL INFORMATION:
 ; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 ; STREET: 7 Clarke Drive
 ; CITY: Cranbury
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 08512
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/093,972C
 ; FILING DATE: 09-Jun-1998
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 08/757,024
 ; FILING DATE: 26-11-1996
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 09/016,464
 ; FILING DATE: 30-January-1998
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel, Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: EPI-00672
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-409-3035
 ; TELEFAX: 413-254-9245
 ; TELEX: <Unknown>
 ;
 ; INFORMATION FOR SEQ ID NO: 711:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 711:
 US-09-093-972C-711

Query Match 1.1%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGGCGGC 79
 Db 3 GGGCGGCATGGCGGC 18

RESULT 215
 US-09-093-972C-730
 ; Sequence 730, Application US/09093972C
 ; Patent No. 6825174
 ; GENERAL INFORMATION:
 ; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 ; STREET: 7 Clarke Drive
 ; CITY: Cranbury
 ; STATE: New Jersey
 ; COUNTRY: USA

; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 ; STREET: 7 Clarke Drive
 ; CITY: Cranbury
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 08512
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/093,972C
 ; FILING DATE: 09-Jun-1998
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 08/757,024
 ; FILING DATE: 26-11-1996
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 09/016,464
 ; FILING DATE: 30-January-1998
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel, Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: EPI-00672
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-409-3035
 ; TELEFAX: 413-254-9245
 ; TELEX: <Unknown>
 ;
 ; INFORMATION FOR SEQ ID NO: 730:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 730:
 US-09-093-972C-730

Query Match 1.1%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGGCGGC 79
 Db 2 GGGCGGCATGGCGGC 17

RESULT 216
 US-09-093-972C-748
 ; Sequence 748, Application US/09093972C
 ; Patent No. 6825174
 ; GENERAL INFORMATION:
 ; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 ; STREET: 7 Clarke Drive
 ; CITY: Cranbury
 ; STATE: New Jersey
 ; COUNTRY: USA

Fri Aug 19 10:59:59 2005

ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 748:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 748:
US-09-093-972C-748
Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 GGGAGCATGGCGGCG 79
DB 1 GGGCGCATGGCGGCG 16
RESULT 217
US-09-918-186A-116
Sequence 116, Application US/09918186A
Patent No. 6838283
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swayze
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0585
CURRENT APPLICATION NUMBER: US/09/918,186A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/496,694
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 250
SEQ ID NO 116
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-186A-116

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 953 CCACTCTGGACCCAGG 968
DB 1 CCACTCTGGACCCAGG 16
RESULT 218
PCT-US95-03731-34
Sequence 34, Application PC/TUS9503731
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03731
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224982
FILING DATE: 07-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 884P1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-03731-34
Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TTAACCTCTCTGGGTG 1095
DB 1 TTAACCTCTCTGGGTG 16
RESULT 219
US-08-785-750-2/c
Sequence 2, Application US/08785750
Patent No. 5846528
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES

STREET: 90 MIDDLEFIELD ROAD, SUITE 200
 CITY: MENLO PARK
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/785,750
 FILING DATE: 16-JAN-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/588,355
 FILING DATE: 18-JAN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: MCCracken, THOMAS P.
 REGISTRATION NUMBER: 38,548
 REFERENCE/DOCKET NUMBER: 0800-0009.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 325-7812
 TELEFAX: (415) 325-7823
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-785-750-2

Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCGAGCTGCC 753
 ||| ||||| |||||
 Db 14 TGCAGGCGAGCTGCC 1

RESULT 220
 US-08-588-355-1/c
 ; Sequence 1, Application US/08588355
 ; Patent No. 5858351
 ; GENERAL INFORMATION:
 ; APPLICANT: PODSAKOFF, GREGORY M.
 ; APPLICANT: KESSLER, PAUL D.
 ; APPLICANT: BYRNE, BARRY J.
 ; APPLICANT: KURTZMAN, GARY J.
 ; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
 ; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ROBINS & ASSOCIATES
 ; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
 ; CITY: MENLO PARK
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/588,355
 ; FILING DATE: 18-JAN-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: MCCracken, THOMAS P.
 REGISTRATION NUMBER: 38,548
 REFERENCE/DOCKET NUMBER: 0800-0009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 325-7812
 TELEFAX: (650) 325-7823
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-588-355-1

Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCGAGCTGCC 753
 ||| ||||| |||||
 Db 14 TGCAGGCGAGCTGCC 1

RESULT 221
 US-09-116-780-5/c
 ; Sequence 5, Application US/09116780
 ; Patent No. 5945335
 ; GENERAL INFORMATION:
 ; APPLICANT: Colosi, Peter
 ; TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
 ; TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences
 ; FILE REFERENCE: 2555.2.2
 ; CURRENT APPLICATION NUMBER: US/09/116,780
 ; CURRENT FILING DATE: 1998-07-16
 ; EARLIER APPLICATION NUMBER: 08/745,957
 ; EARLIER FILING DATE: 1996-11-07
 ; EARLIER APPLICATION NUMBER: 60/006,402
 ; EARLIER FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
 US-09-116-780-5

Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCGAGCTGCC 753
 ||| ||||| |||||
 Db 14 TGCAGGCGAGCTGCC 1

RESULT 222
 US-08-812-102-1/c
 ; Sequence 1, Application US/08812102
 ; Patent No. 5952221
 ; GENERAL INFORMATION:
 ; APPLICANT: KURTZMAN, GARY J.
 ; APPLICANT: COLOSI, PETER C.
 ; APPLICANT: YOSHIDA, JUN
 ; APPLICANT: MIZUNO, MASAAKI
 ; APPLICANT: OKADA, HIDEHO
 ; TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
 ; TITLE OF INVENTION: TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:

iss.res

Fri Aug 19 10:59:59 2005

```

; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/784,757
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,355

; Query Match 1.1%; Score 12.4; DB 1; Length 14;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCGAGCTGCC 753
DB 14 TGCAGGCGAGCTGCC 1

RESULT 223
US-08-784-757-1/c
; Sequence 1, Application US/08/784/757
; Patent No. 5962313
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/784,757
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,355

; Query Match 1.1%; Score 12.4; DB 1; Length 14;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCGAGCTGCC 753
DB 14 TGCAGGCGAGCTGCC 1

RESULT 224
US-08-745-957-1/c
; Sequence 1, Application US/08/745/957
; Patent No. 6004797
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
; RECOMBINANT AAV VIRION PRODUCTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,957
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,402
; FILING DATE: 09-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-745-957-1

; Query Match 1.1%; Score 12.4; DB 1; Length 14;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCGAGCTGCC 753
DB 14 TGCAGGCGAGCTGCC 1

RESULT 225
US-08-812-102-1
; Sequence 1, Application US/08/812/102
; Patent No. 6004797
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
; RECOMBINANT AAV VIRION PRODUCTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,957
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,402
; FILING DATE: 09-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-812-102-1

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QY 740 TGTAGGAGCTGCC 753
Db 14 TGCAGGAGCTGCC 1

RESULT 225
US-08-646-789A-13/c
; Sequence 13, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-646-789A-13

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 499 TTAGAACTCATCT 512
Db 14 TTAGAACTCAACT 1

RESULT 226
US-08-646-789A-83/c
; Sequence 83, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-646-789A-83

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 499 TTAGAACTCATCT 512
Db 14 TTAGAACTCAACT 1

RESULT 227
US-09-309-042-1/c
; Sequence 1, Application US/09309042
; Patent No. 6211163
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,042
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, Thomas P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-309-042-1
;
; Query Match
; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Length 14;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 740 TGTAGGCAGCTGCC 753
Db 14 TGCAGGCAGCTGCC 1
;
RESULT 228
US-09-205-337-2/c
; Sequence 2, Application US/09205337
; Patent No. 6325998
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
;
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,337
; FILING DATE: 04-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,750
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-205-337-2
;
; Query Match
; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Length 14;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 740 TGTAGGCAGCTGCC 753
Db 14 TGCAGGCAGCTGCC 1
;
RESULT 229
US-09-406-362-1/c
; Sequence 1, Application US/09406362
; Patent No. 6335011
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
;
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,362
; FILING DATE: 28-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/784,757
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-406-362-1
;
; Query Match
; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Length 14;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 740 TGTAGGCAGCTGCC 753
Db 14 TGCAGGCAGCTGCC 1
;
RESULT 230
US-09-755-734-1/c
; Sequence 1, Application US/09755734
; Patent No. 6391858
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
;
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA

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Matches	13;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	740	TGTAGGCAGCTGCC	753						
DB	14	TGCAGGCAGCTGCC	1						
RESULT 233									
US-09-969-204A-1/c									
; Sequence 1, Application US/09969204A									
; Patent No. 6610290									
; GENERAL INFORMATION:									
; APPLICANT: PODSAKOFF, GREGORY M.									
; KESSLER, PAUL D.									
; BYRNE, BARRY J.									
; KURTZMAN, GARY J.									
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE									
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS									
; VIRIONS									
; NUMBER OF SEQUENCES: 9									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: ROBINS & ASSOCIATES									
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200									
; CITY: MENLO PARK									
; STATE: CA									
; COUNTRY: USA									
; ZIP: 94025									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: Patent in Release #1.0, Version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/09/969,204A									
; FILING DATE: 01-Oct-2001									
; CLASSIFICATION: <Unknown>									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US/09/406,362									
; FILING DATE: 28-Sep-1999									
; APPLICATION NUMBER: 08/784,757									
; FILING DATE: <Unknown>									
; ATTORNEY/AGENT INFORMATION:									
; NAME: MCCracken, Thomas P.									
; REGISTRATION NUMBER: 38,548									
; REFERENCE/DOCKET NUMBER: 0800-0009.20									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (415) 325-7812									
; TELEFAX: (415) 325-7823									
; INFORMATION FOR SEQ ID NO: 1:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 14 base pairs									
; TYPE: nucleic acid									
; STRANDEDNESS: single									
; TOPOLOGY: linear									
; MOLECULE TYPE: DNA (genomic)									
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:									
US-09-969-204A-1									
Query Match 1.1%; Score 12.4; DB 1; Length 14;									
Best Local Similarity 92.9%; Pred. No. 2.1e-02;									
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	740	TGTAGGCAGCTGCC	753						
DB	14	TGCAGGCAGCTGCC	1						
RESULT 234									
US-08-182-968A-118									
; Sequence 118, Application US/08182968A									
; Patent No. 5610054									
; GENERAL INFORMATION:									
; APPLICANT: Draper, Kenneth G.									

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-119

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Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Qy 683 ACTGTTGGTGT 696
Db 1 ACUGGUUUGGCU 14

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RESULT 236
US-08-373-124A-94
; Sequence 94, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327

```

```

; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-94

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 294 CTGGAATTGTGTT 307
Db 1 CUGGAUUGGCU 14

RESULT 237
US-08-435-628-94
; Sequence 94, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 94:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-94

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 294 CTGGAATTGGTGT 307
Db 1 CUGGAUUGGUGU 14

RESULT 238
US-08-774-306A-118
; Sequence 118, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-119

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 683 ACTTGTGGCTGT 696
Db 1 ACUGGUUGGUGU 14

RESULT 240
US-08-667-939A-10
; Sequence 10, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LJO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: L00=2A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-667-939A-10

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 455 GAGCAGTGGTAGCA 468
Db 1 GAGCAGTGGCAGCA 14

RESULT 241
US-08-667-939A-21/c
; Sequence 21, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: L00=2A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; MEDIUM TYPE: linear
; MOLECULE TYPE: cdna
US-08-667-939A-21

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 455 GAGCAGTGGTAGCA 468
Db 15 GAGCAGTGGCAGCA 2

RESULT 242
US-09-284-782-13/c
; Sequence 13, Application US/09284782
; Patent No. 6057111
; GENERAL INFORMATION:
; APPLICANT: ENTERPRISES, LTD., QBI
; APPLICANT: Deiss, Louis P.
; APPLICANT: Yehiely, Fruma
; APPLICANT: Efimova, Elena
; APPLICANT: Vasquez-Iaslop, No. 6057111a C.
; APPLICANT: Einat, Paz
; TITLE OF INVENTION: GENE IDENTIFICATION METHOD
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6057111thwestern Highway, Suite 410
; CITY: Fawington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 0168-00022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
US-09-284-782-13

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 841 GGCCGGGTGGATC 854
Db 14 GGCCGAGGTGGATC 1

RESULT 243
US-09-064-156A-118
; Sequence 118, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
```

Fri Aug 19 10:59:59 2005

```

;
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
;
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-064-156A-119
;
; Query Match 1.1%; Score 12.4; DB 1; Length 15;
; Best Local Similarity 50.0%; Pred. No. 2.1e+02;
; Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
;
; QY 683 ACTTGTTGGCTGT 696
; ||:|::|::|:|:
; Db 1 ACUGGUUUGGCGU 14
;
; RESULT 245
; US-09-081-646-526
; Sequence 526, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 0107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 526
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-09-081-646-526
;
; Query Match 1.1%; Score 12.4; DB 1; Length 15;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 977 ATGAGATCCCAAGG 990
; |||||
; Db 2 ATGAGATCCCAAGG 15
;
;
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
;
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-064-156A-118
;
; Query Match 1.1%; Score 12.4; DB 1; Length 15;
; Best Local Similarity 50.0%; Pred. No. 2.1e+02;
; Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
;
; QY 683 ACTTGTTGGCTGT 696
; ||:|::|::|:|:
; Db 2 ACUGGUUUGGCGU 15
;
; RESULT 244
; US-09-064-156A-119
; Sequence 119, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:

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RESULT 246
US-08-584-040-8484
; Sequence 8484, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8484:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-8484

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATCA 1028
Db 1 GAAGCAUCAGCAUA 14

RESULT 247
US-08-433-123-10
; Sequence 10, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-433-123-10

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 455 GAGCAGTGTGACGA 468
Db 1 GAGCAGTGTGACGA 14

RESULT 248
US-08-433-123-21/c
; Sequence 21, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs

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Fri Aug 19 10:59:59 2005

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4138
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-4138

Query Match      1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1015 GAAGCATCATCATCA 1028
Db      1 GAAGCAUCAGCAUA 14

RESULT 251
US-07-696-793A-18
; Sequence 18, Application US/07696793A
; Patent No. 5220004
; GENERAL INFORMATION:
; APPLICANT: Saiiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/696,793A
; FILING DATE: 19910507
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin R. Kaaster
; REGISTRATION NUMBER: 32704
; REFERENCE/DOCKET NUMBER: 2598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3444
; TELEFAX: (415) 658-5239
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-07-696-793A-18

Query Match      1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1042 CACACCCCACTTCC 1055
Db      1 CACACCCAGCTTCC 14

RESULT 252
US-07-977-694-18
; Sequence 18, Application US/07977694
```

Patent No. 5273883
GENERAL INFORMATION:
APPLICANT: Saiki, Randall K.
APPLICANT: Nasarabadi, Shanavaz L.
TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,694
FILING DATE: 19921117
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stacey R. Sias, Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8733
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-07-977-694-18

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCAACTTCC 1055
DB 1 CACACCCAGCTTCC 14

RESULT 253
US-09-479-005A-12/c
Sequence 12, Application US/09479005A
Patent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBH00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/444,209
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens

US-09-479-005A-12

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 387 ATGCAGTCATTTTC 400
DB 14 ATTCAGTCATTTTC 1

RESULT 254
US-09-410-416-19/c
Sequence 19, Application US/09410416
Patent No. 6743906
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Wang, Steven Sizing
APPLICANT: Epllin, Edward D.
APPLICANT: Li, Jia Ling
APPLICANT: Huang, Liying
TITLE OF INVENTION: PPP2R1B is a Tumor Suppressor
FILE REFERENCE: UTS0574
CURRENT APPLICATION NUMBER: US/09/410,416
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 60/102,952
EARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 16
TYPE: DNA
ORGANISM: Homo sapiens
US-09-410-416-19

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 571 TAATACCTTTTATAT 584
DB 14 TAATCTCTTTATAT 1

RESULT 255
US-07-696-793A-19
Sequence 19, Application US/07696793A
Patent No. 5220004
GENERAL INFORMATION:
APPLICANT: Saiki, Randall K.
APPLICANT: Nasarabadi, Shanavaz L.
TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,793A
FILING DATE: 19910507
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

```

ATTORNEY/AGENT INFORMATION:
NAME: Kevin R. Kaster
REGISTRATION NUMBER: 32704
REFERENCE/DOCKET NUMBER: 2598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3444
TELEFAX: (415) 658-5239
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-07-696-793A-19

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCACTTCC 1055
DB 111111111111111111
3 CACACCCCACTTCC 16

RESULT 256
US-07-696-793A-20
Sequence 20, Application US/07696793A
Patent No. 5220004
GENERAL INFORMATION:
APPLICANT: Saiki, Randall K.
APPLICANT: Nasarabadi, Shanavaz L.
TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,793A
FILING DATE: 19910507
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kevin R. Kaster
REGISTRATION NUMBER: 32704
REFERENCE/DOCKET NUMBER: 2598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3444
TELEFAX: (415) 658-5239
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-07-696-793A-20

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,694
; FILING DATE: 19921117
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8733
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-07-977-694-20

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCACTCC 1055
DB 1 CACACCCCACTCC 14

RESULT 259
US-08-095-726-46/c
; Sequence 46, Application US/08095726
; Patent No. 5530188
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Beta-Carotene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,726
; FILING DATE: 21-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,566
```

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; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5530189val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-095-726-46

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCCGGGCGGTGGCA 33
DB 17 CCCGGGCGGTGGCA 4

RESULT 260
US-08-096-043-43/c
; Sequence 43, Application US/08096043
; Patent No. 5530189
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Lycopene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,043
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,568
; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5530189val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-096-043-43

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
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Fri Aug 19 10:59:59 2005

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 CCCGGGCGGTGGCA 33
Db 17 CCCGGGCGGTGGCA 4

RESULT 261
US-08-093-577-39/c
; Sequence 39, Application US/08093577
; Patent No. 5545816
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Phytoene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,577
; FILING DATE: 19-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,569
; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5545816val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-093-577-39
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 CCCGGGCGGTGGCA 33
Db 17 CCCGGGCGGTGGCA 4

RESULT 262
US-08-390-850-601/c
; Sequence 601, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,850
FILING DATE: February 17, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354,920
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
FILING DATE: No. 5612215ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 601:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-390-850-601
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 925 CCTTATTAGAAATG 938
Db 17 CCTTATCAGAAATG 4

RESULT 263
US-08-373-124A-572
; Sequence 572, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 572:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-572

```

```

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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QY 294 CTGGAATTGTTGTT 307
|:||||:|:|:|
DB 2 CUGGAUUGUGCU 15

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RESULT 264
US-08-373-124A-1611
; Sequence 1611, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-1611

```

```

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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QY 294 CTGGAATTGTTGTT 307
|:||||:|:|:|
DB 2 CUGGAUUGUGCU 15

```

```

RESULT 265
US-08-373-124A-1917/C
; Sequence 1917, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992

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; TELEFAX: (312) 655-1501
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-096-623A-51

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCCGGCGCGTGGCA 33
Db 17 CCCGGCGCATGGCA 4

RESULT 268
US-08-434-402-55/c
; Sequence 55, Application US/08434402
; Patent No. 5714581
; GENERAL INFORMATION:
; APPLICANT: KUGA, TETSURO
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: SATO, MORIYUKI
; APPLICANT: OKABE, MASAMI
; APPLICANT: MORIMOTO, MAKOTO
; APPLICANT: ITOH, SEIGA
; APPLICANT: YAMASAKI, MOTOO
; APPLICANT: YOKOO, YOSHIHARU
; APPLICANT: YAMAGUCHI, KAZUO
; APPLICANT: YOSHIDA, HAJIME
; APPLICANT: YOSHINORI, KOMATSU
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,402
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306799/86
; FILING DATE: 23-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 51357/88
; FILING DATE: 04-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 80088/88
; FILING DATE: 31-MAR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR
; REGISTRATION NUMBER: 25327
; REFERENCE/DOCKET NUMBER: 249-72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-434-402-55

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAGGCGCGGG 848
Db 17 CAGGAGGCGCGGG 4

RESULT 269
US-08-435-634-601/C
; Sequence 601, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295 September 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-601

Query Match          1.1%; Score 12.4; DB 1; Length 17;

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Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 925 CCTTATTAGAAATG 938
Db 17 CCTTATCAGAAATG 4

RESULT 270
US-08-783-288-55/c
; Sequence 55, Application US/08783288
; Patent No. 5795968
; GENERAL INFORMATION:
; APPLICANT: KUGA, TETSURO
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: SATO, MORIYUKI
; APPLICANT: OKABE, MASAMI
; APPLICANT: MORIMOTO, MAKOTO
; APPLICANT: ITOH, SEIGA
; APPLICANT: YAMASAKI, MOTOO
; APPLICANT: YOKOO, YOSHIHARU
; APPLICANT: YAMAGUCHI, KAZUO
; APPLICANT: YOSHIDA, HAJIME
; APPLICANT: YOSHINORI, KOMATSU
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783,288
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,411
; FILING DATE: 03-MAY-1995
; APPLICATION NUMBER: JP 306799/86
; FILING DATE: 23-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 51357/88
; FILING DATE: 04-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 80088/88
; FILING DATE: 31-MAR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR
; REGISTRATION NUMBER: 25327
; REFERENCE/DOCKET NUMBER: 249-73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-783-288-55

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 835 CAGGAGCGCGGG 848
Db 17 CAGGAGCGCGGG 4

RESULT 271
US-08-435-628-572
; Sequence 572, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 572:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-572

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 294 CTGGAATTGTGTT 307
Db 2 CUGGAUUGUUGCU 15

```

RESULT 272
US-08-435-628-1611
; Sequence 1611, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1611

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 294 CTGGAATTCGTTGTT 307
|:|||||:|:|:|
Db 2 CUGGAUUGUUCU 15

RESULT 273
US-08-435-628-1917/c
; Sequence 1917, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:

```

```

; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1917:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1917

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 274 ACTGGCATATTTCT 287
|:|||||:|:|:|
Db 14 ACTGGCATATTTCT 1

RESULT 274
US-08-313-185-35/c
; Sequence 35, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio

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[illegible]

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-35

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1021 TCATCATGAGAAG 1034
Db 14 TCATCATAGGGAAG 1

RESULT 277
US-09-306-595C-27
; Sequence 27, Application US/09306595C
; Patent No. 6284506
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/306,595C
; CURRENT FILING DATE: 1999-05-06
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of genomic DNA containing MVX gene
US-09-306-595C-27

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 863 TGTGTAGTCCATG 876
Db 4 TGTGTAGTCCATG 17

RESULT 278
US-08-584-040-2568
; Sequence 2568, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2568:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2568

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 689 TTGCTGTTCATG 702
Db 1 UUAGCGUUGAUG 14

RESULT 279
US-08-584-040-3886
; Sequence 3886, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2568:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-3886

```

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Fri Aug 19 10:59:59 2005

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3886:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-3886

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATTA 1028
Db 2 GAAGCAUCAGCAUA 15

RESULT 280
US-09-634-918-1
; Sequence 1, Application US/09634918
; Patent No. 6379931
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
; FILE REFERENCE: 2124-302
; CURRENT APPLICATION NUMBER: US/09/634,918
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/148,339
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Residues 1-9 are DNA; residues 10-17 are RNA.
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: DNA/RNA ribozyme sequence
US-09-634-918-1

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 469 CTTTATTCTGATTA 482

Db 3 CTTTATTCTGATTA 16

RESULT 281
US-09-634-918-3
; Sequence 3, Application US/09634918
; Patent No. 6379931
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Swiderski, Piotr M.
; TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
; FILE REFERENCE: 2124-302
; CURRENT APPLICATION NUMBER: US/09/634,918
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/148,339
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Residues 1-9 are DNA; residues 10-17 are RNA.
; OTHER INFORMATION: Residue 10 is cm. Residues 11 and 14 are um.
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: DNA/RNA ribozyme sequence
US-09-634-918-3

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 469 CTTTATTCTGATTA 482
Db 3 CTTTATTCTGATTA 16

RESULT 282
US-09-474-432B-475
; Sequence 475, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleo
; FILE REFERENCE: MHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 475
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-475

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 2.1e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 305 GTTCTGCTTTGG 318
 Db 3 GUUUUGCCUUGG 16

RESULT 283
 US-09-474-432B-667/c
 ; Sequence 667, Application US/09474432B
 ; Patent No. 6528640
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Beigelman, Leo
 ; APPLICANT: Burgin, Alex
 ; APPLICANT: Beaudry, Amber
 ; APPLICANT: Karpeisky, Alex
 ; APPLICANT: Adamic, Jasenka
 ; APPLICANT: Sweedler, David
 ; APPLICANT: Zinnen, Shawn
 ; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
 ; FILE REFERENCE: MBHB00-831-B (247/276)
 ; CURRENT APPLICATION NUMBER: US/09/474,432B
 ; CURRENT FILING DATE: 1999-12-19
 ; PRIOR APPLICATION NUMBER: US 60/064,866
 ; PRIOR FILING DATE: 1997-11-05
 ; PRIOR APPLICATION NUMBER: US 60/084,727
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: US 09/186,675
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: US 09/301,511
 ; PRIOR FILING DATE: 1999-04-28
 ; NUMBER OF SEQ ID NOS: 1526
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 667
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-474-432B-667

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCGAGGCTGCCGG 24
 Db 15 GCGAGGCTGTCCGG 2

RESULT 284
 US-09-371-772B-1092
 ; Sequence 1092, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBHB00,876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1092

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 2.1e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGCTGTTCATGT 702
 Db 1 UUAGCUGUUGCAUGU 14

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 2.1e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGCTGTTCATGT 702
 Db 1 UUAGCUGUUGCAUGU 14

RESULT 285
 US-09-371-772B-1653
 ; Sequence 1653, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBHB00,876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1653
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-371-772B-1653

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 78.6%; Pred. No. 2.1e+02;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
 Db 2 GAAGCAUCAGCAUA 15

RESULT 286
 US-09-371-772B-5446
 ; Sequence 5446, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBHB00,876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5446
 ; LENGTH: 17

Fri Aug 19 10:59:59 2005

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5446

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY      689 TTGGCTGTTTCATGT 702
Db      ::|||::|||:
          4 UUAGCUGUUGCAUG 17

RESULT 287
US-09-371-772B-6259
; Sequence 6259, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6259
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6259

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1015 GAAGCATCATCATCA 1028
Db      |||||::|||:
          4 GAAGCAUCAGCAUA 17

RESULT 288
US-09-371-772B-6260
; Sequence 6260, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6260
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6260

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1015 GAAGCATCATCATCA 1028
Db      |||||::|||:
          4 GAAGCAUCAGCAUA 14

; ORGANISM: Homo sapiens
US-09-371-772B-6260

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1015 GAAGCATCATCATCA 1028
Db      |||||::|||:
          1 GAAGCAUCAGCAUA 14

RESULT 289
US-09-925-388-27
; Sequence 27, Application US/09925388
; Patent No. 6586202
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/925,388
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of genomic DNA containing MVX gene
US-09-925-388-27

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      863 TGTGTAGTCCATG 876
Db      |||||::|||:
          4 TGTGTAGTCCATG 17

RESULT 290
US-09-476-387-474
; Sequence 474, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zimen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
```



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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 474
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-474

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 305 GTTCTGCTTGG 318
Db 3 GUUUUUGCCUUGG 16

RESULT 291
US-09-476-387-666/c
; Sequence 666, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleob
; FILE REFERENCE: MBH00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 666
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-666

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCGAGCTGCCCGG 24
Db 15 GCGAGCTGCCCGG 2

RESULT 292
US-09-827-998-513/c
; Sequence 513, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-05-26

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; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecmica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 513
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-513

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 312 CCTTTGGATTTCCT 325
Db 17 CCTTTGAATTCCT 4

RESULT 293
US-09-827-998-514/c
; Sequence 514, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecmica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 514
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-514

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 312 CCTTTGGATTTCCT 325
Db 16 CCTTTGAATTCCT 3

RESULT 294
US-09-866-108A-1694/c
; Sequence 1694, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecmeca Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1694
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-1694

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 505 CTCATACATCTGTGT 518
Db 17 CTCATACCATCTGT 4

RESULT 295
US-09-866-108A-1695/c
; Sequence 1695, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecmeca Sequence Listing Engine

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; Sequence 1697, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1697
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-1697

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 505 CTCATCATCTGTGT 518
|||||
Db 14 CTCATACCATCTGT 1

RESULT 298
US-09-866-108A-2568/c
; Sequence 2568, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2568
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-2568

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACC 756
|||||
Db 14 AGGCAGCTGCCGCC 1

RESULT 299
US-09-866-108A-6286
; Sequence 6286, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00685
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755

Fri Aug 19 10:59:59 2005

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; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6286
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6286

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e-02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CGGGCGGTGGCAG 34
Db 4 CGGGCTGTGGCAG 17

RESULT 300
US-09-866-108A-6290
; Sequence 6290, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6290
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6290

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e-02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 CGGGCGGTGGCAGG 35
Db 1 CGGGCTGTGGCAGG 14

RESULT 301
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6290
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6290

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e-02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 CGGGCGGTGGCAGG 35
Db 1 CGGGCTGTGGCAGG 14

RESULT 302
US-09-866-108A-6310/c
; Sequence 6310, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6310
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6310

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e-02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTGCC 148
Db 15 TGCTGGGATGTGCC 2

RESULT 302
US-09-866-108A-6311/c
; Sequence 6311, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6311
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-6311

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTC 148
DB 14 TGCTGGGATGTC 1

RESULT 303
US-09-866-108A-7015/c
; Sequence 7015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6311
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-6311

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTC 148
DB 14 TGCTGGGATGTC 1

RESULT 303
US-09-866-108A-7015/c
; Sequence 7015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6311
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-6311

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; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7015
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7015

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 745 GCAGCTGCCACCTT 758
DB 17 GCAGCTGCCACCTT 4

RESULT 304
US-09-866-108A-7016/c
; Sequence 7016, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7016
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7016

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 745 GCAGCTGCCACCTT 758
DB 16 GCAGCTGCCACCTT 3

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iss.res

Fri Aug 19 10:59:59 2005

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7020

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACC 756
DB 14 AAGCAGCTGCCACC 1

RESULT 307
US-09-866-108A-7789/c
; Sequence 7789, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

RESULT 306
US-09-866-108A-7020/c
; Sequence 7020, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACC 756
DB 15 AAGCAGCTGCCACC 2

RESULT 306
US-09-866-108A-7020/c
; Sequence 7020, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7789
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7789

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      812 GCTGAAGCAGGCT 825
      ||||| |||||
DB      17 GCTGAAGCTGGCCT 4

RESULT 308
US-09-866-108A-7790/c
; Sequence 7790, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7791
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7791

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      812 GCTGAAGCAGGCT 825
      ||||| |||||
DB      15 GCTGAAGCTGGCCT 2

RESULT 310
US-09-866-108A-7792/c
; Sequence 7792, Application. US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7790
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7790

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      812 GCTGAAGCAGGCT 825
      ||||| |||||
DB      16 GCTGAAGCTGGCCT 3
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Fri Aug 19 10:59:59 2005

PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7792
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7792

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1;

Qy 812 GCTGAAGCAGGCGCT 825
Db 14 GCTGAAGCTGGCGCT 1

RESULT 311
US-09-866-108A-9275/c
; Sequence 9275, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7792
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7792

PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9275
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9275

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1;

Qy 505 CTCATACATCTCTGT 518
Db 17 CTCATAGTATCTGT 4

RESULT 312
US-09-866-108A-9276/c
; Sequence 9276, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9276
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9276

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1;

Qy 505 CTCATACATCTCTGT 518
Db 16 CTCATAGTATCTGT 3


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RESULT 313
US-09-866-108A-9277/c
; Sequence 9277, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9277
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9277

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 505 CTCATCTACTCTGT 518
Db 15 CTCATAGTATCTGT 2

RESULT 314
US-09-866-108A-9278/c
; Sequence 9278, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9277
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9277

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 505 CTCATCTACTCTGT 518
Db 15 CTCATAGTATCTGT 2

RESULT 315
US-09-404-912-589
; Sequence 589, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
; APPLICANT: John Landers
; APPLICANT: David Houseman
; APPLICANT: Barbara Jordan
; APPLICANT: Alain Charest
; TITLE OF INVENTION: Methods and Products Related to
; FILE REFERENCE: M0656/7045 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/404,912
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,757
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22283
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 589
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-589

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 450 GCTGGGAGCAGTGG 463
Db 2 GCTGGGCGCAGTGG 15
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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9278
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9278

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 505 CTCATCTACTCTGT 518
Db 14 CTCATAGTATCTGT 1

RESULT 315
US-09-404-912-589
; Sequence 589, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
; APPLICANT: John Landers
; APPLICANT: David Houseman
; APPLICANT: Barbara Jordan
; APPLICANT: Alain Charest
; TITLE OF INVENTION: Methods and Products Related to
; FILE REFERENCE: M0656/7045 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/404,912
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,757
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22283
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 589
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-589

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 450 GCTGGGAGCAGTGG 463
Db 2 GCTGGGCGCAGTGG 15
```

iss.res

Fri Aug 19 10:59:59 2005

```
RESULT 316
US-09-155-885A-14
; Sequence 14, Application US/09155885A
; Patent No. 6709812
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-155-885A-14
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 845 GGGGTGGATCCCTC 858
; | | | | | | | | | |
; Db 2 GGGGTGGAGCCCTC 15
;
; RESULT 317
US-09-155-885A-33/C
; Sequence 33, Application US/09155885A
; Patent No. 6709812
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-155-885A-14
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 845 GGGGTGGATCCCTC 858
; | | | | | | | | | |
; Db 2 GGGGTGGAGCCCTC 15
;
; RESULT 318
US-09-685-664B-1092
; Sequence 1092, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1092
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-155-885A-33
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 845 GGGGTGGATCCCTC 858
; | | | | | | | | | |
; Db 16 GGGGTGGAGCCCTC 3
;
; RESULT 318
US-09-685-664B-1092
; Sequence 1092, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1092
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
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US-09-685-664B-1092
Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGGCTGTTTCATGT 702
DB 1  UUAGCUGUUCAGU 14

RESULT 319
US-09-685-664B-1653
; Sequence 1653, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1653
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1653

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATCA 1028
DB 2  GAAGCAUCAGCAUA 15

RESULT 320
US-09-993-192A-5/c
; Sequence 5, Application US/09993192A
; Patent No. 6838555
; GENERAL INFORMATION:
; APPLICANT: Korea Research Institute of Bioscience and Biotechnology
; APPLICANT: Dong Kook Pharmaceutical Co.
; APPLICANT: Rhee, Sangki
; APPLICANT: Choi, Euisung
; APPLICANT: Kang, Hyunah
; APPLICANT: Sohn, Junghoon
; APPLICANT: Bae, Junghoon
; APPLICANT: Kim, Moowoong
; APPLICANT: Agaphonov, Michasael
; TITLE OF INVENTION: Hansenua polymorpha mutants and process for the preparation of recombinant proteins using the same
; FILE REFERENCE: 4220-116.1 US
; CURRENT APPLICATION NUMBER: US/09/993,192A
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/674,617
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5

US-09-685-664B-1092
Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGGCTGTTTCATGT 702
DB 1  UUAGCUGUUCAGU 14

RESULT 319
US-09-685-664B-1653
; Sequence 1653, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1653
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1653

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATCA 1028
DB 2  GAAGCAUCAGCAUA 15

RESULT 320
US-09-993-192A-5/c
; Sequence 5, Application US/09993192A
; Patent No. 6838555
; GENERAL INFORMATION:
; APPLICANT: Korea Research Institute of Bioscience and Biotechnology
; APPLICANT: Dong Kook Pharmaceutical Co.
; APPLICANT: Rhee, Sangki
; APPLICANT: Choi, Euisung
; APPLICANT: Kang, Hyunah
; APPLICANT: Sohn, Junghoon
; APPLICANT: Bae, Junghoon
; APPLICANT: Kim, Moowoong
; APPLICANT: Agaphonov, Michasael
; TITLE OF INVENTION: Hansenua polymorpha mutants and process for the preparation of recombinant proteins using the same
; FILE REFERENCE: 4220-116.1 US
; CURRENT APPLICATION NUMBER: US/09/993,192A
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/674,617
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
```

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR primer for S. cerevisiae PRC1 gene
US-09-993-192A-5

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 414 GGTTTTCCTTATA 427
DB 15 GGTTTTCCTTATA 2

RESULT 321
5194592-80/c
; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,647
; FILING DATE: 22-DEC-1987
; SEQ ID NO:80:
; LENGTH: 17
5194592-80

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAAGCGCGGG 848
DB 17 CAGGACGCGCGGG 4

RESULT 322
5194592-80/c
; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,647
; FILING DATE: 22-DEC-1987
; SEQ ID NO:80:
; LENGTH: 17
5194592-80

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAAGCGCGGG 848
DB 17 CAGGACGCGCGGG 4

RESULT 323
US-08-390-850-479/c
; Sequence 479, Application US/08390850
```

Patent No. 5612215
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: February 17, 1995
PRIORITY APPLICATION NUMBER: US/08/390,850
PRIORITY APPLICATION DATA:
FILING DATE: December 13, 1994
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
FILING DATE: NO. 5612215ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 479:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-390-850-479

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0;
Gaps 0;

Qy 902 AGAGCGCTCAACATTC 918
Db 17 ATGAGCCAAAACATTC 1

RESULT 324
US-08-390-850-480/C
Sequence 480, Application US/08390850
Patent No. 5612215
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: February 17, 1995
PRIORITY APPLICATION NUMBER: US/08/390,850
PRIORITY APPLICATION DATA:
FILING DATE: December 13, 1994
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
FILING DATE: NO. 5612215ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 480:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-390-850-480

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0;
Gaps 0;

Qy 901 CAAGAGCGCTCAACATTT 917
Db 17 CATGAGCCAAAACATTT 1

RESULT 325
US-08-373-124A-456/c
Sequence 456, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 456:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-456

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 598 TTAAGAAAGACTTCATAA 614
Db 17 TTAAGAAAGAACTCTATA 1

RESULT 326
US-08-373-124A-458/c
Sequence 458, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 458:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-458

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 597 TTAAGAAAGACTTCATA 613
Db 17 TTAAGAAAGAACTCTATA 1

RESULT 327
US-08-373-124A-504
Sequence 504, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035

QY
4 TGGCTTGGGCAGGCTGC 20

Db 17 TGCCTTTGGAAGGCTTC 1

RESULT 330

US-08-373-124A-1559
; Sequence 1559, Application US/08373124A
; Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 1559:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1559

Query Match 1.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 499 TTGAAGCTCATCTATC 515

Db 1 UUGAACUCCAGCUAUC 17

RESULT 331

US-08-373-124A-2393
; Sequence 2393, Application US/08373124A
; Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 2393:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-2393

Query Match 1.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTCTAGAGCC 926

Db 1 CACCAUUCAUAGAGAC 17

RESULT 332

US-08-373-124A-2437
; Sequence 2437, Application US/08373124A
; Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

```

STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373.124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2437:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-2437
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 546 ATGAATTTTAAATGCT 562
DB 1 AAGAAUUAUAUGGU 17

RESULT 333
US-08-373-124A-2563
Sequence 2563, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

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INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-200-232-5

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 839 AAGGCGGGTGGATCC 855
 DB 1 AAGGCTGGTGGATAC 17

RESULT 335
 US-08-435-634-479/c
 ; Sequence 479, Application US/08435634
 ; Patent No. 5731295

GENERAL INFORMATION:
 ; APPLICANT: Draper, Kenneth G.
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Gustofson, John
 ; APPLICANT: Stinchcomb, Dan T.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
 ; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
 ; NUMBER OF SEQUENCES: 1151

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,634
 ; FILING DATE: 05-MAY-1995

CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/390,850
 ; FILING DATE: February 17, 1995
 ; APPLICATION NUMBER: 08/354,920
 ; FILING DATE: December 13, 1994
 ; APPLICATION NUMBER: 08/152,487
 ; FILING DATE: No. 5731295, September 12, 1993
 ; APPLICATION NUMBER: 07/989,848
 ; FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 211/084
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 479:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-435-634-479

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 902 AAGAGCCTCAACATTT 918
 DB 17 ATGAGCCAAACATTT 1

RESULT 336
 US-08-435-634-480/c
 ; Sequence 480, Application US/08435634
 ; Patent No. 5731295

GENERAL INFORMATION:
 ; APPLICANT: Draper, Kenneth G.
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Gustofson, John
 ; APPLICANT: Stinchcomb, Dan T.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
 ; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
 ; NUMBER OF SEQUENCES: 1151

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,634
 ; FILING DATE: 05-MAY-1995

CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/390,850
 ; FILING DATE: February 17, 1995
 ; APPLICATION NUMBER: 08/354,920
 ; FILING DATE: December 13, 1994
 ; APPLICATION NUMBER: 08/152,487
 ; FILING DATE: No. 5731295, September 12, 1993
 ; APPLICATION NUMBER: 07/989,848
 ; FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 211/084
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 480:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-435-634-480

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 901 CAAGAGCCTCAACATTT 917
 DB 17 CATGAGCCAAACATTT 1

Fri Aug 19 10:59:59 2005

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 456:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-456

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 598 TAAGAAAGACTTCATTA 614
Db 17 TAAGAAAGACTTCATTA 1

RESULT 339
US-08-435-628-458/c
Sequence 458, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California

```

```

; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-458

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 597 TTAAGAAGACTTCATA 613
Db 17 TTAAGAAGACTTCATA 1

RESULT 340
US-08-435-628-504
; Sequence 504, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514

```

```

; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 504:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-504

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTCCTAGAGCC 926
Db 1 CACCAUUCUAUAGAGAC 17

RESULT 341
US-08-435-628-716
; Sequence 716, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514

```

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
0. Mismatches 3; Indels 0; Gaps 0;

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1559:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-1559

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 499 TTAGAACTCATCTATC 515
DB 1 UUAGACUCCAGCAUC 17

RESULT 344
US-08-435-628-2393
Sequence 2393, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2393:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-2393
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 910 CAACATTTCTTAGAGCC 926
DB 1 CACCAUUCUAGAGAC 17
RESULT 345
US-08-435-628-2437
Sequence 2437, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2437:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-435-628-2437

Query Match
Best Local Similarity 1.1%; Score 12.2; DB 1; Length 17;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 546 ATGAAATTTAAATGCT 562
Db 1 AAGAAAUAAUAUGGU 17

RESULT 346
US-08-435-628-2563
; Sequence 2563, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2563:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-2563

Query Match
Best Local Similarity 1.1%; Score 12.2; DB 1; Length 17;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

TOPOLOGY: linear
US-08-985-162-157/c

Query Match
Best Local Similarity 1.1%; Score 12.2; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 982 ATCCAAAGGAGGTGTAT 998
Db 17 ATCCAGAGGAGGAGTAT 1

RESULT 348
US-08-985-162-283
; Sequence 283, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-157

Query Match
Best Local Similarity 1.1%; Score 12.2; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-283

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTCCTAGACC 926
DB 1 CAACAUCUCCGAAGCC 17

RESULT 349
US-08-985-162-337
; Sequence 337, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.

```

```

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 337:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-337

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCTCCATCC 212
DB 1 CGAGAUCUCCUCCAUCC 17

RESULT 350
US-08-985-162-631/c
; Sequence 631, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.

```

iss.res

Fri Aug 19 10:59:59 2005

```

;
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 631:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-985-162-631

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 613 AAGTAGGAGATGAGTTT 629
Db 17 AATTAGGAGATGCTTT 1

RESULT 351
US-08-985-162-653
; Sequence 653, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 653:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 653:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-985-162-653

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 654 AATTAGATTATGTTTAC 670
Db 1 AAUAGUUGUGUACU 17

RESULT 352
US-08-985-162-654
; Sequence 654, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 654:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 654:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-985-162-654

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.3e+02;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 655 AATTAGATTATGTTTACT 671
Db 1 AAUAGUUGUGUACU 17

RESULT 353
US-08-988-706-45
; Sequence 45, Application US/08988706
; Patent No. 6083698
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,706
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 653:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 653:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-985-162-653
```


APPLICANT: OLSEN, Sheri J.
APPLICANT: ANGELLY, Tracy S.
APPLICANT: LAWRENCE, Tammy
APPLICANT: LESCALLET, Jennifer L.
APPLICANT: MURPHY, Patricia D.
APPLICANT: ALLEN, Antonette P.
APPLICANT: THRUBER, Denise B.
APPLICANT: WHITE, Marga B.
APPLICANT: ZENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oncormed, Inc.
STREET: 205 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCZA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFAX: 301-926-6125
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PROBE"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
US-08-988-706-45
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 927 TTATTAGAAATGCAGAA 943
Db 1 TTATTATTAATGAAGAA 17
RESULT 354
US-09-192-104-7/c
Sequence 7, Application US/09192104B
Patent No. 6184020
GENERAL INFORMATION:
APPLICANT: Alexander Blinkovsky
APPLICANT: Tony Byun
APPLICANT: Alan V. Klotz
APPLICANT: Alan Sloma
APPLICANT: Maria Tang
APPLICANT: Mikio Fujii
APPLICANT: Chigusa Marumoto
APPLICANT: Lene Venke Kofod

TITLE OF INVENTION: Polypeptides Having Aminopeptidase
TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
FILE REFERENCE: 5379.200-US
CURRENT APPLICATION NUMBER: US/09/192,104B
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/069719
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 1465/97
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: PA 1998 00670
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 17
TYPE: DNA
ORGANISM: Sphingomonas
US-09-192-104-7
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 797 GGAGAGCGAGATAACGC 813
Db 17 GGAGAGCGATATGACGC 1
RESULT 355
US-09-275-680-7
Sequence 7, Application US/09275680
Patent No. 6221630
GENERAL INFORMATION:
APPLICANT: Hopper, James E
TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
FILE REFERENCE: 98428
CURRENT APPLICATION NUMBER: US/09/275,680
CURRENT FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 17
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 263 GCCTGTGCGGAACCTGGC 279
Db 1 GCCTGTTGACAACTGGC 17
RESULT 356
US-09-324-867-24
Sequence 24, Application US/09324867A
Patent No. 6251632
GENERAL INFORMATION:
APPLICANT: Lillcrap, David
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-059

Query Match	Best Local Similarity	Score 12.2;	DB 1;	Length 17;
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	895 ACAGACCAAGAGCTTCA 911			
Db	1 ACAGCCCAAGAGCTCCA 17			
<p>RESULT 357</p> <p>US-09-543-446-7/c</p> <p>Sequence 7, Application US/09543446</p> <p>Patent No. 6303360</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Alexander Blinkovsky</p> <p>APPLICANT: Tony Byun</p> <p>APPLICANT: Alan V. Klotz</p> <p>APPLICANT: Alan Sloma</p> <p>APPLICANT: Maria Tang</p> <p>APPLICANT: Mikio Fujii</p> <p>APPLICANT: Chigusa Marumoto</p> <p>APPLICANT: Lene Venke Kofod</p> <p>TITLE OF INVENTION: Polypeptides Having Aminopeptidase</p> <p>TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same</p> <p>FILE REFERENCE: 5379.210-US</p> <p>CURRENT APPLICATION NUMBER: US/09/543,446</p> <p>CURRENT FILING DATE: 2000-04-05</p> <p>EARLIER APPLICATION NUMBER: 60/069719</p> <p>EARLIER FILING DATE: 1997-12-16</p> <p>EARLIER APPLICATION NUMBER: 1465/97</p> <p>EARLIER FILING DATE: 1997-12-16</p> <p>EARLIER APPLICATION NUMBER: PA 1998 00670</p> <p>EARLIER FILING DATE: 1998-05-15</p> <p>EARLIER APPLICATION NUMBER: 09/192,104</p> <p>EARLIER FILING DATE: 1998-11-13</p> <p>NUMBER OF SEQ ID NOS: 9</p> <p>SOFTWARE: FastSeq for Windows Version 4.0</p> <p>SEQ ID NO 7</p> <p>LENGTH: 17</p> <p>TYPE: DNA</p> <p>ORGANISM: Sphingomonas</p> <p>US-09-543-446-7</p>				
Query Match	Best Local Similarity	Score 12.2;	DB 1;	Length 17;
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	797 GGAGAGCGCATATGACGC 813			
Db	17 GGAGAGCGCATATGACGC 1			
<p>RESULT 358</p> <p>US-08-584-040-1689/c</p> <p>Sequence 1689, Application US/08584040</p> <p>Patent No. 6346398</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Pavco, Pamela</p> <p>APPLICANT: McSwiggen, James</p> <p>APPLICANT: Stinchcomb, Dan T.</p> <p>APPLICANT: Escobedo, Jaime</p> <p>TITLE OF INVENTION: METHOD AND REAGENT FOR THE</p> <p>TITLE OF INVENTION: TREATMENT OF DISEASES OR</p> <p>TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS</p> <p>TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL</p> <p>TITLE OF INVENTION: GROWTH FACTOR</p> <p>NUMBER OF SEQUENCES: 8502</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Lyon & Lyon</p> <p>STREET: 633 West Fifth Street</p> <p>CITY: Suite 4700</p> <p>STATE: Los Angeles</p> <p>COUNTRY: U.S.A.</p> <p>ZIP: 90071-2066</p>				

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1739:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1739

```

```

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 320 TTCTCTGTTATCTTGC 336
Db 17 TTCTCTCTATTATGTC 1

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RESULT 360

```

; US-08-584-040-2165
; Sequence 2165, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974

```

```

; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2165

```

```

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Qy 1050 ACTTCCTTATCTTTCCA 1066
Db 1 ACACCUUUAUCUUCCA 17

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RESULT 361

```

; US-08-584-040-2167
; Sequence 2167, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

```

iss.res

Fri Aug 19 10:59:59 2005

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2167
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1054 CCTTATCTTTCCAGTGG 1070
| :|:|:|:|:|
Db 1 CUUUAUCUUUCCAUAGG 17

RESULT 362
US-08-584-040-4021
; Sequence 4021, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4021:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-4021

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 881 TAAAGTGTGCCACCA 897
| :|:|:|:|:|
Db 1 UACAAGCUUGGCCCA 17

```

```

RESULT 363
US-08-584-040-5664/c
; Sequence 5664, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5664:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-5664

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 421 CCTTATTTTGAAGAG 437
| :|:|:|:|:|
Db 17 CCTTATTATGAAGAG 1

RESULT 364
US-08-584-040-5710/c
; Sequence 5710, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

```

```

; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5710:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-5710

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Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. NO. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 219 TCATTGCCAAGAGTC 235
Db 17 TCATTGCCAAGAGTC 1

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RESULT 365
US-08-584-040-7398/c
; Sequence 7398, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```

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; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7398:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-7398

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```

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. NO. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 564 GGTGTTTAAATACCTTT 580
Db 17 GGTGTTTAAATAGCCTT 1

```

```

RESULT 366
US-08-584-040-8014
; Sequence 8014, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-790

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 622 ATGAGTTTATTCCTCAG 638
DB 17 ATAGGATTATTCCTCAG 1

RESULT 369
US-09-371-772B-234/c
; Sequence 234, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-234

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 GGTTTTAAATACCTTT 580
DB 17 GGTTTTAAACACATTT 1

RESULT 370
US-09-371-772B-284/c
; Sequence 284, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

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```

; ORGANISM: Homo sapiens
US-09-371-772B-284

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 320 TTTCCTGTATTCTTGC 336
DB 17 TTTCCTCTATTATTGC 1

RESULT 371
US-09-371-772B-710
; Sequence 710, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 710
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-710

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCA 1066
DB 1 ACACCUUUAUCUUCCA 17

RESULT 372
US-09-371-772B-712
; Sequence 712, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 712
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

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Fri Aug 19 10:59:59 2005

US-09-371-772B-712

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1054 CCTATCTTTCCAGTGG 1070
| :|:|:|:|:|:|
Db 1 CUUUAUUUUUCCAUUGG 17

RESULT 373

US-09-371-772B-1788

; Sequence 1788, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1788
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1788

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 881 TAAAGTGTGCCACCA 897
:|:|:|:|:|:|:|
Db 1 UACAAGCUUGGCCACCA 17

RESULT 374

US-09-371-772B-2553/c

; Sequence 2553, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2553
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2553

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 421 CCTATATTGGAAGAG 437
|:|:|:|:|:|:|:|
Db 17 CCTTCTATTATGAAGAG 1

RESULT 375

US-09-371-772B-2594/c

; Sequence 2594, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2594
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2594

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 219 TCATTGCCAAAGAGTC 235
|:|:|:|:|:|:|:|
Db 17 TCATTGCCAAAGAGTC 1

RESULT 376

US-09-371-772B-3206/c

; Sequence 3206, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3206
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3206

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 GGTGTTTAAATACCTTT 580
 |||||
 DB 17 GGTGTTTAAATAGCCTT 1

RESULT 377
 US-09-371-772B-3797
 ; Sequence 3797, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBH00.876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3797
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Mus sp.
 US-09-371-772B-3797

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 41.2%; Pred. No. 2.3e+02;
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 465 AGCACTTTATTCGATT 481
 |||||:::|:|:|
 DB 1 AGCACUUUAUGCCUCCU 17

RESULT 378
 US-09-371-772B-4538/c
 ; Sequence 4538, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBH00.876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4538
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-371-772B-4538

Query Match 1.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1033 AGTAAACATCACACCA 1049
 |||||
 DB 17 AGTTAACATGAACCCA 1

RESULT 379
 US-09-371-772B-4854/c
 ; Sequence 4854, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBH00.876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4854
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-371-772B-4854

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 TCCCTCTTTGTGTGTA 869
 |||||
 DB 17 TCGCTCTTGTGCTGTA 1

RESULT 380
 US-09-371-772B-6139/c
 ; Sequence 6139, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MBH00.876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6139
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-371-772B-6139

Query Match 1.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.3e+02;

Fri Aug 19 10:59:59 2005

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 123 TGACTTTTCTTATGCTG 139
|| ||||| |||||

Db 17 TGTCTTTTGTATGCTG 1

RESULT 381
US-09-401-063-157/C
; Sequence 157, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-157

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 982 ATCCAGAGGAGGTAT 998
||||| ||||| |||||

Db 17 ATCCAGAGGAGGTAT 1

RESULT 382
US-09-401-063-283
; Sequence 283, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-157

APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-401-063-283

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 910 CAACATTTCCTAGAGCC 926
||||| :||| |||||

Db 1 CAACAUCUCGGAAGCC 17

RESULT 383
US-09-401-063-337
; Sequence 337, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-283

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 337:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-337

```

```

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 196 CGCATCTCCCCCATCC 212
|||:|:|:|:|:|:|
Db 1 CGAGAUCCUCCAUCC 17

```

```

RESULT 384
US-09-401-063-631/c
; Sequence 631, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063

```

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 631:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-631

```

```

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 613 AAGTAGGAGATGAGTTT 629
|||||:|:|:|:|:|
Db 17 AATTAGGAGATGAGTTT 1

```

```

RESULT 385
US-09-401-063-653
; Sequence 653, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:

```

```

/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 653:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-401-063-653

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 654 AATTAGATTATGTTAC 670
Db 1 AAAUAGUUUGUUGUAC 17
|| :|| :|| :|| :||
/

RESULT 386
US-09-401-063-654
/ Sequence 654, Application US/09401063
/ Patent No. 6623962
/ GENERAL INFORMATION:
/ APPLICANT: Akhtar, Saghir
/ APPLICANT: Fell, Patricia
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
/ TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
/ TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
/ TITLE OF INVENTION: FACTOR RECEPTORS
/ NUMBER OF SEQUENCES: 1877
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/401,063
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/985,162
/ FILING DATE: 04 December 1997
/ APPLICATION NUMBER: 60/036,476
/ FILING DATE: 31 January 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 230/107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 654:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-401-063-654

Query Match 1.1%; Score 12.2; DB 1; Length 17;

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RESULT 389

US-09-957-189-7/c
; Sequence 7, Application US/09957189
; Patent No. 6673571

GENERAL INFORMATION:

; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto

; APPLICANT: Lene venke korof

; TITLE OF INVENTION: Polypeptides Having Aminoacidase

; FILE REFERENCE: 5379.200-US

; CURRENT APPLICATION NUMBER: US/09/957,189

; CURRENT FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/192,104

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-13

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1465/97

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00670

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-15

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Sphingomonas

US-09-957-189-7

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 797 GGAGAGGCAGATPAACGC 813

||||| ||||| |||||

DB 17 GGAGAGGCATATGAGC 1

RESULT 390

US-09-866-108A-400/c

; Sequence 400, Application US/09866108A

; Patent No. 6686188

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOmica-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 400
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-400

Query Match

1.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAATTGTTGTT 307

||||| ||||| |||||

DB 17 CTGCTGGACTTGCTGTT 1

RESULT 391

US-09-866-108A-401/c

; Sequence 401, Application US/09866108A

; Patent No. 6686188

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOmica-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 401

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-401

Query Match

1.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Fri Aug 19 10:59:59 2005

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; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 437
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-437

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCTCTCATGAC 833
DB 1 AGCAGATCTCTCAGGAC 17

RESULT 394
US-09-866-108A-733/c
; Sequence 733, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 402
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-402

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 289 CACTACTGGAATGTGTG 305
DB 17 CACTGTGCTGACTTGCTG 1

RESULT 393
US-09-866-108A-437
; Sequence 437, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

```


isb.res

Fri Aug 19 10:59:59 2005

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1487
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1487

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 32 CAGGAAGCGGAGCAG 48
DB 1 CAGGAAGCGTGGGCAG 17

RESULT 398
US-09-866-108A-6438/c
; Sequence 6438, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6440
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6440

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6438
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6438

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 964 CCAGGACATTTTGATGA 980
DB 17 CCGGACCTTTTGATCA 1

RESULT 399
US-09-866-108A-6440/c
; Sequence 6440, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6440
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6440

Query Match 1.1%; Score 12.2; DB 1; Length 17;
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```

Best Local Similarity 82.4%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3;

QY 962 ACCGAGCATTTTGAT 978
Db 17 AGCGCGGACCTTTGAT 1

RESULT 400
US-09-866-108A-6618/c
; Sequence 6618, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6618
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6618

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 896 CAGACCAAGAGCCTCAA 912
Db 17 CAGACGAGAGCCTCAA 1

RESULT 401
US-09-866-108A-6751
; Sequence 6751, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6618
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6618

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 838 GAAGCGCGGTGGATC 854
Db 1 GAAGCGCGGTGGAGGC 17

RESULT 402
US-09-866-108A-7102/c
; Sequence 7102, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6751
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6751

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iss.res

Fri Aug 19 10:59:59 2005

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7102
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7102

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 853 TCCTCTTTGTGTGTA 869
Db 17 TCCGCTCTAGCGTTGTA 1

RESULT 403
US-09-866-108A-7368/c
; Sequence 7368, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7368
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7368

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 116 ATTGGACTGACTTTTCT 132
Db 17 ATTCAACTGAATTTTCT 1

RESULT 404
US-09-866-108A-7438
; Sequence 7438, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7438
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7438

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 345 CTGTGATCAAAATGGGA 361
Db 1 CTGTGCTCAGATGAGA 17

RESULT 405
US-09-866-108A-7964/c
; Sequence 7964, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.

```
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7964
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7964

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 316 TGGATTCTCTGTATTC 332
Db 17 TGGATTCTCTGTGTC 1

RESULT 406
US-09-866-108A-7969/C
; Sequence 7969, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David R.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7964
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7964

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 316 TGGATTCTCTGTATTC 332
Db 17 TGGATTCTCTGTGTC 1

RESULT 406
US-09-866-108A-7969/C
; Sequence 7969, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David R.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7970
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7970
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7969
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7969

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 311 GCCTTTGGATTTCTGT 327
Db 17 GGCTCTGGATTTCTGT 1

RESULT 407
US-09-866-108A-7970/C
; Sequence 7970, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David R.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7970
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7970
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;
;
; ORGANISM: Homo sapiens
US-09-866-108A-9279

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      501 AGAACTCATACTACTG 517
      || ||||| |||||
Db       17 AGTCCTCATAGTATCTG 1

RESULT 410
US-09-866-108A-9317
; Sequence 9317, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 686188
; SEQ ID NO 9317
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9317

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      44  AGCAGCGCGGCCCGCAG 60
Db      1  AGCAGCGCGCATCCTCAG 17

RESULT 411
US-09-404-912-319
; Sequence 319, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
; APPLICANT: John Landers
; APPLICANT: David Houseman
; APPLICANT: Barbara Jordan
; APPLICANT: Alain Charest
; TITLE OF INVENTION: Methods and Products Related to
; TITLE OF INVENTION: Genotyping and DNA Analysis
; FILE REFERENCE: M0656/7045(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/404,912
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,757
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22283
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-319

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      672  CAATTAATGTTACTTGT 688
Db      1  CAATAAATGTTAGTTAT 17

RESULT 412
US-09-685-664B-234/c
; Sequence 234, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-234

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      564  GGTTTTAAATACCTTT 580
Db      17  GGTTTTAAACACATTT 1

RESULT 413
US-09-685-664B-284/c
; Sequence 284, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-284

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      320  TTTCCTGTTATTCTTGC 336
Db      17  TTTCCTCTATTATGC 1

RESULT 414
US-09-685-664B-710
; Sequence 710, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
```

Fri Aug 19 10:59:59 2005

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; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 710
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-710

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1050 ACTTCCTATCTTCCCA 1066
Db      1 ACACCUUUCUUCGA 17

RESULT 415
US-09-685-664B-712
; Sequence 712, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 712
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-712

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1054 CCTTATCTTCCAGTGG 1070
Db      1 CUUUAUCUUCUUGGG 17

RESULT 416
US-09-685-664B-1788
; Sequence 1788, Application US/09685664B

```

```

; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1788
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1788

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      881 TAAAGTGTGCCCA 897
Db      1 UACAGCUUGGCCCA 17

RESULT 417
US-09-685-664B-2553/C
; Sequence 2553, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2553
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2553

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      421 CCTTATTTGGAAGAG 437
Db      17 CCTTATTTGGAAGAG 1

```

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RESULT 418
US-09-685-664B-2594/c
; Sequence 2594, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2594
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2594

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 219 TCATTGCCAAAGAGTC 235
DB 17 TCATTGCCAAAGAGTC 1

RESULT 419
US-09-685-664B-3206/c
; Sequence 3206, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3206
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3206

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 GGTTTTTAATACCTT 580
DB 17 GGTTTTTAATACCTT 1

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Db 17 GGTTTTTAATACCTT 1

RESULT 420
US-09-685-664B-3797
; Sequence 3797, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3797
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3797

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 465 AGCATTATTCTGATT 481
DB 1 AGCATTATTCTGATT 17

RESULT 421
PCT-US95-02219-5
; Sequence 5, Application PC/TUS9502219
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880

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```
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-02219-5
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 839 AAGCGCGGGTGGATCC 855
DB 1 AAGCGTGGTGGATAC 17

RESULT 422
PCT-US95-02219A-5
; Sequence 5, Application PC/TUS9502219A
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tumuru, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND THE RELATED METHODS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-02219A-5
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 839 AAGCGCGGGTGGATCC 855
DB 1 AAGCGTGGTGGATAC 17

RESULT 423
US-09-338-907-372
```

```
; Sequence 372, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-338-907-372
Query Match 1.0%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 850 GGATCCCTCTTTGTGTTG 867
DB 2 GGCTCCCTTTTGAGTTG 19

RESULT 424
US-09-218-207-372
; Sequence 372, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-218-207-372
Query Match 1.0%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 850 GGATCCCTCTTTGTGTTG 867
```


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Fri Aug 19 10:59:59 2005

```

; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 514
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-514

Query Match 1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 GAAGCCGGAGCAGCC 50
DB 2 GAAGCGCGCAGCTGCC 17

RESULT 429
US-09-827-998-515
; Sequence 515, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 515
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-515

Query Match 1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 976 GATGAGATCCAAAGGA 991
DB 1 GAGGAAATTCAAAGGA 16

RESULT 430
US-09-827-998-514
; Sequence 514, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong

```

```

; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 514
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-514

Query Match 1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 976 GATGAGATCCAAAGGA 991
DB 2 GAGGAAATTCAAAGGA 17

RESULT 431
US-09-324-867-24/c
; Sequence 24, Application US/09324867A
; Patent No. 6251632
; GENERAL INFORMATION:
; APPLICANT: Lillcrap, David
; APPLICANT: Cameron, Cherie
; APPLICANT: No. 6251632ley, Colleen
; APPLICANT: Horrocks, L. Suzanne Hoyle
; APPLICANT: Hough, Christine
; TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
; FILE REFERENCE: 1669.0010002/JAG/BJD
; CURRENT APPLICATION NUMBER: US/09/324,867A
; CURRENT FILING DATE: 1999-06-03
; EARLIER APPLICATION NUMBER: 09/035,141
; EARLIER FILING DATE: 1998-03-059
; EARLIER APPLICATION NUMBER: 60/039,953
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Synthetic oligonucleotide
; US-09-324-867-24

Query Match 1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 109 TGGGGCTATTGGACTG 124
DB 17 TGGAGCTCTTGGGCTG 2

RESULT 432
US-09-392-580-12
; Sequence 12, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580

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```

; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-580-12

Query Match      1.0%; Score 11; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 586 TCATGTTTCATTAAAGAA 604
    ||||| ||||| |||||
DB 2 TCATCTCTCTTGAAATA 20

RESULT 433
US-09-371-772B-4538
; Sequence 4538, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4538
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4538

Query Match      1.0%; Score 10.8; DB 1; Length 17;
Best Local Similarity 35.7%; Pred. No. 3.9e+02;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 316 TGGATTTCCTGTGA 329
    ||| :|| :|| :||
DB 1 UGGGUUUCAGUUA 14

RESULT 434
US-09-433-699-36
; Sequence 36, Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; FILE REFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433,699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

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US-09-433-699-36

Query Match      1.0%; Score 10.8; DB 1; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 391 AGTCATTTCCTTA 404
    ||||| ||||| |||||
DB 7 AGTCATCTCTCTCA 20

RESULT 435
US-09-866-108A-7015
; Sequence 7015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEONICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7015
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7015

Query Match      1.0%; Score 10.6; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 736 GTCTTGTAGGAGCTGC 752
    ||||| ||||| |||||
DB 1 GCCATGGTGGCAGCTGC 17

RESULT 436
US-09-422-978-4732
; Sequence 4732, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta

```

```
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4732
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798,
US-09-422-978-4732

Query Match 1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 350 ATCAAAATGGGGAGCCTG 366
||| ||||| ||||| |||
Db 2 ATGAATGCTGAGGCTG 18

RESULT 437
US-09-422-978-6041/c
; Sequence 6041, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6041
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-09-422-978-6041

Query Match 1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 614 ACTGAGAGATGATGTTT 630
||| ||||| ||||| |||
Db 17 AGTGGGGTTCGAGATT 1

RESULT 438
US-09-422-978-7460
; Sequence 7460, Application US/09422978
; Patent No. 6537751
```

```
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7460
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-49 for SEQ 3526,
US-09-422-978-7460

Query Match 1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 932 AGAAATGCGAGATCTGA 948
||||| ||||| ||||| |||
Db 1 AGAAATCCACAGTCAGA 17

RESULT 439
US-09-198-452A-5159/c
; Sequence 5159, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment...
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev...
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5159

Query Match 1.0%; Score 10.6; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 599 AAGAAAGACTTCATAAG 615
||||| ||||| ||||| |||
Db 18 AACACGACTCCAGAAG 2

RESULT 440
US-09-198-452A-5166/c
; Sequence 5166, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment...
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev...
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
```

```
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5166

Query Match      1.0%; Score 10.6; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 599 AAGAAAGACTTCATAG 615
Db 18 AACACGACTCCAGAAG 2

RESULT 441
US-09-657-472-1733
; Sequence 1733, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825 1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1733
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1733

Query Match      1.0%; Score 10.6; DB 1; Length 21;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 TGGCAGGCTGCCCGGCC 27
Db 1 TGGACAGCTRCCCCAGGC 19

RESULT 442
US-08-373-124A-2437/c
; Sequence 2437, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles

Query Match      0.9%; Score 10.4; DB 1; Length 17;
Best Local Similarity 91.7%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 489 ATTGAATTTCTT 500
Db 12 ATTGAATTTCTT 1

RESULT 443
US-08-435-628-2437/c
; Sequence 2437, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
```

QY 886 GTGTGGCCACA 897

925 CCTATTAGAA 936
Ov

Db ||||||| |||
 3 CCTATTAAAA 14

RESULT 447
US-09-081-646-526/C
; Sequence 526, Application US/09081646
; Patent No. 633152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 633152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 526
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-526

Query Match 0.9%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 312 CTTTGGATTTCCTG 326
 ||||| ||| |||
Db 15 CTTGGGATCTCATG 1

RESULT 448
US-09-866-108A-2566
; Sequence 2566, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2566
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2566

Query Match 0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 AAGCGGGAAGCAGCC 50
 ||||| ||| |||
Db 1 AAGCGGCGAGCTGCC 15

RESULT 449
US-09-866-108A-2563
; Sequence 2563, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2563

Query Match 0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 GAAGCGGGAAGCAGC 49
 ||||| ||| |||
Db 3 GAAGCGGCGAGCTGC 17

Fri Aug 19 10:59:59 2005

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; Patent No. 6686188
; SEQ ID NO 7017
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7017

Query Match      0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      738 CTTGTAGGCGAGTGC 752
Db      1 CATGGTGCAGCTGC 15

RESULT 452
US-09-827-998-513
; Sequence 513, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 513
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-513

Query Match      0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      976 GATGATCCAAAGG 990
Db      3 GAGAAATTCAAAGG 17

RESULT 453
US-09-866-108A-7016
; Sequence 7016, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

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RESULT 450
US-09-827-998-516
; Sequence 516, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 516
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-516

Query Match      0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      977 ATGAGTCCAAAGGA 991
Db      1 AGGAAATTCAAAGGA 15

RESULT 451
US-09-866-108A-7017
; Sequence 7017, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine

```


Db 16 AGACACAACAATTCC 2

RESULT 457

US-08-836-261A-72/c

Sequence 72, Application US/08836261A

Patent No. 6221582

GENERAL INFORMATION:

APPLICANT: GIESENDORF, BELINDA

APPLICANT: QUINT, WILHELMUS

APPLICANT: VAN DOORN, LEENBERT-JAN

TITLE OF INVENTION: NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE

TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF PROKARYOTIC ORGANISMS

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,261A

FILING DATE: 25 Apr 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/04264

FILING DATE: 30 Oct 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94870171.9

FILING DATE: 28 Oct 1994

ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: INNS:005

INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-836-261A-72

Query Match 0.9%; Score 10.2; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 526 TGCACATGCGGCATT 540

Db 20 TGCAGATTCGTGATT 6

RESULT 458

US-09-980-052-219/c

Sequence 219, Application US/09980052

Patent No. 6670130

GENERAL INFORMATION:

APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.

APPLICANT: KIM, Cheol Min

APPLICANT: PARK, Hee Kyung

TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria

FILE REFERENCE: PP05020/PCT

CURRENT APPLICATION NUMBER: US/09/980,052

CURRENT FILING DATE: 2001-11-28

PRIOR APPLICATION NUMBER: KR 10-1999-0019631

PRIOR FILING DATE: 1999-05-29

PRIOR APPLICATION NUMBER: KR 10-1999-0019632

PRIOR FILING DATE: 1999-05-29

PRIOR APPLICATION NUMBER: KR 10-1999-0019633

PRIOR FILING DATE: 1999-05-29

PRIOR APPLICATION NUMBER: KR 10-1999-0019634

PRIOR FILING DATE: 1999-05-29

PRIOR APPLICATION NUMBER: KR 10-1999-0019635

PRIOR FILING DATE: 1999-05-29

PRIOR APPLICATION NUMBER: KR 10-2000-0018189

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 243

SOFTWARE: KopatentIn 1.71

SEQ ID NO 219

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium

OTHER INFORMATION: diernhoferi

US-09-980-052-219

Query Match 0.9%; Score 10.2; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 668 TACTCAATTATGTT 682

Db 20 TTCTCAAGTTTGT 6

RESULT 459

US-08-785-750-2

Sequence 2, Application US/08785750

Patent No. 5846528

GENERAL INFORMATION:

APPLICANT: PODSAKOFF, GREGORY M.

APPLICANT: KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING

TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBINS & ASSOCIATES

STREET: 90 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK

STATE: CA

COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/785,750

FILING DATE: 16-JAN-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/588,355

FILING DATE: 18-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.

REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 0800-0009.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 325-7812

TELEFAX: (415) 325-7823

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-785-750-2

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
|||||
DB 1 GGCAGCTGCC 10

RESULT 460
US-08-588-355-1
; Sequence 1, Application US/08588355
; Patent No. 5858351
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,355
; FILING DATE: 18-JAN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-588-355-1

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
|||||
DB 1 GGCAGCTGCC 10

RESULT 461
US-09-116-780-5
; Sequence 5, Application US/09116780
; Patent No. 5945335
; GENERAL INFORMATION:
; APPLICANT: Colosi, Peter
; TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
; TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences

FILE REFERENCE: 2555.2.2
; CURRENT APPLICATION NUMBER: US/09/116,780
; CURRENT FILING DATE: 1998-07-16
; EARLIER APPLICATION NUMBER: 08/745,957
; EARLIER FILING DATE: 1996-11-07
; EARLIER APPLICATION NUMBER: 60/006,402
; EARLIER FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-09-116-780-5

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
|||||
DB 1 GGCAGCTGCC 10

RESULT 462
US-08-812-102-1
; Sequence 1, Application US/08812102
; Patent No. 5952221
; GENERAL INFORMATION:
; APPLICANT: KURTZMAN, GARY J.
; APPLICANT: COLOSI, PETER C.
; APPLICANT: YOSHIDA, JUN
; APPLICANT: MIZUNO, MASAOKI
; APPLICANT: OKADA, HIDEHO
; TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
; TITLE OF INVENTION: TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,102
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,209
; FILING DATE: 06-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-812-102-1

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Query Match          0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
Db      1 GGCAGCTGCC 10

RESULT 463
US-08-784-757-1
; Sequence 1, Application US/08784757
; Patent No. 5962313
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,757
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,355
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-784-757-1

Query Match          0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
Db      1 GGCAGCTGCC 10

RESULT 464
US-08-745-957-1
; Sequence 1, Application US/08745957
; Patent No. 6004797
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN

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; TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,957
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,402
; FILING DATE: 09-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-745-957-1

Query Match          0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
Db      1 GGCAGCTGCC 10

RESULT 465
US-09-309-042-1
; Sequence 1, Application US/09309042
; Patent No. 6211163
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,042
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/598,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-309-042-1

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
DB 1 GGCAGCTGCC 10

RESULT 466
US-09-205-337-2
; Sequence 2, Application US/09205337
; Patent No. 6325998
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,337
; FILING DATE: 04-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,750
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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US-09-205-337-2
Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
DB 1 GGCAGCTGCC 10

RESULT 467
US-09-406-362-1
; Sequence 1, Application US/09406362
; Patent No. 6335011
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,362
; FILING DATE: 28-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/784,757
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-406-362-1

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
DB 1 GGCAGCTGCC 10

RESULT 468
US-09-755-734-1
; Sequence 1, Application US/09755734
; Patent No. 6391858
; GENERAL INFORMATION:

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,363
FILING DATE: 28-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,957
FILING DATE: 11-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO:1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-406-363-1

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
Db 1 GGCAGCTGCC 10

RESULT 470
US-09-649-890-1
Sequence 1, Application US/09649890
Patent No. 6531456
GENERAL INFORMATION:
APPLICANT: KURTZMAN, GARY J.
COLOSI, PETER C.
YOSHIDA, JUN
MIZUNO, MASAHI
OKADA, HIDSHO
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/649,890
FILING DATE: 28-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/812,102
FILING DATE: 05-MAR-1997
APPLICATION NUMBER: US 60/013,209
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812

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TELEFAX: (415) 325-7823
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-649-890-1

Query Match 0.9%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GGCAGCTGCC 753
 |||||
 Db 1 GGCAGCTGCC 10

RESULT 471

US-09-969-204A-1
 ; Sequence 1, Application US/09969204A
 ; Patent No. 6610290
 ; GENERAL INFORMATION:
 ; APPLICANT: PODSAKOFF, GREGORY M.
 ; KESSLER, PAUL D.
 ; BYRNE, BARRY J.
 ; KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
 CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS
 VIRIONS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBINS & ASSOCIATES
 STREET: 90 MIDDLEFIELD ROAD, SUITE 200
 CITY: MENLO PARK
 STATE: CA
 COUNTRY: USA
 ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/969,204A
 FILING DATE: 01-Oct-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/406,362
 FILING DATE: 28-Sep-1999
 APPLICATION NUMBER: 08/784,757
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.
 REGISTRATION NUMBER: 38,548
 REFERENCE/DOCKET NUMBER: 0800-0009.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 325-7812
 TELEFAX: (415) 325-7823

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-969-204A-1

Query Match 0.9%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 744 GGCAGCTGCC 753
 |||||
 Db 1 GGCAGCTGCC 10

Search completed: August 19, 2005, 10:54:27
 Job time : 9 secs

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:52:25 ; Search time 5 Seconds
(without alignments)
2.757 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gctcgttggcgaggtgc.....gttacctgcattgttga 1114

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 325 seqs, 6187 residues

Total number of hits satisfying chosen parameters: 650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 326 summaries

Database : gedb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	5.4	60	1	ACCESSION:AX677227
2	51	4.6	51	1	ACCESSION:AX189878
3	49.4	4.4	51	1	ACCESSION:AX189879
4	22	2.0	22	1	ACCESSION:AX860120
5	21	1.9	21	1	ACCESSION:AX783362
6	20	1.8	20	1	ACCESSION:AX784159
7	20	1.8	20	1	ACCESSION:AX860090
8	20	1.8	20	1	ACCESSION:AX860110
9	20	1.8	20	1	ACCESSION:AX860111
10	20	1.8	20	1	ACCESSION:AX860112
11	20	1.8	20	1	ACCESSION:AX860113
12	20	1.8	20	1	ACCESSION:AX860114
13	20	1.8	20	1	ACCESSION:AX860115
14	20	1.8	20	1	ACCESSION:AX860116
15	20	1.8	20	1	ACCESSION:AX860117
16	20	1.8	20	1	ACCESSION:AX860118
17	20	1.8	20	1	ACCESSION:AX860119
18	20	1.8	20	1	ACCESSION:AX860121
19	20	1.8	20	1	ACCESSION:AX860122
20	20	1.8	20	1	ACCESSION:AX783361
21	20	1.8	20	1	ACCESSION:BD128083
22	20	1.8	21	1	ACCESSION:AX860126
23	19.8	1.8	25	1	ACCESSION:AX378941
24	19.4	1.7	21	1	ACCESSION:AX860125
25	19	1.7	19	1	ACCESSION:AX166701
26	18	1.6	18	1	ACCESSION:AX166700
27	18	1.6	18	1	ACCESSION:AX302819
28	18	1.6	18	1	ACCESSION:AR302820
29	17.6	1.6	24	1	ACCESSION:AX412234
30	17.6	1.6	24	1	ACCESSION:AX548339
31	17	1.5	17	1	ACCESSION:AX738199
32	16.8	1.5	21	1	ACCESSION:BD223822
33	16.8	1.5	24	1	ACCESSION:EI3776

34	16.8	1.5	24	1	AX420107
35	16.6	1.5	23	1	AX487296
36	16.2	1.5	21	1	AR067252
37	16.2	1.5	21	1	I31384
38	16.2	1.5	23	1	AX665946
39	16	1.4	15	1	CO860133
40	16	1.4	17	1	AX738983
41	16	1.4	20	1	AX298650
42	16	1.4	20	1	AX298652
43	15.8	1.4	19	1	AX795189
44	15.8	1.4	20	1	AS0630
45	15.8	1.4	20	1	AR147307
46	15.8	1.4	22	1	AX241144
47	15.8	1.4	22	1	AX486731
48	15.6	1.4	20	1	BD009437
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VERSION AX677227.1 GI:29334643
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Legrain, P. and Daviet, L.
TITLE Protein-protein interactions in adipocytes
JOURNAL Patent: WO 02086122-A 5 31-OCT-2002;
Hybrigenics (FR)
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ACCESSION AX189878
VERSION AX189878.1 GI:15143249
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147942-A 57 05-JUL-2001;
Curagen Corporation (US)
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 VERSION AX189879.1 GI:15143250
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shimkets,R.A. and Leach,M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
 JOURNAL Patent: WO 0147942-A 58 05-JUL-2001;
 Curagen Corporation (US)
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 LOCUS CQ860120 22 bp DNA linear PAT 10-SEP-2004
 DEFINITION Sequence 32 from Patent WO2004072293.
 ACCESSION CQ860120
 VERSION CQ860120.1 GI:51982008
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
 TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
 JOURNAL Patent: WO 2004072293-A 32 26-AUG-2004;
 Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
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 Db 22 CCTGTGGGAACTGGCATATTT 1
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 DEFINITION Sequence 15 from Patent WO2004080272.
 ACCESSION CQ878362

VERSION CQ878362.1 GI:53790915
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1
 AUTHORS Baillleul,B., Rouille,Y., Seron,K. and Belouzard,S.
 TITLE Use of the genes leptin and ob-rgrp for the screening of active compounds for weight gain or loss or diabetes in human or animal subjects
 JOURNAL Patent: WO 2004080272-A 15 23-SEP-2004;
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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 ACCESSION CQ784159
 VERSION CQ784159.1 GI:45538647
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.
 TITLE Primers for synthesizing full length cDNA clones and their use
 JOURNAL Patent: EP 1396543-A 4299 10-MAR-2004;
 Research Association for Biotechnology (JP)
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 DEFINITION Sequence 2 from Patent WO2004072293.
 ACCESSION CQ860090
 VERSION CQ860090.1 GI:51981978
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

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REFERENCE
AUTHORS      1 Jockers,R., Couturier,C. and Uhlmann,E.
TITLE        Oligonucleotides which inhibit the expression of the ob-rgrp
              protein and method for detection of compounds modifying the
              interaction between the proteins of the ob-rgrp family and the
              leptin receptor
JOURNAL      Patent: WO 2004072293-A 2 26-AUG-2004;
              Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
              RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
              Scientifique (CNRS) (FR)
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DEFINITION Sequence 22 from Patent WO2004072293.
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VERSION    CQ860110.1  GI:51981998
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jockers,R., Couturier,C. and Uhlmann,E.
TITLE      Oligonucleotides which inhibit the expression of the ob-rgrp
            protein and method for detection of compounds modifying the
            interaction between the proteins of the ob-rgrp family and the
            leptin receptor
JOURNAL    Patent: WO 2004072293-A 22 26-AUG-2004;
            Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
            RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
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Db      20 CCCGGGCGGTGGCAGGAGC 1

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LOCUS      CQ860111          20 bp      DNA          linear          PAT 10-SEP-2004
DEFINITION Sequence 23 from Patent WO2004072293.
ACCESSION  CQ860111
VERSION    CQ860111.1  GI:51981999
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jockers,R., Couturier,C. and Uhlmann,E.
TITLE      Oligonucleotides which inhibit the expression of the ob-rgrp
            protein and method for detection of compounds modifying the
            interaction between the proteins of the ob-rgrp family and the
            leptin receptor
JOURNAL    Patent: WO 2004072293-A 23 26-AUG-2004;
            Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
            RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
            Scientifique (CNRS) (FR)
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Db      20 CCCAGTTGCGGAGACATGGC 1

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DEFINITION Sequence 24 from Patent WO2004072293.
ACCESSION  CQ860112
VERSION    CQ860112.1  GI:51982000
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jockers,R., Couturier,C. and Uhlmann,E.
TITLE      Oligonucleotides which inhibit the expression of the ob-rgrp
            protein and method for detection of compounds modifying the
            interaction between the proteins of the ob-rgrp family and the
            leptin receptor
JOURNAL    Patent: WO 2004072293-A 24 26-AUG-2004;
            Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
            RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
            Scientifique (CNRS) (FR)
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LOCUS      CQ860113          20 bp      DNA          linear          PAT 10-SEP-2004
DEFINITION Sequence 25 from Patent WO2004072293.
ACCESSION  CQ860113
VERSION    CQ860113.1  GI:51982001
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jockers,R., Couturier,C. and Uhlmann,E.

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TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 25 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

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DEFINITION Sequence 26 from Patent WO2004072293.
ACCESSION CQ860114
VERSION CQ860114.1 GI:51982002
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 26 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

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LOCUS 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 27 from Patent WO2004072293.
ACCESSION CQ860115
VERSION CQ860115.1 GI:51982003
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp

protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 27 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

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DEFINITION Sequence 28 from Patent WO2004072293.
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KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 28 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

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DEFINITION Sequence 29 from Patent WO2004072293.
ACCESSION CQ860117
VERSION CQ860117.1 GI:51982005
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the

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interaction between the proteins of the ob-rgrp family and the
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Patent: WO 2004072293-A 29 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
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  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="AS08"

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 GAGGATTATGGCGTTTACTG 171
Db 20 GAGGATTATGGCGTTTACTG 1

RESULT 16
CQ860118/c
LOCUS CQ860118 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 30 from Patent WO2004072293.
ACCESSION CQ860118
VERSION CQ860118.1 GI:51982006
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL
Patent: WO 2004072293-A 30 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES
  Location/Qualifiers
  1..20
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="AS09"

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 GCGGTTTACTGCCCTTATT 180
Db 20 GCGGTTTACTGCCCTTATT 1

RESULT 17
CQ860119/c
LOCUS CQ860119 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 31 from Patent WO2004072293.
ACCESSION CQ860119
VERSION CQ860119.1 GI:51982007
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
Patent: WO 2004072293-A 31 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
JOURNAL
source
FEATURES
  Location/Qualifiers
  1..20
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="AS10"

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TGCCTGTGCGGAACCTGGCAT 281
Db 20 TGCCTGTGCGGAACCTGGCAT 1

RESULT 18
CQ860121/c
LOCUS CQ860121 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 33 from Patent WO2004072293.
ACCESSION CQ860121
VERSION CQ860121.1 GI:51982009
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL
Patent: WO 2004072293-A 33 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES
  Location/Qualifiers
  1..20
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="AS12"

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 269 CGGGAACCTGGCATATTCTT 288
Db 20 CGGGAACCTGGCATATTCTT 1

RESULT 19
CQ860122/c
LOCUS CQ860122 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 34 from Patent WO2004072293.
ACCESSION CQ860122
VERSION CQ860122.1 GI:51982010
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
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JOURNAL Patent: WO 2004072293-A 34 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS13"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 370 CCTTGTGTTGGCAGGCAATG 389
Db 20 CCTTGTGTTGGCAGGCAATG 1
RESULT 20
CO878361 20 bp DNA linear PAT 04-OCT-2004
LOCUS
DEFINITION Sequence 14 from Patent WO2004080272.
ACCESSION CO878361
VERSION CO878361.1 GI:53790914
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Baillieu, B., Rouille, Y., Seron, K. and Belouzard, S.
TITLE Use of the genes leptin and ob-rgr for the screening of active
compounds for weight gain or loss or diabetes in human or animal
subjects
JOURNAL Patent: WO 2004080272-A 14 23-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
misc_feature 1..20
/note="Amorce sens pour PCR en temps r el de OB-RGRP"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 44 ACCAGCCGCGCCCGTTC 63
Db 1 ACCAGCCGCGCCCGTTC 20
RESULT 21
BD128083 20 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD128083
VERSION BD128083.1 GI:23223028
KEYWORDS JP 2002017375-A/3514.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
Koga, H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 3514 22-JAN-2002;
HELIIX RESEARCH INSTITUTE
COMMENT OS Unidentified
PN JP 2002017375-A/3514

PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Description of Artificial Sequence: an artificially CC
synthesized primer
CC sequence
FH Key Location/Qualifiers
FT source 1..20
FT /organism="Unidentified".
FEATURES
source
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1029 GAGAGTAACATCACACCC 1048
Db 20 GAGAGTAACATCACACCC 1
RESULT 22
CO860126/c 21 bp DNA linear PAT 10-SEP-2004
LOCUS
DEFINITION Sequence 38 from Patent WO2004072293.
ACCESSION CO860126
VERSION CO860126.1 GI:51982014
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Jockers, R., Couturier, C. and Uhlmann, E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgr
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgr family and the
leptin receptor
JOURNAL Patent: WO 2004072293-A 38 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES
source
1..21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial"
Query Match 1.8%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 260 AGTGCCTGTCTGGGAACCTGCG 279
Db 20 AGTGCCTGTCTGGGAACCTGCG 1
RESULT 23
AX378941/c 25 bp DNA linear PAT 18-MAR-2002
LOCUS
DEFINITION Sequence 59 from Patent WO0210347.
ACCESSION AX378941


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VERSION      AX378941.1  GI:19574784
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1
JOURNAL      Benvenisty,N.
FEATURES     Directed differentiation of embryonic cells
SOURCE       Patent: WO 0210347-A 59 07-FEB-2002;
              Yissum Research and Dev. Company of the Hebrew Univ. of Jerusalem
              (IL)
              Location/Qualifiers
                1..25
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
                  /note="3' primer of Parathyroid Hormone"

Query Match      1..8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 7.6;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 794 CTTGGAGAGGAGGAGTAACGCTGA 816
      |||||
Db 23 CTTGGAGAGGAGGAGCAAAAGCTGA 1

RESULT 24
CQ860125 Q860125 21 bp DNA linear PAT 10-SEP-2004
LOCUS
DEFINITION Sequence 37 from Patent WO2004072293.
ACCESSION CQ860125
VERSION CQ860125.1 GI:51982013
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.

REFERENCE    1
AUTHORS      Jockers,R., Couturier,C. and Uhlmann,E.
TITLE        Oligonucleotides which inhibit the expression of the ob-rgrp
              protein and method for detection of compounds modifying the
              interaction between the proteins of the ob-rgrp family and the
              leptin receptor
              Patent: WO 2004072293-A 37 26-AUG-2004;
              Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
              RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
              Scientifique (CNRS) (FR)
JOURNAL      Scientificque (CNRS) (FR)
FEATURES     Location/Qualifiers
SOURCE       1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Artificiel"

Query Match      1.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 261 GTGCCTGTGGGAACGGCAT 281
      |||||
Db 1 GTGCCTGTGGGAACGGCTT 21

RESULT 25
AR166701 AR166701 19 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 51 from patent US 6281346.
ACCESSION AR166701
VERSION AR166701.1 GI:16242129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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REFERENCE    1 (bases 1 to 19)
AUTHORS      Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sean.
TITLE        Rat ob-receptors and nucleotides encoding them
JOURNAL      Patent: US 6281346-A 51 28-AUG-2001;
FEATURES     Location/Qualifiers
SOURCE       1..19
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 TCGTGGCATTATCCTTCAG 108
      |||||
Db 1 TCGTGGCATTATCCTTCAG 19

RESULT 26
AR166700 AR166700 18 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 50 from patent US 6281346.
ACCESSION AR166700
VERSION AR166700.1 GI:16242127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE    1 (bases 1 to 18)
AUTHORS      Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sean.
TITLE        Rat ob-receptors and nucleotides encoding them
JOURNAL      Patent: US 6281346-A 50 28-AUG-2001;
FEATURES     Location/Qualifiers
SOURCE       1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 CTTATGCTGGGATGTGCC 148
      |||||
Db 1 CTTATGCTGGGATGTGCC 18

RESULT 27
AR302819/c AR302819 18 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 30 from patent US 6541604.
ACCESSION AR302819
VERSION AR302819.1 GI:31691306
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE    1 (bases 1 to 18)
AUTHORS      Bennett,B. and Matthews,W.
TITLE        Leptin receptor having a WSX motif
JOURNAL      Patent: US 6541604-A 30 01-APR-2003;
FEATURES     Location/Qualifiers
SOURCE       1..18
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTGCCTTAGA 153
      |||||
Db 18 GCTGGGATGTGCCTTAGA 1
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RESULT 28
LOCUS      AR302820          18 bp      DNA
DEFINITION Sequence 31 from patent US 6541604.
ACCESSION  AR302820
VERSION     AR302820.1  GI:31691307
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Bennett,B. and Matthews,W.
TITLE      Leptin receptor having a WSX motif
JOURNAL    Patent: US 6541604-A 31 01-APR-2003;
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1..6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      136  GCTGGGATGTCCTTAGA 153
          |||||
Db       1  GCTGGGATGTCCTTAGA 18

RESULT 29
LOCUS      AX412234/c      24 bp      DNA
DEFINITION Sequence 60 from Patent WO0222879.
ACCESSION  AX412234
VERSION     AX412234.1  GI:21444692
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Bacher,J.W., Flanagan,L. and Nasais,N.
TITLE      Detection of microsatellite instability and its use in diagnosis of
            tumors
JOURNAL    Patent: WO 0222879-A 60 21-MAR-2002;
            PROMEGA CORPORATION (US)
FEATURES   Location/Qualifiers
            source
            1..24
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="BAT-25 primer"

Query Match      1..6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921  AGAGCCTTATTAGAAATGCAGAA 944
          |||||
Db       24  AGAGCCATAGTTAAATGCAGAA 1

RESULT 30
LOCUS      AX548339          24 bp      DNA
DEFINITION Sequence 263 from Patent WO0240716.
ACCESSION  AX548339
VERSION     AX548339.1  GI:25813373
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

RESULT 28
LOCUS      AR302820          18 bp      DNA
DEFINITION Sequence 31 from patent US 6541604.
ACCESSION  AR302820
VERSION     AR302820.1  GI:31691307
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Bennett,B. and Matthews,W.
TITLE      Leptin receptor having a WSX motif
JOURNAL    Patent: US 6541604-A 31 01-APR-2003;
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1..6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      136  GCTGGGATGTCCTTAGA 153
          |||||
Db       1  GCTGGGATGTCCTTAGA 18

RESULT 29
LOCUS      AX412234/c      24 bp      DNA
DEFINITION Sequence 60 from Patent WO0222879.
ACCESSION  AX412234
VERSION     AX412234.1  GI:21444692
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Bacher,J.W., Flanagan,L. and Nasais,N.
TITLE      Detection of microsatellite instability and its use in diagnosis of
            tumors
JOURNAL    Patent: WO 0222879-A 60 21-MAR-2002;
            PROMEGA CORPORATION (US)
FEATURES   Location/Qualifiers
            source
            1..24
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="BAT-25 primer"

Query Match      1..6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921  AGAGCCTTATTAGAAATGCAGAA 944
          |||||
Db       24  AGAGCCATAGTTAAATGCAGAA 1

RESULT 30
LOCUS      AX548339          24 bp      DNA
DEFINITION Sequence 263 from Patent WO0240716.
ACCESSION  AX548339
VERSION     AX548339.1  GI:25813373
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

RESULT 31
LOCUS      AX738199          17 bp      DNA
DEFINITION Sequence 3789 from Patent WO03025177.
ACCESSION  AX738199
VERSION     AX738199.1  GI:30517487
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL    Patent: WO 03025177-A 3789 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1..5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      981  GATCCAAAGGAGTTGTA 997
          |||||
Db       1  GATCCAAAGGAGTTGTA 17

RESULT 32
LOCUS      BD223822/c      21 bp      DNA
DEFINITION Novel method of regulating seed development in plants and genetic
            sequences therefor.
ACCESSION  BD223822
VERSION     BD223822.1  GI:33033592
KEYWORDS   JP 2002526052-A/15.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 21)
AUTHORS    Bilodeau,P., Chaudhury,A.M., Dennis,E.S., Koltunow,A.M.G., Luo,M.
            and Peacock,W.J.
TITLE      Novel method of regulating seed development in plants and genetic
            sequences therefor
JOURNAL    Patent: JP 2002526052-A 15 20-AUG-2002;
            COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

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REFERENCE  1
AUTHORS    Palm,K.
TITLE      Profiling tumor specific markers for the diagnosis and treatment of
            neoplastic disease
JOURNAL    Patent: WO 0240716-A 263 23-MAY-2002;
            Cemines, LLC (US)
FEATURES   Location/Qualifiers
            source
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Probe"

Query Match      1..6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      834  CCAGGAGCGCGGGTGGATCCCT 857
          |||||
Db       1  CCAGTATGCGCGGGATGGATACCT 24

RESULT 31
LOCUS      AX738199          17 bp      DNA
DEFINITION Sequence 3789 from Patent WO03025177.
ACCESSION  AX738199
VERSION     AX738199.1  GI:30517487
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL    Patent: WO 03025177-A 3789 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1..5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      981  GATCCAAAGGAGTTGTA 997
          |||||
Db       1  GATCCAAAGGAGTTGTA 17

RESULT 32
LOCUS      BD223822/c      21 bp      DNA
DEFINITION Novel method of regulating seed development in plants and genetic
            sequences therefor.
ACCESSION  BD223822
VERSION     BD223822.1  GI:33033592
KEYWORDS   JP 2002526052-A/15.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 21)
AUTHORS    Bilodeau,P., Chaudhury,A.M., Dennis,E.S., Koltunow,A.M.G., Luo,M.
            and Peacock,W.J.
TITLE      Novel method of regulating seed development in plants and genetic
            sequences therefor
JOURNAL    Patent: JP 2002526052-A 15 20-AUG-2002;
            COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

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COMMENT      OS      Artificial Sequence
              PN      JP 2002526052-A/15
              PD      20-AUG-2002
              PF      21-SEP-1999 JP 2000573582
              PR      21-SEP-1998 US 60/101184,22-SEP-1998 AU PP 6061 PR
              22-SEP-1998 AU PP 6062,22-SEP-1998 AU PP 6063 PR
              01-JUL-1999 AU PP 1345,01-JUL-1999 AU PQ 1346 PI PIERRE
              BILODEAU,ABDUL MUTAKABBIR CHAUDHURY,ELIZABETH SALISBURY
              PI DENNIS,
              PI ANNA MARIA GRAZYNA KOLTUNOW,MING LUO,WILLIAM JAMES PEACOCK PC
              C12N15/09,A01H5/00,C07K14/415,C12N5/10,C12N15/00,C12N5/00 CC
              Description of Artificial Sequence:Primer
              FH      Key      Location/Qualifiers
              FT      Source      1..21
              FT      Location/Qualifiers
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              source
              1..21
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

Query Match      1.5%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      606 ACTTCATAGTAGGAGATGA 625
      |||||
Db      20 ACTTCATAGGAAGATGA 1

RESULT 33
E13776
LOCUS      24 bp      DNA      linear      PAT 27-APR-1998
DEFINITION PCR primer for discriminating genotype 1a of HCV (Hepatitis C virus).
ACCESSION E13776
VERSION E13776.1 GI:3252544
KEYWORDS JP 1997234072-A/28.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Ono,T., Mukaiide,M., Hikichi,K. and Mizogami,M.
TITLE NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
JOURNAL Patent: JP 1997234072-A 28 09-SEP-1997;
S R L:KK
COMMENT      OS      None
              OC      Artificial sequences.
              PN      JP 1997234072-A/28
              PD      09-SEP-1997
              PF      01-FEB-1996 JP 1996038875
              PR      01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI
              ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI MIZOGAMI
              MASAFUMI
              PC      C12N15/09,C07H21/04,C12Q1/68,C12Q1/70,(C12N15/09,C12R1:92); CC
              strandedness: Single;
              CC      topology: Linear;
              CC      hypothetical: No;
              CC      anti-sense: No;
              FH      Key      Location/Qualifiers
              FT      Source      1..24
              FT      /organism="Artificial sequences" FT
              misc_feature 1..24 /note="Primer,MNS54".
              FT      Location/Qualifiers
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              source
              1..24
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

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Query Match      1.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 28;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      9 TGGGCGAGCTGCCCGGGCGGTG 30
      |||||
Db      1 TCGACAGGCKGCCCGGCGCTTG 22

RESULT 34
AX420107
LOCUS      24 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent WO0208409.
ACCESSION AX420107
VERSION AX420107.1 GI:21524406
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ow,D.W.
TITLE Methods for the replacement, translocation and stacking of dna in eukaryotic genomes
JOURNAL Patent: WO 0208409-A 1 31-JAN-2002;
The Secretary of Agriculture (US)
FEATURES      Location/Qualifiers
              source
              1..24
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Primer"

Query Match      1.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      294 CTGGAATTGTTGTTCTGCC 313
      |||||
Db      5 CTGAAATTGTTGTTCTGCC 24

RESULT 35
AX487296/C
LOCUS      23 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 4596 from Patent WO02053728.
ACCESSION AX487296
VERSION AX487296.1 GI:22321444
KEYWORDS Candida albicans
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE 1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4596 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES      Location/Qualifiers
              source
              1..23
              /organism="Candida albicans"
              /mol_type="unassigned DNA"
              /db_xref="taxon:5476"

Query Match      1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      477 TGATTACAGTCGATTGAATTTCT 499
      |||||
Db      23 TGATTGCAAGTCGTTGAAATTTT 1

RESULT 36

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Fri Aug 19 10:59:59 2005

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AR067252          21 bp  DNA          PAT 29-SEP-1999
LOCUS              Sequence 600 from patent US 5851760.
ACCESSION          AR067252
VERSION            AR067252.1  GI:5998474
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 21)
AUTHORS             Evans,G.A. and Smith,M.W.
TITLE               Method for generation of sequence sampled maps of complex genomes
JOURNAL             Patent: US 5851760-A 600 22-DEC-1998;
FEATURES            Location/Qualifiers
source              1..21
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match        1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 37
I31384
LOCUS              I31384
DEFINITION         Sequence 296 from patent US 5582979.
ACCESSION          I31384
VERSION            I31384.1  GI:1822175
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 21)
AUTHORS             Weber,J.L.
TITLE               Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
JOURNAL             Patent: US 5582979-A 296 10-DEC-1996;
FEATURES            Location/Qualifiers
source              1..21
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match        1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 38
AX665946/c
LOCUS              AX665946
DEFINITION         Sequence 23 from Patent WO0242458.
ACCESSION          AX665946
VERSION            AX665946.1  GI:29290816
KEYWORDS
SOURCE             synthetic construct
ORGANISM            other sequences; artificial sequences.
REFERENCE           1
AUTHORS             Tian,H., Zhao,J., Chen,J.L., Cutler,G., An,S., Dai,K. and
TITLE               G-protein coupled receptors
JOURNAL             Patent: WO 0242458-A 23 30-MAY-2002;
FEATURES            Tularik Inc. (US)
                      Location/Qualifiers

source              1..21
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match        1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 39
CQ860133/c
LOCUS              CQ860133
DEFINITION         Sequence 45 from Patent WO2004072293.
ACCESSION          CQ860133
VERSION            CQ860133.1  GI:51982021
KEYWORDS
SOURCE             synthetic construct
ORGANISM            other sequences; artificial sequences.
REFERENCE           1
AUTHORS             Jockers,R., Couturier,C. and Uhlmann,E.
TITLE               Oligonucleotides which inhibit the expression of the ob-rgrp
JOURNAL             Patent: WO 2004072293-A 45 26-AUG-2004;
FEATURES            Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
                      RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
                      Scientifique (CNRS) (FR)
                      Location/Qualifiers

source              1..16
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial"

Query Match        1.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 CTTGCTCGTGTGGCTG 347
Db 16 CTTGCTCGTGTGGCTG 1

RESULT 40
AX738983
LOCUS              AX738983
DEFINITION         Sequence 4573 from Patent WO03025177.
ACCESSION          AX738983
VERSION            AX738983.1  GI:30518273
KEYWORDS
SOURCE             Homo sapiens (human)
ORGANISM            Homo sapiens
REFERENCE           1
AUTHORS             Telerman,A., Anson,R. and Tuijnder,M.
TITLE               Sequences involved in phenomena of tumour suppression, tumour
JOURNAL             thereof as medicaments
FEATURES            Patent: WO 03025177-A 4573 27-MAR-2003;
                      Molecular Engines Laboratories (FR)
                      Location/Qualifiers

source              1..17
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"

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source              1..23
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TGR342Right PCR expression profiling primer"

Query Match        1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 117 TTGGACTGACTTTTCTTATGC 137
Db 22 TTGGAATGCCTTTTCTTATTC 2

RESULT 39
CQ860133/c
LOCUS              CQ860133
DEFINITION         Sequence 45 from Patent WO2004072293.
ACCESSION          CQ860133
VERSION            CQ860133.1  GI:51982021
KEYWORDS
SOURCE             synthetic construct
ORGANISM            other sequences; artificial sequences.
REFERENCE           1
AUTHORS             Jockers,R., Couturier,C. and Uhlmann,E.
TITLE               Oligonucleotides which inhibit the expression of the ob-rgrp
JOURNAL             Patent: WO 2004072293-A 45 26-AUG-2004;
FEATURES            Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
                      RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
                      Scientifique (CNRS) (FR)
                      Location/Qualifiers

source              1..16
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial"

Query Match        1.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 CTTGCTCGTGTGGCTG 347
Db 16 CTTGCTCGTGTGGCTG 1

RESULT 40
AX738983
LOCUS              AX738983
DEFINITION         Sequence 4573 from Patent WO03025177.
ACCESSION          AX738983
VERSION            AX738983.1  GI:30518273
KEYWORDS
SOURCE             Homo sapiens (human)
ORGANISM            Homo sapiens
REFERENCE           1
AUTHORS             Telerman,A., Anson,R. and Tuijnder,M.
TITLE               Sequences involved in phenomena of tumour suppression, tumour
JOURNAL             thereof as medicaments
FEATURES            Patent: WO 03025177-A 4573 27-MAR-2003;
                      Molecular Engines Laboratories (FR)
                      Location/Qualifiers

source              1..17
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"

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/db_xref=taxon:9606"

Query Match 1.4%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGTTGT 996
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 Db 1 GATCCAAAGGAGTTGT 16

RESULT 41
 AX298650/c
 LOCUS AX298650 20 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 284 from Patent WO0183749.
 ACCESSION AX298650
 VERSION AX298650.1 GI:17128640
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Bachmanov A.A., Beauchamp G.K., Chatterjee A., de Jong P.J., Li S.,
 Li X., Ohnen J.D., Reed D.R., Ross D. and Tordoff M.G.
 TITLE Gene and sequence variation associated with sensing carbohydrate
 compounds and other sweeteners
 JOURNAL Patent: WO 0183749-A 284 08-NOV-2001;
 WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center
 (US)

FEATURES
 source
 1..20
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref=taxon:9606"

Query Match 1.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACTGCTCAT 1107
 |||||
 Db 16 GGTGTTACTGCTCAT 1

RESULT 42
 AX298652/c
 LOCUS AX298652 20 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 286 from Patent WO0183749.
 ACCESSION AX298652
 VERSION AX298652.1 GI:17128642
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Bachmanov A.A., Beauchamp G.K., Chatterjee A., de Jong P.J., Li S.,
 Li X., Ohnen J.D., Reed D.R., Ross D. and Tordoff M.G.
 TITLE Gene and sequence variation associated with sensing carbohydrate
 compounds and other sweeteners
 JOURNAL Patent: WO 0183749-A 286 08-NOV-2001;
 WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center
 (US)

FEATURES
 source
 1..20
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref=taxon:9606"

Query Match 1.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACTGCTCAT 1107
 |||||
 Db 16 GGTGTTACTGCTCAT 1

RESULT 43
 AX795189
 LOCUS AX795189 19 bp DNA linear PAT 04-OCT-2003
 DEFINITION Sequence 19 from Patent EP1323825.
 ACCESSION AX795189
 VERSION AX795189.1 GI:37515950
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Giuliano G., Rosati C., Dharmapuri S., Pallara P. and Camara B.
 TITLE Recombinant plants and dna constructs
 JOURNAL Patent: EP 1323825-A 19 02-JUL-2003;
 ENEA ENTE PER LE NUOVE TECNOLOGIE, L'ENERGIA E L'AMBIENTE (IT);
 Biogen S.r.l. (IT)
 FEATURES
 Location/Qualifiers
 1..19
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref=taxon:32630"
 /note="Upstream primer used to detect the expression of
 the Lycopersicon esculentum Chy2 gene by RT-PCR"
 primer_bind 1..19
 /note="Le -Chy2 Upstream Primer"

Query Match 1.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 47;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 435 GAGGAGATGATTTAGCTG 453
 |||||
 Db 1 GAGGAGAGAGCTTTAGCTG 19

RESULT 44
 A50630
 LOCUS A50630 20 bp DNA linear PAT 07-MAR-1997
 DEFINITION Sequence 72 from Patent WO9613608.
 ACCESSION A50630
 VERSION A50630.1 GI:2303510
 KEYWORDS unidentified
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Giesendorf B., Quint W. and Van D.L.
 TITLE NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE DETECTION AND
 DIFFERENTIATION OF PROKARYOTIC ORGANISMS
 JOURNAL Patent: WO 9613608-A 72 09-MAY-1996;
 INNOGENETICS NV (BE)
 COMMENT Other publication AU 3845795 960523.
 FEATURES
 Location/Qualifiers
 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref=taxon:32644"

Query Match 1.4%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 46;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 TAGAAATGCAGAACTCGAA 949
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 Db 2 TAGCAATGCAGAACTCGCA 20

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RESULT 45
AR147307
LOCUS AR147307 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 72 from patent US 6221582.
ACCESSION AR147307
VERSION AR147307.1 GI:15111110
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
AUTHORS Giesendorf,B., Quint,W. and Van Doorn,L.-J.
TITLE Polynucleic acid sequences for use in the detection and
differentiation of prokaryotic organisms
JOURNAL Patent: US 6221582-A 72 24-APR-2001;
FEATURES
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 931 TAGAATGCAGATCTCAA 949
|||||
Db 2 TAGCAATGCAGATCTGCA 20

RESULT 46
AX241144/c
LOCUS AX241144 22 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 382 from Patent WO0160975.
ACCESSION AX241144
VERSION AX241144.1 GI:15798019
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Roemer,T., Jiang,B., Boone,C. and Bussey,H.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 0160975-A 382 23-AUG-2001;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DNA primer"

Query Match 1..4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 337 TCGTGTGGCTGTGATCAA 355
|||||
Db 19 TCGTGTGGCTGTCTCAA 1

RESULT 47
AX486731/c
LOCUS AX486731 22 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4031 from Patent WO02053728.
ACCESSION AX486731
VERSION AX486731.1 GI:2320879
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE
AUTHORS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.

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TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4031 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
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/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match 1..4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 337 TCGTGTGGCTGTGATCAA 355
|||||
Db 19 TCGTGTGGCTGTCTCAA 1

RESULT 48
BD009437
LOCUS BD009437 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples.
ACCESSION BD009437
VERSION BD009437.1 GI:18637810
KEYWORDS JP 2001502536-A/29.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Quint,W. and Doorn,L.J.V. for detection and typing of Helicobacter
pylori nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 29 27-FEB-2001;
INNOGENETICS NV, DDL BV
COMMENT
OS Unidentified
PN JP 2001502536-A/29
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C12Q1/68,C07K14/205,C12N15/11
CC CC
FH Key Location/Qualifiers
FT source 1..20 /organism='Unidentified'.

FEATURES
source
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1..4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 103 CTTTCAGTGGGCTATTGG 120
|||||
Db 2 CTTTAGTGGGTATTGG 19

RESULT 49
AX422712
LOCUS AX422712 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1048 from Patent WO0188124.
ACCESSION AX422712
VERSION AX422712.1 GI:21526094
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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AUTHORS Jarvis,T., von Carlowitz,I., Mewswigen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1048 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 958 CTGGACCCAGGACATT 974
Db 1 CTGGACTCAGGACATT 17
RESULT 50
AX732552/c
LOCUS AX732552 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4186 from Patent WO03025175.
ACCESSION AX732552
VERSION AX732552.1 GI:30511895
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 4186 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 838 GAAGCCCGGGTGGATC 854
Db 17 GAAGGCTGGGTGGATC 1
RESULT 51
AX759882/c
LOCUS AX759882 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3203 from Patent WO03040369.
ACCESSION AX759882
VERSION AX759882.1 GI:32254498
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 3203 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 838 GAAGCCCGGGTGGATC 854
Db 17 GAAGGCTGGGTGGATC 1
RESULT 52
AX732552/c
LOCUS AX732552 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4186 from Patent WO03025175.
ACCESSION AX732552
VERSION AX732552.1 GI:30511895
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 4186 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 838 GAAGCCCGGGTGGATC 854
Db 17 GAAGGCTGGGTGGATC 1
RESULT 53
AX713192/c
LOCUS AX713192 18 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 78 from Patent WO03018837.
ACCESSION AX713192
VERSION AX713192.1 GI:29823781
KEYWORDS synthetic construct
SOURCE
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Waschuetza,S., Schnakenberg,B. and Lustig,M.
TITLE Method and diagnostic kit for the molecular diagnosis of pharmacologically relevant genes
JOURNAL Patent: WO 03018837-A 78 06-MAR-2003;
Adnagen AG (DE)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 19 GCCCGGGCGGTGGCAGG 35
Db 17 GCCCGGGCAGTGGCAGG 1

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 838 GAAGCCCGGGTGGATC 854
Db 17 GAAGGCTGGGTGGATC 1
RESULT 52
AR299925
LOCUS AR299925 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 11660 from patent US 6537751.
ACCESSION AR299925
VERSION AR299925.1 GI:31687209
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11660 25-MAR-2003;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 104 TTCAGTGGGGCTATTGG 120
Db 2 TTCAATGGGGCTATTGG 18
RESULT 53
AX713192/c
LOCUS AX713192 18 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 78 from Patent WO03018837.
ACCESSION AX713192
VERSION AX713192.1 GI:29823781
KEYWORDS synthetic construct
SOURCE
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Waschuetza,S., Schnakenberg,B. and Lustig,M.
TITLE Method and diagnostic kit for the molecular diagnosis of pharmacologically relevant genes
JOURNAL Patent: WO 03018837-A 78 06-MAR-2003;
Adnagen AG (DE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 19 GCCCGGGCGGTGGCAGG 35
Db 17 GCCCGGGCAGTGGCAGG 1

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RESULT 54
AX132091/c
LOCUS           19 bp      DNA      linear      PAT 15-MAY-2001
DEFINITION      Sequence 3309 from Patent WO0130362.
ACCESSION       AX132091
VERSION         AX132091.1 GI:14138396
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL
FEATURES        source
                1..19
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Cyclin B1 ribozyme binding site"
Query Match     1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 790 TGTGCTTGGAGAGGAGCAG 806
Db 18 TGGGCTTGGAGAGGAGCAG 2
RESULT 55
I88036/c
LOCUS           20 bp      DNA      linear      PAT 10-AUG-1998
DEFINITION      Sequence 14 from patent US 5716846.
ACCESSION       I88036
VERSION         I88036.1 GI:3407976
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 20)
AUTHORS         Brown,S.Joel., Dattagupta,N. and Naidu,Y.M.
TITLE           Method for inhibiting cellular proliferation using antisense
                oligonucleotides to interleukin-6 receptor mRNA
JOURNAL          Patent: US 5716846-A 14 10-FEB-1998;
FEATURES        source
                1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match     1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 54;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 32 CAGGAAGCCGGAGGAGCAG 48
Db 18 CAGGAAGCCGGAGGAGCAG 2
RESULT 56
ARI36416/c
LOCUS           20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION      Sequence 11 from patent US 6136604.
ACCESSION       ARI36416
VERSION         ARI36416.1 GI:14477088
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
Query Match     1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 743 AGCGAGCTGCCACCTTATGC 762
Db 1 AGCGAGCTGCCACCTTATGC 20
RESULT 57
CO767202
LOCUS           20 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION      Sequence 30 from Patent WO2004005513.
ACCESSION       CO767202
VERSION         CO767202.1 GI:44909292
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE       1
AUTHORS         Besterman,J.M., Li,Z., Delorme,D. and Bonfils,C.
TITLE           Methods for specifically inhibiting histone deacetylase-7 and 8
JOURNAL          Patent: WO 2004005513-A 30 15-JAN-2004;
                MethyIgene, Inc. (CA)
FEATURES        source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of Combined DNA/RNA Molecule: Synthetic
                oligonucleotide-description of Artificial Sequence:
                Synthetic oligonucleotide"
Query Match     1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 743 AGCGAGCTGCCACCTTATGC 762
Db 1 AGCGAGCTGCCACCTTATGC 20
RESULT 58
ARI315527/c
LOCUS           20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION      Sequence 6064 from patent US 6559294.
ACCESSION       ARI315527
VERSION         ARI315527.1 GI:31708953
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 20)
AUTHORS         Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
                Sankaran,B. and Fletcher,L.D.
TITLE           Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL          Patent: US 6559294-A 6064 06-MAY-2003;
FEATURES        source
                1..20
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match     1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 459 AGTGGTAGCACCATTATCTG 478
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Db 20 AGCGGTAGCAGTTCTCTG 1

RESULT 59
AR442611
LOCUS AR442611 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 219 from patent US 6670130.
ACCESSION AR442611
VERSION AR442611.1 GI:42669868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,C.M., Park,H.K. and Jang,H.J.
TITLE Oligonucleotide for detection and identification of Mycobacteri
JOURNAL Patent: US 6670130-A 219 30-DEC-2003;
FEATURES
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 998 TGCACATGAAGTTTGAGAA 1017
||||| ||| |||||
Db 1 TGCACAACAACCTTGAGAA 20

RESULT 60
AX293011/c
LOCUS AX293011 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 4773 from Patent WO0179548.
ACCESSION AX293011
VERSION AX293011.1 GI:17054694
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 4773 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)

FEATURES
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 CATCGAACCTTTGCTGG 786
||||| ||| |||||
Db 20 CATCGACACGTTGCTCG 1

RESULT 61
AX456087
LOCUS AX456087 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 17 from Patent WO0170675.
ACCESSION AX456087
VERSION AX456087.1 GI:21715042

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Delorme,D., Woo,S.H. and Vaisburg,A.
TITLE Inhibitors of histone deacetylase
JOURNAL Patent: WO 0170675-A 17 27-SEP-2001;
Methylgene, Inc. (CA)

FEATURES
Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
||||| ||| |||||
Db 1 AGGCAGCTGCCACTTGATGC 20

RESULT 62
AX589807/c
LOCUS AX589807 20 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02079249.
ACCESSION AX589807
VERSION AX589807.1 GI:27901058
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Escary,J.L.
TITLE New polynucleotides and polypeptides of the ifn_g(a)-21 gene
JOURNAL Patent: WO 02079249-A 9 10-OCT-2002;
GenOdysee (FR)

FEATURES
Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 608 TTCATAAGTAGGAGATGAGT 627
||||| ||| |||||
Db 20 TTCCCAAGTAGCAGATGAGT 1

RESULT 63
AX703629
LOCUS AX703629 20 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 33 from Patent WO03006652.
ACCESSION AX703629
VERSION AX703629.1 GI:29538528
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Li,Z., Bonfile,C. and Besterman,J.
TITLE Inhibition of specific histone deacetylase isoforms
JOURNAL Patent: WO 03006652-A 33 23-JAN-2003;
Methylgene, Inc. (CA)

FEATURES
Location/Qualifiers

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source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGCAGCTGCCACTTATGC 762
||| ||||| ||||| ||||| |||||
Db 1 AGCCAGCTGCCACTTATGC 20

RESULT 64
LOCUS AX962777/c 20 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 33 from Patent WO03104458.
ACCESSION AX962777
VERSION AX962777.1 GI:40881890
KEYWORDS
ORGANISM
SOURCE
SYNTHETIC CONSTRUCT
OTHER SEQUENCES; artificial sequences.
REFERENCE
AUTHORS Baker,B.F., Freier,S.M. and Dobie,K.W.
TITLE Antisense modulation of il-1 receptor-associated kinase-1
JOURNAL
JOURNAL
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCTCTCATGACCCA 836
||| ||||| ||||| ||||| |||||
Db 20 AGGAGGCTCTCATGACCCA 1

RESULT 65
LOCUS AX962848 20 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 104 from Patent WO03104458.
ACCESSION AX962848
VERSION AX962848.1 GI:40881971
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Baker,B.F., Freier,S.M. and Dobie,K.W.
TITLE Antisense modulation of il-1 receptor-associated kinase-1
expression
JOURNAL
JOURNAL
FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCTCTCATGACCCA 836
||| ||||| ||||| ||||| |||||
Db 20 AGGAGGCTCTCATGACCCA 1

RESULT 66
LOCUS BD012571 20 bp DNA linear PAT 02-AUG-2002
DEFINITION Human cytochrome P450-transgenic mouse.
ACCESSION BD012571
VERSION BD012571.1 GI:22092760
KEYWORDS
SOURCE
SYNTHETIC CONSTRUCT
OTHER SEQUENCES; artificial sequences.
REFERENCE
AUTHORS Ishida,I., Tomizuka,K., Kuroiwa,Y., Oshima,T., Suzuki,M. and Ito,K.
TITLE Human cytochrome P450-transgenic mouse
JOURNAL
JOURNAL
COMMENT
OS Artificial Sequence
PN WO 011951-A/10
PD 22-FEB-2001
PF 11-AUG-2000 WO 2000JP005424
PR 13-AUG-1999 JP 99P 229094
PI ISAO ISHIDA, KAZUMA TOMIZUKA, YOSHIMI KUROIWA, TAKESHI OSHIMA, PI
MUTSUMI SUZUKI,
KUNIO ITO
PC A01K67/027,C12N15/00,C12Q1/68,C12N15/85,C12N5/10,G01N33/50, PC
GO1N33/15
CC Description of Artificial Sequence:primer
for detecting CYP3A4 cDNA
CC
FH Key Location/Qualifiers.
1..20 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 105 TCAGTGGGCTCTTGGACTG 124
||| ||||| ||||| ||||| |||||
Db 1 TCAGTGAGGCTGTGGATTG 20

RESULT 67
LOCUS BD143015 21 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of assaying human ABC transporter and probe and kit
thereof.
ACCESSION BD143015
VERSION BD143015.1 GI:27848773
KEYWORDS
SOURCE
UNIDENTIFIED
ORGANISM
unclassified.
REFERENCE
AUTHORS Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
TITLE Method of assaying human ABC transporter and probe and kit therefor
JOURNAL
JOURNAL
COMMENT
OS human ABCB4 gene
PN JP 2002112775-A/86
PD 16-APR-2002
PF 03-OCT-2000 JP 2000303404
PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAOKA
PC C12N15/09,C12Q1/68,C12N15/00
CC Method of assaying human ABC transporter and probe and kit
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therefor
FH Key Location/Qualifiers
FT source 1..21
FT /organism='human ABCB4 gene'.
FEATURES
    source
        1..21
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            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'
Query Match
    Best Local Similarity 1.4%; Score 15.2; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 295 TCGAATGTGTTCTGCGCT 314
    ||||| ||||| |||||
Db 1 TGGAGTCTCTGTTGCTGCT 20
    ||||| ||||| |||||

RESULT 68
E12685
LOCUS AX095512/c 21 bp DNA linear PAT 27-APR-1998
DEFINITION Sequence 690 from Patent WO0118250.
ACCESSION AX095512
VERSION AX095512.1 GI:3251517
KEYWORDS unidentifed
SOURCE unclassified
ORGANISM Homo sapiens
REFERENCE
    1 (bases 1 to 21)
    Tanida,E., Oue,C., Yagi,S., Hasegawa,A., Kiyozawa,K. and Yano,A.
    ASTALOGLYCOPROTEIN RECEPTOR DERIVATIVE AND ITS USE
    Patent: JP 1997056380-A 2 04-MAR-1997;
    TONEN CORP., INTERNATL REAGENTS CORP, KIYOZAWA KENDOU
COMMENT
    OS None
    OC Artificial sequences.
    PN JP 1997056380-A/2
    PD 04-MAR-1997
    PF 21-AUG-1995 JP 1995212118
    PI TANIDA EMIKO, OUE CHIHARU, YAGI SHINTARO, HASEGAWA AKIRA, PI
    KIYOZAWA KENDOU,
    PI YANO AKIHIKO
    PC C12N15/09,C07H21/04,C07K14/705,C12N1/21,C12N5/10,C12P21/02, PC
    G01N33/53,
    PC G01N33/566,G01N33/576,(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),
    PC C12P21/02,
    PC C12R1:19),(C12P21/02,C12R1:91);
    CC strandedness: Single;
    CC topology: Linear;
    CC hypothetical: No;
    FH Key Location/Qualifiers
    FH source 1..21
    FT /organism='Artificial sequences'.
FEATURES
    source
        1..21
            Location/Qualifiers
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'
Query Match
    Best Local Similarity 1.4%; Score 15.2; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 820 AGGCTCTCATGACCCAGGA 839
    ||||| ||||| |||||
Db 1 AGCCCTATCATGACCAAGGA 20
    ||||| ||||| |||||

RESULT 69
AR529487/c
LOCUS AX956467 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 690 from patent US 6727063.

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ACCESSION AR529487
VERSION AR529487.1 GI:53917924
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
    1 (bases 1 to 21)
    Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.O. and
    McCarthy,J.J.
    Single nucleotide polymorphisms in genes
    Patent: US 6727063-A 690 27-APR-2004;
    Location/Qualifiers
    1..21
        source
            /organism='unknown'
            /mol_type='genomic DNA'
Query Match
    Best Local Similarity 1.4%; Score 15.2; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 733 GCAGTCTTTGTAGGCAGCTGC 752
    ||||| ||||| |||||
Db 20 GCAGTCATTRAGGCAGCTGC 1
    ||||| ||||| |||||

RESULT 70
AX095512/c 21 bp DNA linear PAT 30-MAR-2001
LOCUS AX095512
DEFINITION Sequence 690 from Patent WO0118250.
ACCESSION AX095512
VERSION AX095512.1 GI:13511715
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
    1
    Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.O. and
    McCarthy,J.J.
    Single nucleotide polymorphisms in genes
    Patent: WO 0118250-A 690 15-MAR-2001;
    WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
    Pharmaceuticals, Inc. (US)
    Location/Qualifiers
    1..21
        source
            /organism='Homo sapiens'
            /mol_type='unassigned DNA'
            /db_xref='taxon:9606'
Query Match
    Best Local Similarity 1.4%; Score 15.2; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 733 GCAGTCTTTGTAGGCAGCTGC 752
    ||||| ||||| |||||
Db 20 GCAGTCATTRAGGCAGCTGC 1
    ||||| ||||| |||||

RESULT 71
AX956467 21 bp DNA linear PAT 08-JAN-2004
LOCUS AX956467
DEFINITION Sequence 17 from Patent WO03097869.
ACCESSION AX956467
VERSION AX956467.1 GI:40784976
KEYWORDS Rosa sp.
SOURCE Rosa sp.
ORGANISM Rosa sp.
REFERENCE
    1
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
    Suess,K.H.
    Microsatellite markers for genetic analyses and the differentiation

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1050 ACTTCCTATCTTCCAG 1067

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AUTHORS      Soeda,E.
TITLE        A method of arraying genome clone
JOURNAL      Patent: WO 02072815-A 69 19-SEP-2002;
              EIICHI SOEDA,TAKESHI KUKITA
COMMENT      OS Artificial Sequence
              PN WO 02072815-A/69
              PD 19-SEP-2002
              PF 17-MAY-2001 WO 2001JP004139
              PI 12-MAR-2001 JP 01P 68285
              PC C12N15/09,C12Q1/68
              CC Description of Artificial Sequence: Synthetic DNA FH Key
              FT source 1..20
              FT Location/Qualifiers
              FT Location/Qualifiers
              FT 1..20
              FT /organism="synthetic construct"
              FT /mol_type="genomic DNA"
              FT /db_xref="taxon:32630"

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1010 TTTGAGAGCATCATCAT 1027
Db 1 TTTGAGAGCATCATCAT 18

RESULT 77
BD247804
LOCUS      BD247804 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of interleukin-5 signal transduction.
ACCESSION BD247804
VERSION    BD247804.1 GI:33057574
KEYWORDS   JP 2002539846-A/152.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Dean,N.M., Karras,J.G. and McKay,R.
TITLE      Antisense modulation of interleukin-5 signal transduction
JOURNAL    Patent: JP 2002539846-A 152 26-NOV-2002;
              ISIS PHARMACEUTICALS INC
COMMENT    OS Artificial Sequence
              PN JP 2002539846-A/152
              PD 26-NOV-2002
              PF 17-MAR-2000 JP 2000608790
              PI 26-MAR-1999 US 09/280799
              PC C12N15/09,A61K31/711,A61K48/00,A61P11/06,A61P29/00,A61P35/00,
              PC A61P43/00,
              PC A61P43/00,C12N5/02,C12N15/00
              CC Description of Artificial Sequence:Synthetic
              FH Key Location/Qualifiers
              FT source 1..20
              FT Location/Qualifiers
              FT 1..20
              FT /organism="Artificial Sequence".
              FT Location/Qualifiers
              FT 1..20
              FT /organism="synthetic construct"
              FT /mol_type="genomic DNA"
              FT /db_xref="taxon:32630"

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCTCTG 19

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RESULT 78
E43993/c
LOCUS      E43993 20 bp DNA linear PAT 31-JAN-2002
DEFINITION ACE-analogous gene.
ACCESSION E43993
VERSION    E43993.1 GI:18629196
KEYWORDS   JP 2001046072-A/7.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Sugano,S. and Komatsu,T.
TITLE      ACE-analogous gene
JOURNAL    Patent: JP 2001046072-A 7 20-FEB-2001;
              OTSUKA PHARMACEUT CO LTD
COMMENT    OS Unidentified
              PN JP 2001046072-A/7
              PD 20-FEB-2001
              PF 06-AUG-1999 JP 1999223892
              PR SUMIO SUGANO,TAKAMI KOMATSU
              PC C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,A61K39/395, PC
              PC A61K39/395,
              PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
              C12N1/19,
              PC C12N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC
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              PC C12N5/00
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              FT source 1..20
              FT /organism="Unidentified".
              FT Location/Qualifiers
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              FT /organism="unidentified"
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              FT /db_xref="taxon:32644"

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 182 GTCCTGATTTTCCAGCC 199
Db 18 GTTCTGATTTTCCAGCC 1

RESULT 79
AR183974/c
LOCUS      AR183974 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6342392.
ACCESSION AR183974
VERSION    AR183974.1 GI:20227943
KEYWORDS   AR183974.1
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
TITLE      Nucleotide and deduced amino acid sequences of tumor gene Int6
JOURNAL    Patent: US 6342392-A 9 29-JAN-2002;
              Location/Qualifiers
              FT source 1..20
              FT /organism="unknown"
              FT /mol_type="unassigned DNA"

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 926 CTTATTAGAAATGCAGAA 943

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Db      20 CTAATTAATAAATGCAGAA 3

RESULT 80
AR540678/c
LOCUS      AR540678      20 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 9 from patent US 6737251.
ACCESSION  AR540678
VERSION     AR540678.1  GI:53931994
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS   Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
TITLE     Nucleotide and deduced amino acid sequences of tumor gene Int6
JOURNAL   Patent: US 6737251-A 9 18-MAY-2004;
FEATURES   Location/Qualifiers
            source
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            /organism="unknown"
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Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      926 CTTATTAGAAATGCAGAA 943
        |||||
        20 CTAATTAATAAATGCAGAA 3

Db

RESULT 81
AX417273/c
LOCUS      AX417273      20 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 2 from Patent EP1197553.
ACCESSION  AX417273
VERSION     AX417273.1  GI:21522583
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE 1
AUTHORS   Kronenwett,R., Graef,T., Haas,R. and Nedbal,W.
TITLE     Antisense nucleic acid against alphav integrin
JOURNAL   Patent: EP 1197553-A 2 17-APR-2002;
          A3D GmbH, Antisense Design & Drug Development (DE)
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Antisense ODN directed against alphav integrin chain"

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      417 TTTTCCTTATATTGGAA 434
        |||||
        18 TTTTCCTTATATTCCAA 1

Db

RESULT 82
AX467276/c
LOCUS      AX467276      20 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 2 from Patent WO0231142.
ACCESSION  AX467276
VERSION     AX467276.1  GI:21900554
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE 1
AUTHORS   Kronenwett,R., Graef,T., Haas,R. and Nedbal,W.
TITLE     Antisense nucleic acid against alphav integrin
JOURNAL   Patent: EP 1197553-A 2 17-APR-2002;
          A3D GmbH, Antisense Design & Drug Development (DE)
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Antisense ODN directed against alphav integrin chain"

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      417 TTTTCCTTATATTGGAA 434
        |||||
        18 TTTTCCTTATATTCCAA 1

Db

RESULT 83
AX544228/c
LOCUS      AX544228      20 bp      DNA      linear      PAT 23-NOV-2002
DEFINITION Sequence 52 from Patent WO0244426.
ACCESSION  AX544228
VERSION     AX544228.1  GI:25277780
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE 1
AUTHORS   Nunez,G., Inohara,N., Ogura,Y., Cho,J., Nicolae,D.L. and Bonen,D.
TITLE     Nod2 nucleic acids and proteins
JOURNAL   Patent: WO 0244426-A 52 06-JUN-2002;
          THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US) ; The University of Chicago (US)
FEATURES   Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic"

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      784 TGGGGATGTGCTTGAGAA 801
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        18 TGGGGATGTGTTGAAGA 1

Db

RESULT 84
BD090191
LOCUS      BD090191      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION  BD090191
VERSION     BD090191.1  GI:22635801
KEYWORDS   JP 2001321190-A/2435.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS   Soda,E.
TITLE     A method of arraying genome clone
JOURNAL   Patent: JP 2001321190-A 2435 20-NOV-2001;
          THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA GENOTECHS
COMMENT    OS Artificial Sequence
          PN JP 2001321190-A/2435
          PD 20-NOV-2001

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PF 12-MAR-2001 JP 2001068285
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PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 1.3%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1010 TTGAGAGCATCATCAT 1027
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Db 1 TTTGAAAGCATCAGCAT 18

RESULT 85
AR530530/c
LOCUS AR530530 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1733 from patent US 6727063.
ACCESSION AR530530
VERSION AR530530.1 GI:53918967
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolck,S., Daley,G.O. and
McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 1733 27-APR-2004;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 14.8; DB 1; Length 21;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTGGCTTGGCAGGTGCCC 22
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Db 21 CTGCCTGGGGYAGGCTGTC 2

RESULT 86
AX096555/c
LOCUS AX096555 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1733 from Patent WO0118250.
ACCESSION AX096555
VERSION AX096555.1 GI:13512809
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolck,S., Daley,G.O. and
McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1733 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.3%; Score 14.8; DB 1; Length 21;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTGGCTTGGCAGGTGCCC 22
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Db 21 CTGCCTGGGGYAGGCTGTC 2

RESULT 87
AX539512
LOCUS AX539512 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 299 from Patent WO02059142.
ACCESSION AX539512
VERSION AX539512.1 GI:25273003
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 299 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
source
Location/Qualifiers
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Query Match
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
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Db 4 AATCACTCAACCTCTCTG 21

RESULT 88
AX539513/c
LOCUS AX539513 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 300 from Patent WO02059142.
ACCESSION AX539513
VERSION AX539513.1 GI:25273004
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 300 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
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Location/Qualifiers
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/mol_type="unassigned DNA"
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091

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AUTHORS Heinrich, G. and Kerb, R.
 TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5
 JOURNAL Patent: WO 03013534-A 293 20-FEB-2003;
 Epidauros Biotechnologie AG (DE)

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 68;
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Qy 1074 AACCACTTAACCTCTCTG 1091

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 Db 4 AATCACTAAACCTCTCTG 21

RESULT 94
 AX706597/c
 LOCUS AX706597 21 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 294 from Patent WO03013534.
 ACCESSION AX706597
 VERSION AX706597.1 GI:29563020

KEYWORDS

source

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/organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

REFERENCE 1
 AUTHORS Heinrich, G. and Kerb, R.
 TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5
 JOURNAL Patent: WO 03013534-A 294 20-FEB-2003;
 Epidauros Biotechnologie AG (DE)

FEATURES

Location/Qualifiers
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 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091

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 Db 18 AATCACTAAACCTCTCTG 1

RESULT 95
 AX706598
 LOCUS AX706598 21 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 295 from Patent WO03013534.
 ACCESSION AX706598
 VERSION AX706598.1 GI:29563021

KEYWORDS

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REFERENCE 1
 AUTHORS Heinrich, G. and Kerb, R.
 TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5
 JOURNAL Patent: WO 03013534-A 295 20-FEB-2003;
 Epidauros Biotechnologie AG (DE)

FEATURES

Location/Qualifiers
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Qy 1074 AACCACTTAACCTCTCTG 1091

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 Db 4 AATCACTAAACCTCTCTG 21

RESULT 96
 AX706599/c
 LOCUS AX706599 21 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 296 from Patent WO03013534.
 ACCESSION AX706599
 VERSION AX706599.1 GI:29563022

KEYWORDS

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/organism="Homo sapiens"
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REFERENCE 1
 AUTHORS Heinrich, G. and Kerb, R.
 TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5
 JOURNAL Patent: WO 03013534-A 296 20-FEB-2003;
 Epidauros Biotechnologie AG (DE)

FEATURES

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misc_feature

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 Db 18 AATCACTAAACCTCTCTG 1

RESULT 97
 AX707526
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 DEFINITION Sequence 293 from Patent WO03013536.
 ACCESSION AX707526
 VERSION AX707526.1 GI:29563699

KEYWORDS

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 /db_xref="taxon:9606"

REFERENCE 1
 AUTHORS Heinrich, G. and Kerb, R.
 TITLE Methods for treatment of cancer using irinotecan based on UGT1A1
 JOURNAL Patent: WO 03013536-A 293 20-FEB-2003;
 Epidauros Biotechnologie AG (DE)

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Location/Qualifiers
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Query Match 1.3%; Score 14.8; DB 1; Length 21;
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 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091

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 Db 4 AATCACTAAACCTCTCTG 21

JP 2002509721-A/1997.
 Homo sapiens (human)
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Pavco, P.A., Jarvis, T., Coeshott, C. and Meswiggen, J.A.
 AUTHORS

TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 200209721-A 1797 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 200209721-A/1797
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
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concerning molecule
CC participating in vasculogenic response
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/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1023 ATCATAGAGAGTAA 1038
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Db 2 ATCATAGAGTAA 17
RESULT 103
CQ617825/c
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2565 from Patent WO0192524.
ACCESSION CQ617825
VERSION CQ617825.1 GI:41668043
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2565 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
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Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
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Db 17 AGGCAGCTGCCACCTT 2
RESULT 104
CQ617826/c
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2566 from Patent WO0192524.
ACCESSION CQ617826
VERSION CQ617826.1 GI:41668044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2565 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
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Db 17 AGGCAGCTGCCACCTT 2
RESULT 106
CQ617826/c
LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2566 from patent US 6686188.
ACCESSION AR458889
VERSION AR458889.1 GI:42693946
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2565 03-FEB-2004;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
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Db 17 AGGCAGCTGCCACCTT 2
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LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2566 from patent US 6686188.
ACCESSION AR458889
VERSION AR458889.1 GI:42693946
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle

ACCESSION CQ617826
VERSION CQ617826.1 GI:41668044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2566 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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/db_xref='taxon:9606'
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
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Db 16 AGGCAGCTGCCACCTT 1
RESULT 105
AR458888/c
LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2565 from patent US 6686188.
ACCESSION AR458888
VERSION AR458888.1 GI:42693945
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2565 03-FEB-2004;
Aeomica, Inc. (US)
FEATURES
source
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Location/Qualifiers
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
||||| ||||||| ||||
Db 17 AGGCAGCTGCCACCTT 2
RESULT 106
AR458889/c
LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2566 from patent US 6686188.
ACCESSION AR458889
VERSION AR458889.1 GI:42693946
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle

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JOURNAL Patent: US 6686188-A 2566 03-FEB-2004;
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
Db 16 AGGCAGCTGCCGCTT 1

RESULT 107
AX421988 17 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 324 from Patent WO0188124.
ACCESSION AX421988
VERSION AX421988.1 GI:21525370
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 324 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 958 CTGGACCCAGGACATT 973
Db 2 CTGGACTCAGGACATT 17

RESULT 108
AX423718 17 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 2054 from Patent WO0188124.
ACCESSION AX423718
VERSION AX423718.1 GI:21527100
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 2054 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 959 TGGACCCAGGACATTT 974
Db 1 TGGACTCAGGACATTT 16

RESULT 109
AX674053/c 17 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 2498 from Patent WO03004526.
ACCESSION AX674053
VERSION AX674053.1 GI:29332401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 2498 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 969 ACATTTTCATGAGATC 984
Db 16 ACATTTTCATGAGATC 1

RESULT 110
AX726789 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 4476 from Patent WO03025176.
ACCESSION AX726789
VERSION AX726789.1 GI:30506132
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4476 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 519 ATACATGTGCACATGC 534
Db 2 ATCCATGTGCACATGC 17

RESULT 111
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AX736977/c
LOCUS       AX736977               17 bp    DNA          linear      PAT 08-MAY-2003
DEFINITION   Sequence 2567 from Patent WO03025177.
ACCESSION   AX736977
VERSION     AX736977.1  GI:30516265
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman, A., Amson, R. and Tuijinder, M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL     Patent: WO 03025177-A 2567 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      839  AAGCGCGGGTGGATC 854
Db      16  AAGGCTGGGTGGATC 1

RESULT 112
LOCUS       AX762887/c            17 bp    DNA          linear      PAT 25-JUN-2003
DEFINITION   Sequence 6208 from Patent WO03040369.
ACCESSION   AX762887
VERSION     AX762887.1  GI:32257503
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman, A., Amson, R. and Tuijinder, M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 6208 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      839  AAGCGCGGGTGGATC 854
Db      16  AAGGCTGGGTGGATC 1

RESULT 113
LOCUS       AX132090/c            19 bp    DNA          linear      PAT 15-MAY-2001
DEFINITION   Sequence 3308 from Patent WO0130362.
ACCESSION   AX132090
VERSION     AX132090.1  GI:14138395
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens

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ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Robbins, J.M. and Tritz, R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
JOURNAL     Patent: WO 0130362-A 3308 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES    Location/Qualifiers
            source
            1..19
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Cyclin B1 ribozyme binding site"
Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      791  CTGCTTGGAGAGGCAG 806
Db      19  GGGCTTGGAGAGGCAG 4

RESULT 114
LOCUS       BD266785             20 bp    DNA          linear      PAT 17-JUL-2003
DEFINITION   Methods for treating cancer and for mediating chemotaxis of
            dendritic cells.
ACCESSION   BD266785
VERSION     BD266785.1  GI:33076553
KEYWORDS    JP 2002533402-A/5.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Keting, C., Xin, H., Chan, V.W.F., Kothakota, S., Williams, L.T. and
            Winter, J.A.
TITLE       Methods for treating cancer and for mediating chemotaxis of
            dendritic cells
JOURNAL     Patent: JP 2002533402-A 5 08-OCT-2002;
            CHIRON CORP
COMMENT     OS Artificial Sequence
            PN JP 2002533402-A/5
            PD 08-OCT-2002
            PF 28-DEC-1999 JP 2000590657
            PR 31-DEC-1998 US 60/114498
            PI CHU KETING,HONG XIN,VIVIEN W F CHAN,SRINIVAS
            KOTHAKOTA,LEWIS T
            PI WILLIAMS,
            PI JILL A WINTER
            PC
            A61K38/00,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
            A61P35/00,
            PC A61P37/00,A61P43/00,C07K14/47//C12N15/02,A61K37/02,C12N15/00
            CC PCR Primer
            FH Key
            FT source
            1..20
                Location/Qualifiers
                /organism="Artificial Sequence".
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      781  GCTTGGGATGTGCTT 796
Db      2   GCTTGGTGTGTGCTT 17

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receptor-1 expression
JOURNAL Patent: US 6710174-A 37 23-MAR-2004;
FEATURES Location/Qualifiers
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 1..3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 626 GTTTTATCTCAGCAA 641
Db 4 GTTTTATGCTCAGCAA 19

RESULT 118
AR565745/c
LOCUS AR565745 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 91 from patent US 6767739.
ACCESSION AR565745
VERSION AR565745.1 GI:53981799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Crooke,R.M. and Graham,M.J.
TITLE Antisense modulation of microsomal triglyceride transfer protein
JOURNAL expression
FEATURES Patent: US 6767739-A 91 27-JUL-2004;
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 1..3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 130 TCTTATGCTGGCATGT 145
Db 18 TCTTATGCTGGCATGT 3

RESULT 119
BD185951
LOCUS BD185951 19 bp DNA linear PAT 17-JUN-2003
DEFINITION A stabilization method and a preservation method for a reagent for
    nucleic acid amplification or detection reaction.
ACCESSION BD185951.1 GI:31878151
VERSION WO 02101042-A/147.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Sagawa,H., Uemori,T., Mukai,H., Yamamoto,J., Tomono,J.,
    Kobayashi,E., Enoki,T., Asada,K. and Kato,I.
TITLE A stabilization method and a preservation method for a reagent for
    nucleic acid amplification or detection reaction
JOURNAL Patent: WO 02101042-A 147 19-DEC-2002;
    TAKARA BIO INC,HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO
    YAMAMOTO, JUN TOMONO,EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO
    ASADA,IKUNOSHIN KATO
COMMENT OS Artificial Sequence
    PN WO 02101042-A/147
    PD 19-DEC-2002
    PF 12-JUN-2002 WO 2002JP005832
    PR 12-JUN-2001 JP 01P 177737,20-AUG-2001 JP 01P 249689 PI
    HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO YAMAMOTO, PI
    JUN TOMONO,
    EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO ASADA,IKUNOSHIN KATO PC
    PI

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RESULT 115
AR295060
LOCUS AR295060 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6795 from patent US 6537751.
ACCESSION AR295060
VERSION AR295060.1 GI:31682344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
    disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6795 25-MAR-2003;
FEATURES Location/Qualifiers
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 1..3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 218 TTCTTGGCCAAAGAG 233
Db 5 TTCTTGGCCAAAGAG 20

RESULT 116
AR311266/c
LOCUS AR311266 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1803 from patent US 6559294.
ACCESSION AR311266
VERSION AR311266.1 GI:31704692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Hojseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
    Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1803 06-MAY-2003;
FEATURES Location/Qualifiers
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 1..3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 287 TTCCTACTGGGAATTG 302
Db 19 TTCCTACTGGGAATTG 4

RESULT 117
AR489914
LOCUS AR489914 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 37 from patent US 6710174.
ACCESSION AR489914
VERSION AR489914.1 GI:47257027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Watt,A.T.
TITLE Antisense inhibition of vascular endothelial growth factor

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C12N15/09,C12Q1/68
CC Designed oligonucleotide probe as Mycol70-probe to detect a
CC DNA fragment
CC amplifying a portion of ATPase operon from Mycoplasma CC
pneumoniae.
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial Sequence'.
FEATURES
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        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1064 CCAGTGGCTAACCACTTA 1082
DB 1 CCAGAGGCTGAACCACTTA 19
RESULT 120
BD004746 19 bp DNA linear PAT 31-JAN-2002
LOCUS BD004746 Method for detecting specific nucleic acid sequence.
ACCESSION BD004746
VERSION BD004746.1 GI:18632707
KEYWORDS JP 2001013147-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ishiguro,T., Otsuka,M., Inoue,T., Yahata,H. and Sugiur,Y.
TITLE Method for detecting specific nucleic acid sequence
JOURNAL Patent: JP 2001013147-A 4 19-JAN-2001;
TOSOH CORP
COMMENT OS Artificial Sequence
PN JP 2001013147-A/4
PD 19-JAN-2001
PF 22-MAY-2000 JP 2000154431
PR TAKAHIKO ISHIGURO,MASAMI OTSUKA,TERUHIKO INOUE,HIDEO YAHATA,
PI YUKIO SUGIURA
PC G01N33/566,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/536,
PC C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..19
FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"
FEATURES
    source
        Location/Qualifiers
            1..19
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 189 TTTTCCAGCCATCTCCCC 207
DB 1 TTTTCTCTCTCCCTCTCCCC 19
RESULT 121
A36286/c 20 bp DNA linear PAT 04-MAR-1997
LOCUS A36286 Sequence 9 from Patent EP0574345.
DEFINITION A36286
ACCESSION A36286
VERSION A36286.1 GI:2293718
KEYWORDS
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unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bardosa,N.N., De,B.B., Borja,T.M., Pons,A.F. and Torres,P.V.
TITLE Procedure for the detection and identification of viral and
subviral pathogens
JOURNAL Patent: EP 0574345-A 9 15-DEC-1993;
COMMENT INST NACIONAL DE INVESTIGACION (IS)
Other publication JP 6062900 940308
Other publication AU 4120093 931223
Other publication CA 2098270 931213
Other publication ES 2044784 940101.
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 857 TCTTTGTCTTGTACTCCAT 875
DB 19 TCTTTGTCTTGTCTGCCAT 1
RESULT 122
AR011463 20 bp DNA linear PAT 04-DEC-1998
LOCUS AR011463 Sequence 336 from patent US 5762938.
DEFINITION AR011463
ACCESSION AR011463
VERSION AR011463.1 GI:3969453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Paoletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,W.I., Audonnet,J.-C.Francis. and Gettig,R.Robert.
TITLE Modified recombinant vaccinia virus and expression vectors thereof
JOURNAL Patent: US 5762938-A 336 09-JUN-1998;
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 394 CATTTTCCTTACATTCAA 412
DB 1 CATGTCTCTTCAAGTCAA 19
RESULT 123
AR071524/c 20 bp DNA linear PAT 18-FEB-2000
LOCUS AR071524 Sequence 24 from patent US 5911982.
DEFINITION AR071524
ACCESSION AR071524
VERSION AR071524.1 GI:7222412
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chao,Y.-C.
TITLE H2-1 virus persistence-associated-gene 1 (PAG1) promoter usage
thereof, and compositions containing same or products therefrom
JOURNAL Patent: US 5911982-A 24 15-JUN-1999;
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FEATURES             source
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 566 TTTTAAATACCTTATAT 584
    |||||||
Db 19 TTGTTAAATACCTTGGTT 1

RESULT 124
AR076721/c
LOCUS          20 bp      DNA      linear      PAT 30-AUG-2000
DEFINITION     Sequence 86 from patent US 5959096.
ACCESSION      AR076721
VERSION        AR076721.1 GI:10003467
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Bennett,C.Frank. and Dean,N.
TITLE         Antisense oligonucleotides against human protein kinase C
JOURNAL       Patent: US 5959096-A 86 28-SEP-1999;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTAGCT 452
    |||||
Db 19 AGAGAAGAGGATTTGGCT 1

RESULT 125
AR103292/c
LOCUS          20 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION     Sequence 12 from patent US 6087173.
ACCESSION      AR103292
VERSION        AR103292.1 GI:12814880
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.
TITLE         Antisense modulation of X-linked inhibitor of apoptosis expression
JOURNAL       Patent: US 6087173-A 12 11-JUL-2000;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 426 TATTTGGAAGAGGATGA 444
    |||||
Db 20 TATTTTCAGAGAAGATGA 2

RESULT 126
BD144123/c
LOCUS          20 bp      DNA      linear      PAT 17-JAN-2003

DEFINITION     Cell cycle regulatory protein.
ACCESSION      BD144123
VERSION        BD144123.1 GI:27849881
KEYWORDS       JP 2002101891-A/6.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Yamaguchi,T. and Tajima,M.
TITLE         Cell cycle regulatory protein
JOURNAL       Patent: JP 2002101891-A 6 09-APR-2002;
COMMENT        NIPPON SHINYAKU CO LTD
              OS Artificial Sequence
              PN JP 2002101891-A/6
              PD 09-APR-2002
              PF 02-OCT-2000 JP 200302674
              PI TORU YAMAGUCHI,MASAYA TAJIMA
              PC C12N15/09,A61K31/711,A61K39/395,A61K45/00,A61P9/10,
              PC A61P11/00,
              PC A61P13/08,A61P13/12,A61P29/00,A61P35/00,A61P37/02,C07K14/47,
              PC C07K16/18,
              PC
              C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,G01N33/15,G01N33/ PC
              50//
              PC A61K48/00,C12P21/08,(C12P21/02,C12R1.91),C12N15/00,C12N5/00 CC
              Designed primer based on nucleotide sequence of Human SKP2 CC
              mRNA.
              FH Key Location/Qualifiers
              FT source 1..20
              /organism='Artificial Sequence'.
              Location/Qualifiers
              1..20
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1079 CTTAACCTCTCTGGGTGT 1097
    |||||||
Db 19 CTGACCTCTCTGGGTGT 1

RESULT 127
BD174726
LOCUS          20 bp      DNA      linear      PAT 18-MAR-2003
DEFINITION     Novel cytochrome P450 and gene encoding the same.
ACCESSION      BD174726
VERSION        BD174726.1 GI:29120418
KEYWORDS       JP 2002253248-A/5.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Wariishi,H., Tanaka,H., Ichinose,H. and Okada,K.
TITLE         Novel cytochrome P450 and gene encoding the same
JOURNAL       Patent: JP 2002253248-A 5 10-SEP-2002;
COMMENT        HIROYUKI WARIISHI,KUBOTA CORP
              OS Artificial Sequence
              PN JP 2002253248-A/5
              PD 10-SEP-2002
              PF 28-FEB-2001 JP 2001055452
              PI HIROYUKI WARIISHI,HIROO TANAKA,HIROFUMI ICHINOSE,KOICHI OKADA
              PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/02//A61K38/ PC
              44,
              PC A61P39/02,C07D319/24,C12N15/00,C12N5/00,A61K37/50 CC PCR
              Primer
              FH Key Location/Qualifiers
              FT source 1..20
              /organism='Artificial Sequence'.
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FEATURES
    source
        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Human LRH1 antisense"

Query Match
    Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 952 CCCACTCTGGACCCAGGAC 970
    ||||| ||||| |||||
Db 2 CCCACCAGGACCCAGGAC 20

RESULT 128
LOCUS BD176347 20 bp DNA linear PAT 18-MAR-2003
DEFINITION A method of arraying genome clone.
ACCESSION BD176347
VERSION BD176347.1 GI:29122053
KEYWORDS WO 02072815-A/147.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: WO 02072815-A 147 19-SEP-2002;
COMMENT EIICHI SOEDA, TAKESHI KUKITA
OS Artificial Sequence
PN WO 02072815-A/147
PD 19-SEP-2002
PF 17-MAY-2001 WO 2001JP004139
PI 12-MAR-2001 JP 01P 68285
PC C12N15/09,C12Q1/68
CC Description of Artificial Sequence: Synthetic DNA FH Key
FT source 1..20
FT Location/Qualifiers
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

FEATURES
    source
        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match
    Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 96 CATTATCTTCAGTGGGC 114
    ||||| ||||| |||||
Db 20 CATTAGCTACAGTGGGC 2

RESULT 129
LOCUS CQ763898 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 2516 from Patent WO2004003201.
ACCESSION CQ763898
VERSION CQ763898.1 GI:44907134
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrhl expression
JOURNAL Patent: WO 2004003201-A 2516 08-JAN-2004;
COMMENT Pharmacia Corporation (US)
OS Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Human LRH1 antisense"

Query Match
    Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 433 AAGAGGAGATCATTTTACC 451
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FEATURES
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        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Human LRH1 antisense"

Query Match
    Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 391 AGTCATTTTCCTTACAATT 409
    ||||| ||||| |||||
Db 1 AGTCATTTCCCTTAATATT 19

RESULT 130
LOCUS CQ764016 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 2634 from Patent WO2004003201.
ACCESSION CQ764016
VERSION CQ764016.1 GI:44907252
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrhl expression
JOURNAL Patent: WO 2004003201-A 2634 08-JAN-2004;
COMMENT Pharmacia Corporation (US)
OS Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Human LRH1 antisense"

Query Match
    Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 391 AGTCATTTTCCTTACAATT 409
    ||||| ||||| |||||
Db 2 AGTCATTTCCCTTAATATT 20

RESULT 131
LOCUS CQ764195 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 2813 from Patent WO2004003201.
ACCESSION CQ764195
VERSION CQ764195.1 GI:44907431
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrhl expression
JOURNAL Patent: WO 2004003201-A 2813 08-JAN-2004;
COMMENT Pharmacia Corporation (US)
OS Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Human LRH1 antisense"

Query Match
    Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 433 AAGAGGAGATCATTTTACC 451
    ||||| ||||| |||||

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Db      1  AATAGGCCATGATTTTAGC 19

RESULT 132
LOCUS   CQ764722                20 bp  DNA
DEFINITION   Sequence 3340 from Patent WO2004003201.
ACCESSION   CQ764722
VERSION     CQ764722.1  GI:44907958
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.

REFERENCE 1
AUTHORS    Kane,C.D.
TITLE      Antisense modulation of lrrh1 expression
JOURNAL    Patent: WO 2004003201-A 3340 08-JAN-2004;
            Pharmacia Corporation (US)
FEATURES   Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Human LRH1 antisense"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      433  AAGAGGAGATGATTTTAGC 451
          ||||| ||||| ||||| |||||
Db      2  AATAGGCCATGATTTTAGC 20

RESULT 133
LOCUS   I18101                20 bp  DNA
DEFINITION   Sequence 336 from patent US 5494807.
ACCESSION   I18101
VERSION     I18101.1  GI:1598456
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS    Paolletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
            Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
            Cox,W.I., Audonnet,J.-C.F. and Gettig,R.R.
TITLE      NYVAC vaccinia virus recombinants comprising heterologous inserts
JOURNAL    Patent: US 5494807-A 336 27-FEB-1996;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      394  CATTTCCTTACCAATTCAA 412
          ||||| ||||| ||||| |||||
Db      1  CATGTCCTTCAAGTCAA 19

RESULT 134
LOCUS   I83386/c              20 bp  DNA
DEFINITION   Sequence 9 from patent US 5714312.
ACCESSION   I83386
VERSION     I83386.1  GI:3406916
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.

Unassigned.
1 (bases 1 to 20)
Nuno Bardosa Nolasco,G., De Blas Beorlegui,C., Borja Tome,M.Jose.,
Pons Ascaso,F. and Torres Pascual,V.
Procedure for the detection and identification of viral and
subviral pathogens
Patent: US 5714312-A 9 03-FEB-1998;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      857  TCTTTGTGTGCTAGTCCAT 875
          ||||| ||||| ||||| |||||
Db      19  TCTTTGTGCTGCTGCCAT 1

RESULT 135
LOCUS   AR182778/c            20 bp  DNA
DEFINITION   Sequence 86 from patent US 6339066.
ACCESSION   AR182778
VERSION     AR182778.1  GI:20225985
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS    Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE      Antisense oligonucleotides which have phosphorothioate linkages of
            high chiral purity and which modulate .beta.I., .beta.II., .gamma.,
            .delta., .EPSILON., .zeta. and .eta. isoforms of human protein
            kinase C
JOURNAL    Patent: US 6339066-A 86 15-JAN-2002;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      434  AGAGGAGATGATTTTAGCT 452
          ||||| ||||| ||||| |||||
Db      19  AGAGAGAGAGATTTTGCT 1

RESULT 136
LOCUS   AR212037              20 bp  DNA
DEFINITION   Sequence 4 from patent US 6399379.
ACCESSION   AR212037
VERSION     AR212037.1  GI:21515517
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS    Baker,B.F. and Freier,S.M.
TITLE      Antisense modulation of interleukin 12 p35 subunit expression
JOURNAL    Patent: US 6399379-A 4 04-JUN-2002;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;

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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 822 GCCTCTCATGACCCAGGAA 840
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 Db 1 GCCACTCCAGACCCAGGAA 19

RESULT 137

AR272138/c
 LOCUS AR272138 20 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 208 from patent US 6503756.
 ACCESSION AR272138
 VERSION AR272138.1 GI:29703706

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Freier,S.M. and Wyatt,J.

TITLE Antisense modulation of syntaxin 4 interacting protein expression

JOURNAL Patent: US 6503756-A 208 07-JAN-2003;

FEATURES Location/Qualifiers

1..20

source /organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 932 AGAATCGAGATCTGAAG 950

||||| ||||| ||||| |||||

Db 19 AGAACTCCAGATGTGAAG 1

RESULT 138

AR297674/c
 LOCUS AR297674 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 9409 from patent US 6537751.
 ACCESSION AR297674
 VERSION AR297674.1 GI:31684958

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.

TITLE Biallelic markers for use in constructing a high density

JOURNAL disequilibrium map of the human genome

Patent: US 6537751-A 9409 25-MAR-2003;

FEATURES Location/Qualifiers

1..20

source /organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 427 ATTTCGAGAGGAGATGAT 445

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Db 19 AGTTGGAGGGGAGATGAT 1

RESULT 139

AR300858/c
 LOCUS AR300858 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 86 from patent US 6537973.
 ACCESSION AR300858
 VERSION AR300858.1 GI:31688425

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.

TITLE Biallelic markers for use in constructing a high density

JOURNAL disequilibrium map of the human genome

Patent: US 6537751-A 9409 25-MAR-2003;

FEATURES Location/Qualifiers

1..20

source /organism="unknown"

/mol_type="genomic DNA"

Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett,C.F., Dean,N.M., Holmlund,J.T. and Dorr,F.A.

TITLE Oligonucleotide inhibition of protein kinase C

JOURNAL Patent: US 6537973-A 86 25-MAR-2003;

FEATURES Location/Qualifiers

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source /organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGAGAGATGATTTAGCT 452

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Db 19 AGAGAAGAGGATTTGGCT 1

RESULT 140

AR311588
 LOCUS AR311588 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 2125 from patent US 6559294.
 ACCESSION AR311588
 VERSION AR311588.1 GI:31705014

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,

Sankaran,B. and Fletcher,L.D.

TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 2125 06-MAY-2003;

FEATURES Location/Qualifiers

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source /organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 AGAATCTGAAGCCCACTC 958

||||| ||||| ||||| |||||

Db 1 AGAATCGGAAACCCACGC 19

RESULT 141

AR313584
 LOCUS AR313584 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 4121 from patent US 6559294.
 ACCESSION AR313584
 VERSION AR313584.1 GI:31707010

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,

Sankaran,B. and Fletcher,L.D.

TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 4121 06-MAY-2003;

FEATURES Location/Qualifiers

1..20

source /organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 771 GAAACCTTTGCTGGGGA 789

Fri Aug 19 10:59:59 2005

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AUTHORS   Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL   Patent: US 6559294-A 5159 06-MAY-2003;
FEATURES   Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 460 GTGTAGCACTTTTATCTG 478
Db 2 GTGTAGCACTATAACCTG 20

RESULT 145
LOCUS      AR401413
DEFINITION Sequence 12 from patent US 6623931.
ACCESSION  AR401413
VERSION     AR401413.1 GI:40148727
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Atkinson, R.M. and Tuomanen, E.I.
TITLE      Diagnostic assay for antibiotic tolerance
JOURNAL    Patent: US 6623931-A 12 23-SEP-2003;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 ATTGAATTTCTTAGAATC 507
Db 1 ATTGATTTCTTCTAATC 19

RESULT 146
LOCUS      AR560731
DEFINITION Sequence 79 from patent US 6756200.
ACCESSION  AR560731
VERSION     AR560731.1 GI:53973070
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Sukumar, S., Evron, E., Dooley, W.C., Sacchi, N. and Davidson, N.
TITLE      Aberrantly methylated genes as markers of breast malignancy
JOURNAL    Patent: US 6756200-A 79 29-JUN-2004;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGGCGTTT 167
Db 1 TTCGAGTTTATGGCGTTT 19

AUTHORS   Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL   Patent: US 6559294-A 5159 06-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAAATGTTGTTTC 309
Db 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 142
LOCUS      AR314622
DEFINITION Sequence 5159 from patent US 6559294.
ACCESSION  AR314622
VERSION     AR314622.1 GI:31708048
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE      Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL    Patent: US 6559294-A 5159 06-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAAATGTTGTTTC 309
Db 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 143
LOCUS      AR314629
DEFINITION Sequence 5166 from patent US 6559294.
ACCESSION  AR314629
VERSION     AR314629.1 GI:31708055
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE      Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL    Patent: US 6559294-A 5166 06-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAAATGTTGTTTC 309
Db 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 144
LOCUS      AR316044
DEFINITION Sequence 6581 from patent US 6559294.
ACCESSION  AR316044
VERSION     AR316044.1 GI:31709470
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)

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RESULT 147
AX101073/c
LOCUS AX101073 20 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 47 from Patent WO0121822.
ACCESSION AX101073
VERSION AX101073.1 GI:13619929
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Dean, C. and Levy, Y.Y.
TITLE Methods and means for modification of plant flowering characteristics
JOURNAL Patent: WO 0121822-A 47 29-MAR-2001;
Plant Bioscience Limited (GB)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 448 TAGCTGGGAGCAGTGTAG 466
|||||
Db 19 TAGGTGGGAAGTGTGTAG 1
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 448 TAGCTGGGAGCAGTGTAG 466
|||||
Db 19 TAGGTGGGAAGTGTGTAG 1
RESULT 148
AX259829/c
LOCUS AX259829 20 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 56 from Patent WO0172822.
ACCESSION AX259829
VERSION AX259829.1 GI:16508903
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Hugot, J.P., Thomas, G., Zouali, M., Leage, S. and Chamailard, M.
TITLE Genes involved in intestinal inflammatory diseases and use thereof
JOURNAL Patent: WO 0172822-A 56 04-OCT-2001;
Fondation Jean Dausset-Ceph (FR)
FEATURES
source
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 776 CTTGTGCTGGGATGTC 794
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Db 20 CTTGTGCTGGGATGTC 2
RESULT 149
AX590749/c
LOCUS AX590749 20 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 189 from Patent WO02086113.
ACCESSION AX590749
VERSION AX590749.1 GI:27949298
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

other sequences; artificial sequences.
REFERENCE
1
AUTHORS Cookson, W.O., Moffat, M.F., Allen, M. and Lench, N.
TITLE Enzyme and snp marker for disease
JOURNAL Patent: WO 02086113-A 189 31-OCT-2002;
Isis Innovation Limited (GB)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 472 TATTCGTGATTACAGTGCAT 490
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Db 19 TGTTCGTGTTACAATGCAT 1
RESULT 150
AX601142/c
LOCUS AX601142 20 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 237 from Patent WO02092851.
ACCESSION AX601142
VERSION AX601142.1 GI:28401215
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Binns, M.M. and Swinburne, J.E.
TITLE Genetic typing
JOURNAL Patent: WO 02092851-A 237 21-NOV-2002;
ANIMAL HEALTH TRUST (GB); The British Horseracing Board (GB)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 317 GGATTCCTGTTATTCCTG 335
|||||
Db 19 GGATTCCTGTTGCTTG 1
RESULT 151
AX804893
LOCUS AX804893 20 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 1061 from Patent WO03060160.
ACCESSION AX804893
VERSION AX804893.1 GI:38522034
KEYWORDS Oreochromis niloticus (Nile tilapia)
SOURCE Oreochromis niloticus
ORGANISM Oreochromis niloticus
REFERENCE
1
AUTHORS Lie, Y., Slettan, A., Hoeyum, M. and Lingaas, F.
TITLE Verification of food origin based on nucleic acid pattern recognition
JOURNAL Patent: WO 03060160-A 1061 24-JUL-2003;
Genomar ASA (NO)
FEATURES
Location/Qualifiers

Fri Aug 19 10:59:59 2005

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source
1. .20
/organism="Oreochromis niloticus"
/mol_type="unassigned DNA"
/db_xref="taxon:8128"

Query Match
Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 782 CTTGGGATGCTTGGAG 800
||||| ||||| |||||
Db 2 CTTGGGTTGAGCTTGGAG 20

RESULT 152
AX815889/c
LOCUS
DEFINITION
Sequence 144 from Patent WO0306891.
ACCESSION
AX815889.1 GI:39646569
KEYWORDS
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1
Hardge,T., Schellander,K. and Wimmers,K.
Genetic markers for the diagnosis of the expression of inverted
nipples in pets, breeding animals and domestic cattle
Patent: WO 0306891-A 144 14-AUG-2003;
Foerderverein Biotechnologieforschung der deutschen
Schweineproduktion e.V. (DE)
Location/Qualifiers
1. .20
/organism="Sus scrofa"
/mol_type="unassigned DNA"
/db_xref="taxon:9823"

Query Match
Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 406 AATCAAGGTTTTCCTT 424
||||| ||||| |||||
Db 19 AACTCAAGGGTTTGCCCT 1

RESULT 153
BD016085/c
LOCUS
DEFINITION
Oligonucleotide modulation of protein kinase C-epsilon.
ACCESSION
BD016085
VERSION
BD016085.1 GI:22557223
KEYWORDS
JP 2001224386-A/94.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
Bennett,F.C., Boggs,R.T. and Dean,N.M.
Oligonucleotide modulation of protein kinase C-epsilon
Patent: JP 2001224386-A 94 21-AUG-2001;
ISIS PHARMACEUTICALS INC
OS
Artificial Sequence
PN
JP 2001224386-A/94
PD
21-AUG-2001
PF
13-DEC-2000 JP 2000379218
PR
09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09,A61K48/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,PC
G01N33/53.
PC
G01N33/566,G01N33/573//A61K31/711,A61K31/712,A61K31/7125,PC
A61P35/00,
PC
A61P43/00,A61P43/00,C12N5/10,C12N15/00,C12N5/00 CC synthetic

source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGTATTTAGCT 452
||||| ||||| |||||
Db 19 AGAGAGAGGATTTTGCT 1

RESULT 155
BD017356/c
LOCUS
DEFINITION
Oligonucleotide modulation of protein kinase C-eta.
ACCESSION
BD017356
VERSION
BD017356.1 GI:22558532
KEYWORDS
JP 2001231579-A/94.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.

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REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-eta
JOURNAL Patent: JP 2001231579-A 94 28-AUG-2001;
        ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
        PN JP 2001231579-A/94
        PD 28-AUG-2001
        PF 13-DEC-2000 JP 2000379234
        PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
        FRANK C BENNETT,RUSSELL T BOGGS,NICHOLAS M DEAN PC
        C12N15/09,A61K31/711,A61K31/712,A61K31/7125,A61K48/00,A61P29/ PC
        00,A61P35/00,
        PC A61P43/00,C07H21/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
        G01N33/50,
        PC G01N33/53,G01N33/566//C12N5/10,G01N33/68,C12N15/00,C12N5/00 CC
        synthetic
        FH Key Location/Qualifiers
        FT source 1..20 /organism='Artificial Sequence'.
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTAGCT 452
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Db 19 AGAGAAGAGGATTTGGCT 1

RESULT 156
BD089267/c
LOCUS A method of arraying genome clone. 20 bp DNA linear PAT 27-AUG-2002
DEFINITION
ACCESSION BD089267
VERSION BD089267.1 GI:22634877
KEYWORDS JP 2001321190-A/1511.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1511 20-NOV-2001;
        THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
        GENOTECHS
COMMENT OS Artificial Sequence
        PN JP 2001321190-A/2513
        PD 20-NOV-2001
        PF 12-MAR-2001 JP 2001068285
        PI EIICHI SOEDA
        PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
        C12N15/00,
        PC C12N15/00
        CC Description of Artificial Sequence:Synthetic DNA FH Key
        FT source 1..20
        FT Location/Qualifiers
            1..20
            /organism='Artificial Sequence'.
            Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 96 CATTATCCTTCAGTGGGC 114
    ||||| ||||| ||||| |||||
Db 20 CATTAGCCTACAGTGGGC 2

RESULT 158
CQ860131
LOCUS Sequence 43 from Patent WO2004072293. 14 bp DNA linear PAT 10-SEP-2004
DEFINITION
ACCESSION CQ860131
VERSION CQ860131.1 GI:51982019
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
        protein and method for detection of compounds modifying the
        interaction between the proteins of the ob-rgrp family and the
        leptin receptor
        Patent: WO 2004072293-A 43 26-AUG-2004;
        Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
        RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
        Scientifique (CNRS) (FR)
JOURNAL
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

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ORGANISM UNKNOWN.
Unclassified.
REFERENCE 1 (bases 1 to 15)


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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.3%; Score 14; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 ATTTGATGAGATC 984
|||||
Db 14 ATTTGATGAGATC 1

RESULT 163
LOCUS AR293818 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5553 from patent US 6537751.
ACCESSION AR293818
VERSION AR293818.1 GI:31681102
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 553 25-MAR-2003;
FEATURES
Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 14; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ATCTCCCCCATCCC 213
|||||
Db 5 ATCTCCCCCATCCC 18

RESULT 164
LOCUS AR292450/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4185 from patent US 6537751.
ACCESSION AR292450
VERSION AR292450.1 GI:31679734
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 4185 25-MAR-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 14; DB 1; Length 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 TCGGTTTTTAATA 575
|||||
Db 19 TCGGTTTTTAATA 6

RESULT 165
LOCUS AR293889 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5624 from patent US 6537751.
ACCESSION AR293889
VERSION AR293889.1 GI:31681173
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 5624 25-MAR-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 14; DB 1; Length 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTGTTATCTTGCT 337
|||||
Db 4 CTGTTATCTTGCT 17

RESULT 166
LOCUS AR432356 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 156 from patent US 6653133.
ACCESSION AR432356
VERSION AR432356.1 GI:40194629
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Marcussen,E.G. and Wyatt,J.
TITLE Antisense modulation of Fas mediated signaling
JOURNAL Patent: US 6653133-A 156 25-NOV-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 14; DB 1; Length 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
|||||
Db 18 AGATGAGTTTATT 5

RESULT 167
LOCUS AR542543 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 55 from patent US 6743909.
ACCESSION AR542543
VERSION AR542543.1 GI:53935031
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cowser,L.M. and Dobie,K.W.
TITLE Antisense modulation of PTPN12 expression
JOURNAL Patent: US 6743909-A 55 01-JUN-2004;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
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<p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>LOCUS AX467285/c DEFINITION Sequence 11 from Patent WO0231142. ACCESSION AX467285 VERSION AX467285.1 GI:21900563 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences.</p> <p>REFERENCE 1 AUTHORS Kronenwett, R., Graef, T., Haas, R. and Nedbal, W. TITLE Antisense nucleic acid against alphav integrin JOURNAL Patent: WO 0231142-A 11 18-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) FEATURES Location/Qualifiers 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Antisense ODN directed against alphav integrin chain"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 417 TTTTCCTTATATT 430 Db 17 TTTTCCTTATATT 4</p> <p>RESULT 169 AX467281/c LOCUS DEFINITION Sequence 7 from Patent WO0231142. ACCESSION AX467281 VERSION AX467281.1 GI:21900559 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences.</p> <p>REFERENCE 1 AUTHORS Kronenwett, R., Graef, T., Haas, R. and Nedbal, W. TITLE Antisense nucleic acid against alphav integrin JOURNAL Patent: EP 1197553-A 7 17-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) FEATURES Location/Qualifiers 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Antisense ODN directed against alphav integrin chain"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 417 TTTTCCTTATATT 430 Db 17 TTTTCCTTATATT 4</p> <p>RESULT 168 AX467281/c LOCUS DEFINITION Sequence 7 from Patent WO0231142. ACCESSION AX467281 VERSION AX467281.1 GI:21900559 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences.</p> <p>REFERENCE 1 AUTHORS Kronenwett, R., Graef, T., Haas, R. and Nedbal, W. TITLE Antisense nucleic acid against alphav integrin JOURNAL Patent: WO 0231142-A 7 18-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) FEATURES Location/Qualifiers 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Antisense ODN directed against alphav integrin chain"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 417 TTTTCCTTATATT 430 Db 17 TTTTCCTTATATT 4</p>	<p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>LOCUS AX467285/c DEFINITION Sequence 11 from Patent WO0231142. ACCESSION AX467285 VERSION AX467285.1 GI:21900563 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences.</p> <p>REFERENCE 1 AUTHORS Kronenwett, R., Graef, T., Haas, R. and Nedbal, W. TITLE Antisense nucleic acid against alphav integrin JOURNAL Patent: WO 0231142-A 11 18-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) FEATURES Location/Qualifiers 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Antisense ODN directed against alphav integrin chain"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 417 TTTTCCTTATATT 430 Db 17 TTTTCCTTATATT 4</p> <p>RESULT 171 AX815827 LOCUS DEFINITION Sequence 82 from Patent WO03066891. ACCESSION AX815827 VERSION AX815827.1 GI:39646507 KEYWORDS Sus scrofa (pig) SOURCE Sus scrofa ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.</p> <p>REFERENCE 1 AUTHORS Hardge, T., Schellander, K. and Wimmers, K. TITLE Genetic markers for the diagnosis of the expression of inverted nipples in pets, breeding animals and domestic cattle JOURNAL Patent: WO 03066891-A 82 14-AUG-2003; Foerderverein Biotechnologieforschung der deutschen Schweineproduktion e.V. (DE) FEATURES Location/Qualifiers 1..20 /organism="Sus scrofa" /mol_type="unassigned DNA" /db_xref="taxon:9823"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 894 CACAGACCAGGC 907 Db 2 CACAGACCAGGC 15</p> <p>RESULT 172 AR083038/c LOCUS DEFINITION Sequence 64 from patent US 5976798. ACCESSION AR083038 VERSION AR083038.1 GI:10009828 KEYWORDS Unknown. SOURCE</p>	<p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>LOCUS AX467281/c DEFINITION Sequence 7 from Patent WO0231142. ACCESSION AX467281 VERSION AX467281.1 GI:21900559 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences.</p> <p>REFERENCE 1 AUTHORS Kronenwett, R., Graef, T., Haas, R. and Nedbal, W. TITLE Antisense nucleic acid against alphav integrin JOURNAL Patent: WO 0231142-A 7 18-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) FEATURES Location/Qualifiers 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Antisense ODN directed against alphav integrin chain"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 417 TTTTCCTTATATT 430 Db 17 TTTTCCTTATATT 4</p> <p>RESULT 169 AX467281/c LOCUS DEFINITION Sequence 7 from Patent WO0231142. ACCESSION AX467281 VERSION AX467281.1 GI:21900559 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences.</p> <p>REFERENCE 1 AUTHORS Kronenwett, R., Graef, T., Haas, R. and Nedbal, W. TITLE Antisense nucleic acid against alphav integrin JOURNAL Patent: WO 0231142-A 7 18-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) FEATURES Location/Qualifiers 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Antisense ODN directed against alphav integrin chain"</p> <p>Query Match Best Local Similarity 1.3%; Score 14; DB 1; Length 20; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 417 TTTTCCTTATATT 430 Db 17 TTTTCCTTATATT 4</p>
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Parker,W.Davis., Hernstadt,C., Ghosh,S. and Fahy,E.D.
TITLE Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid
JOURNAL Patent: US 5976798-A 64 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

RESULT 173
AR124365/c
LOCUS AR124365 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 140 from patent US 6171859.
ACCESSION AR124365
VERSION AR124365.1 GI:14109726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hernstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 140 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

RESULT 174
AR124376/c
LOCUS AR124376 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 151 from patent US 6171859.
ACCESSION AR124376
VERSION AR124376.1 GI:14109737
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hernstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 151 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

Qy 562 TGGGTTTTTAAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

RESULT 175
AR124410/c
LOCUS AR124410 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 185 from patent US 6171859.
ACCESSION AR124410
VERSION AR124410.1 GI:14109771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hernstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 185 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTAAATACCT 578
Db 17 TGGTTTTCTAATACCT 1

RESULT 176
AR124411/c
LOCUS AR124411 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 186 from patent US 6171859.
ACCESSION AR124411
VERSION AR124411.1 GI:14109772
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hernstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 186 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 563 GGGTTTTTAAATACCTT 579
Db 17 GGGTTTTCTAATACCTT 1

RESULT 177
AR124413/c
LOCUS AR124413 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 188 from patent US 6171859.
ACCESSION AR124413
VERSION AR124413.1 GI:14109774
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hernstadt,C. and Parker,W.Davis.

RESULT 179	DEFINITION
BD256418	ACCESSION
LOCUS	VERSION

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FT source 1. .17
FT /organism='Eukaryote'.
FEATURES
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        Location/Qualifiers
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 1.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 396 TTTTCTTACATTCAA 412
Db 1 TTTCTTACAACTCCA 17

RESULT 181
CQ617823/c
LOCUS CQ617823 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2563 from Patent WO0192524.
ACCESSION CQ617823
VERSION CQ617823.1 GI:41668041
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2563 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 745 GCAGCTGCCACCTTATG 761
Db 17 GCAGCTGCCGCTTCTG 1

RESULT 182
CQ617824/c
LOCUS CQ617824 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2564 from Patent WO0192524.
ACCESSION CQ617824
VERSION CQ617824.1 GI:41668042
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2564 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
    source
        1. .17
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 744 GCAGCTGCCACCTTAT 760
Db 17 GCAGCTGCCGCTTCT 1

RESULT 183
CQ622009
LOCUS CQ622009 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 6749 from Patent WO0192524.
ACCESSION CQ622009
VERSION CQ622009.1 GI:41672227
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6749 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
    source
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 836 AGGAGGCCGCGGTGGA 852
Db 1 AGGAAGGCCGCGGAGGA 17

RESULT 184
CQ62376/c
LOCUS CQ62376 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5565323.
ACCESSION CQ62376
VERSION CQ62376.1 GI:1818152
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 17)
Parker,W.Davis. and Herrnstadt,C.
TITLE Cytochrome oxidase mutations aiding diagnosis of sporadic
alzheimer's disease
JOURNAL Patent: US 5565323-A 12 15-OCT-1996;
Aeomica, Inc. (US)
FEATURES
    source
        1. .17
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGCTTTTCTTAATACCT 578
Db 17 TGGTTTCTTAATACCT 1

RESULT 185
CQ62376/c
LOCUS CQ62376 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2563 from patent US 6686188.

```

ACCESSION AR458886
 VERSION AR458886.1 GI:42693943
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 2563 03-FEB-2004;
 FEATURES
 Location/Qualifiers
 source
 1..17
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 745 GCAGCTGCCACCTTATG 761
 Db |||||||
 17 GCAGCTGCCCTTCTG 1
 RESULT 186
 LOCUS AR458887/c 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 2564 from patent US 6686188.
 ACCESSION AR458887
 VERSION AR458887.1 GI:42693944
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 2564 03-FEB-2004;
 FEATURES
 Location/Qualifiers
 source
 1..17
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 744 GCAGCTGCCACCTTAT 760
 Db |||||||
 17 GCAGCTGCCGCTTCT 1
 RESULT 187
 LOCUS AR463072 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 6749 from patent US 6686188.
 ACCESSION AR463072
 VERSION AR463072.1 GI:42698129
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 6749 03-FEB-2004;
 FEATURES
 Location/Qualifiers

source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 836 AGGAGGCGCGGTGGA 852
 Db |||||||
 1 AGGAGGCGCGGTGAGGA 17
 RESULT 188
 LOCUS AX217125/c 17 bp RNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2567 from Patent WO0159103.
 ACCESSION AX217125
 VERSION AX217125.1 GI:15527186
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL Patent: WO 0159103-A 2567 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
 FEATURES
 Location/Qualifiers
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 1..17
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 413 GGGTTTTCCTTATTT 429
 Db |||||||
 17 GAGTTTTCCTTATTT 1
 RESULT 189
 LOCUS AX259837 17 bp DNA linear PAT 26-OCT-2001
 DEFINITION Sequence 64 from Patent WO0172822.
 ACCESSION AX259837
 VERSION AX259837.1 GI:16508911
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Hugot, J.P., Thomas, G., Zouali, M., Lesage, S. and Chamailard, M.
 TITLE Genes involved in intestinal inflammatory diseases and use thereof
 JOURNAL Patent: WO 0172822-A 64 04-OCT-2001;
 Fondation Jean Dausset-Ceph (FR)
 FEATURES
 Location/Qualifiers
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 197 GCCATCTCCCCCATCCC 213

VERSION	AX502936.1	GI:23385229
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Zhan, J.	
TITLE	Human testis expressed patched like protein	
JOURNAL	Patent: EP 1229046-A 4243 07-AUG-2002;	
FEATURES	<p>Acemica, Inc. (US)</p> <p>Location/Qualifiers</p> <p>1. .17</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>	
source	<p>Query Match 1.2%; Score 13.8; DB 1; Length 17;</p> <p>Best Local Similarity 88.2%; Pred. No. 1.1e+02;</p> <p>Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>	
QY	673 AAATTATGTTACTTGGT 689	
DB	1 AGATTATGTTCTTGGT 17	
RESULT 193		
BD070507/c		
LOCUS	BD070507 17 bp DNA linear PAT 27-AUG-2002	
DEFINITION	Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid.	
ACCESSION	BD070507	
VERSION	BD070507.1 GI:22616110	
KEYWORDS	JP 2001514500-A/64.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Parker, W.D., Herrnstadt, C., Ghosh, S. and Fahy, E.D.	
TITLE	Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid	
JOURNAL	Patent: JP 2001514500-A 64 11-SEP-2001;	
COMMENT	MITOKOR	
OS	Unidentified	
PN	JP 2001514500-A/64	
PD	11-SEP-2001	
PF	27-FEB-1998 JP 1998537738	
PR	28-FEB-1997 US 08/810599	
PI	WILLIAM DAVIS PARKER, CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D.	
PI	FAHY	
PC	C1201/68,C07H21/04	
CC	Strandedness: Double;	
CC	Topology: Linear;	
CC	Methods for detecting mitochondrial mutations diagnostic for Alzheimer's	
CC	disease and methods for determining heteroplasmy of CC mitochondrial nucleic acid	
CC	acid	
CC	Location/Qualifiers	
FT	1. .17	
FT	Key source	
FT	source	
FEATURES	<p>Location/Qualifiers</p> <p>1. .17</p> <p>/organism="Unidentified".</p>	
source	<p>Query Match 1.2%; Score 13.8; DB 1; Length 17;</p> <p>Best Local Similarity 88.2%; Pred. No. 1.1e+02;</p> <p>Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>	

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 566 TTTTAAATACCTTAT 582
 |||||
 Db 17 TGTGTTTCTAATACCT 1

RESULT 194
 LOCUS BD104790 17 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD104790
 VERSION WO 0192572-A/894
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 894 06-DEC-2001;
 NISSHINO INDUSTRIES INC.SYTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA

COMMENT OS Artificial Sequence
 PN WO 0192572-A/894
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP OP 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,
 PI SHOGO MORIYA, MICHIO NISHIDA
 CC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
 PC Description of Artificial Sequence: capture
 FH Key Location/Qualifiers
 FT source 1..17
 FT Location/Qualifiers
 FT /organism='Artificial Sequence'.
 FT 1..17
 FT /organism='synthetic construct'
 FT /mol_type='genomic DNA'
 FT /db_xref='taxon:32630'

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 404 ACAATTCAAGGGTTTTT 420
 |||||
 Db 1 ACAATTACAGGGTTTTT 17

RESULT 195
 LOCUS AR071523 18 bp DNA linear PAT 18-FEB-2000
 DEFINITION Sequence 23 from patent US 5911982.
 ACCESSION AR071523
 VERSION AR071523.1 GI:7222411
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Chao,Y.-C.
 TITLE H2-1 virus persistence-associated-gene 1 (PAG1) promoter uses therefor, and compositions containing same or products therefrom
 JOURNAL Patent: US 5911982-A 23 15-JUN-1999;
 FEATURES Location/Qualifiers
 source 1..18
 /organism='unknown'
 /mol_type='unassigned DNA'

Query Match 1.2%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 566 TTTTAAATACCTTAT 582
 |||||
 Db 17 TGTGTTTCTAATACCT 1

RESULT 196
 LOCUS CQ799849 18 bp DNA linear PAT 28-APR-2004
 DEFINITION Sequence 499 from Patent WO2004031413.
 ACCESSION CQ799849
 VERSION CQ799849.1 GI:46848796
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences: artificial sequences.

REFERENCE 1
 AUTHORS Nakamura,Y., Daigo,Y. and Nakatsuru,S.
 TITLE Method for diagnosing non-small cell lung cancers
 JOURNAL Patent: WO 2004031413-A 499 15-APR-2004;
 Oncotherapy Science, Inc. (JP); Japan as represented by the president of the university of Tokyo (JP)

FEATURES Location/Qualifiers
 source 1..18
 /organism='synthetic construct'
 /mol_type='unassigned DNA'
 /db_xref='taxon:32630'
 /note='Artificially synthesized S-oligonucleotide sequence for antisense method'

Query Match 1.2%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 432 GAAGAGGAGATGATTTT 448
 |||||
 Db 18 GAGGAGGAATGATTTT 2

RESULT 197
 LOCUS CQ807685 18 bp DNA linear PAT 10-MAY-2004
 DEFINITION Sequence 1135 from Patent WO2004035803.
 ACCESSION CQ807685
 VERSION CQ807685.1 GI:47113079
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.
 TITLE Method and nucleic acids for the improved treatment of breast cell proliferative disorders
 JOURNAL Patent: WO 2004035803-A 1135 29-APR-2004;
 Epigenomics AG (DE)

FEATURES Location/Qualifiers
 source 1..18
 /organism='synthetic construct'
 /mol_type='unassigned DNA'
 /db_xref='taxon:32630'
 /note='Detection oligonucleotide for CDH1'

Query Match 1.2%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 152 GAGGATTATGCGTTTA 168
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 Db 1 GAGGGTTATCGGTTTA 17


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RESULT 198
127387/c
LOCUS      18 bp      DNA
DEFINITION Sequence 23 from patent US 5565323.
ACCESSION 127387
VERSION    127387.1 GI:1818163
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Parker,W.Davis, and Herrnstadt,C.
TITLE     Cytochrome oxidase mutations aiding diagnosis of sporadic
           alzheimer's disease
JOURNAL    Patent: US 5565323-A 23 15-OCT-1996;
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      562 TGGGTTTTTTTATACCT 578
Db      18 TGGTTTTTCTATACCT 2

RESULT 199
AR292997/c
LOCUS      18 bp      DNA
DEFINITION Sequence 4732 from patent US 6537751.
ACCESSION  AR292997
VERSION     AR292997.1 GI:31680281
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
           disequilibrium map of the human genome
JOURNAL    Patent: US 6537751-A 4732 25-MAR-2003;
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      905 AGCCTCAACATTTCCTA 921
Db      17 AGCCTCAGCATTTTCATA 1

RESULT 200
AR294306
LOCUS      18 bp      DNA
DEFINITION Sequence 6041 from patent US 6537751.
ACCESSION  AR294306
VERSION     AR294306.1 GI:31681590
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
           disequilibrium map of the human genome

JOURNAL    Patent: US 6537751-A 6041 25-MAR-2003;
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      204 CCCCCTATCCCCCATTTTC 220
Db      18 CCTCCATCCCCCATCTC 2

RESULT 202
AX181724
LOCUS      18 bp      DNA
DEFINITION Sequence 6 from Patent WO0146696.
ACCESSION  AX181724
VERSION     AX181724.1 GI:15133047
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
           Mushahwar,I.K.
TITLE      Methods and compositions for detecting hepatitis e virus
           Patent: WO 0146696-A 6 28-JUN-2001;
JOURNAL    ABBOTT LABORATORIES (US)
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Primer C375"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1035 TAAACATCACACCCCAAC 1051
Db      1035 TAAACATCACACCCCAAC 1051

JOURNAL    Patent: US 6537751-A 6041 25-MAR-2003;
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      942 AATCTGAAGCCCACTC 958
Db      2 AATCTCAACCCCACTC 18

RESULT 201
AR299617/c
LOCUS      18 bp      DNA
DEFINITION Sequence 11352 from patent US 6537751.
ACCESSION  AR299617
VERSION     AR299617.1 GI:31686901
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
           disequilibrium map of the human genome
JOURNAL    Patent: US 6537751-A 11352 25-MAR-2003;
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      204 CCCCCTATCCCCCATTTTC 220
Db      18 CCTCCATCCCCCATCTC 2

RESULT 202
AX181724
LOCUS      18 bp      DNA
DEFINITION Sequence 6 from Patent WO0146696.
ACCESSION  AX181724
VERSION     AX181724.1 GI:15133047
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
           Mushahwar,I.K.
TITLE      Methods and compositions for detecting hepatitis e virus
           Patent: WO 0146696-A 6 28-JUN-2001;
JOURNAL    ABBOTT LABORATORIES (US)
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Primer C375"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1035 TAAACATCACACCCCAAC 1051
Db      1035 TAAACATCACACCCCAAC 1051
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Db          2  TGAACATCACGCCCAAC 18

RESULT 203
AX705606
LOCUS      AX705606      18 bp      DNA      linear      PAT 04-APR-2003
DEFINITION Sequence 275 from Patent WO03014388.
ACCESSION  AX705606
VERSION     AX705606.1  GI:29562271
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE
AUTHORS    Distler,J., Model,F. and Taubert,H.
TITLE      Method and nucleic acids for the analysis of colon cancer
JOURNAL    Patent: WO 03014388-A 275 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES   source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for PCR"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 TAGGAGATGAGTTTAT 632
      |||||
Db 2 TAGGAGATGAGATTTT 18

RESULT 204
AX705608/c
LOCUS      AX705608      18 bp      DNA      linear      PAT 04-APR-2003
DEFINITION Sequence 277 from Patent WO03014388.
ACCESSION  AX705608
VERSION     AX705608.1  GI:29562273
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE
AUTHORS    Distler,J., Model,F. and Taubert,H.
TITLE      Method and nucleic acids for the analysis of colon cancer
JOURNAL    Patent: WO 03014388-A 277 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES   source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for PCR"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 TAGGAGATGAGTTTAT 632
      |||||
Db 17 TAGGAGATGAGATTTT 1

RESULT 205
AX837940/c
LOCUS      AX837940      18 bp      DNA      linear      PAT 15-DEC-2003
DEFINITION Sequence 5064 from Patent EP1347046.
ACCESSION  AX837940
VERSION     AX837940.1  GI:39921632
KEYWORDS   .
SOURCE      unidentified

```

```

ORGANISM      unidentified
               unclassified.
REFERENCE
AUTHORS       Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
               Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
               Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
               Masuko,Y.
TITLE         Full-length cDNA sequences
JOURNAL       Patent: EP 1347046-A 5064 24-SRP-2003;
               Research Association for Biotechnology (JP)
FEATURES      Location/Qualifiers
               source
               1..18
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               /note="Description of Artificial Sequence: an artificially
               synthesized primer se q"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 295 TGGATTGTTGTTCTG 311
      |||||
Db 18 TGGATTGTTGTTCTG 2

RESULT 206
BD077127
LOCUS      BD077127      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method and compositions for detecting hepatitis E virus.
ACCESSION  BD077127
VERSION     BD077127.1  GI:22622730
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE
AUTHORS     Schlauer,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
TITLE       Method and compositions for detecting hepatitis E virus
JOURNAL     Patent: JP 2001520384-A 6 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS Artificial Sequence
            PN JP 2001520384-A/6
            PD 30-OCT-2001
            PF 15-OCT-1998 JP 2000516232
            PR 15-OCT-1997 US 60/061199
            PI GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J PI
            DAWSON,
            PT ISA K MASHAWER
            PC G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC C07K14/08,
            PC C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC Primer C375
            FH Key
            FT source
            1..18
            /organism="Artificial Sequence".
            Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1035 TAAACATCACACCCCAAC 1051
      |||||
Db 2 TGAACATCACGCCCAAC 18

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RESULT 207
AX129431/c
LOCUS          AX129431      19 bp      DNA          linear      PAT 15-MAY-2001
DEFINITION     Sequence 649 from Patent WO0130362.
ACCESSION      AX129431
VERSION        AX129431.1  GI:14135736
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Robbins,J.M. and Tritz,R.
TITLE          Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL        Patent: WO 0130362-A 649 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES       source
               1..19
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
               /note="Cdk6 ribozyme binding site"

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      603 AAGACTTCATAGTAGG 619
        ||||| ||||| |||||
Db       19 AACACTTCAGAGTAGG 3

RESULT 208
AX129821/c
LOCUS          AX129821      19 bp      DNA          linear      PAT 15-MAY-2001
DEFINITION     Sequence 1039 from Patent WO0130362.
ACCESSION      AX129821
VERSION        AX129821.1  GI:14136126
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Robbins,J.M. and Tritz,R.
TITLE          Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL        Patent: WO 0130362-A 1039 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES       source
               1..19
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
               /note="Cdk8 ribozyme binding site"

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      415 GTTTTCCTTATATTG 431
        ||||| ||||| |||||
Db       19 GTTTTCCTATATTG 3

RESULT 209
AX149152/c
LOCUS          AX149152      19 bp      DNA          linear      PAT 08-JUN-2001
DEFINITION     Sequence 354 from Patent WO0136625.
ACCESSION      AX149152
VERSION        AX149152.1  GI:14347676
KEYWORDS

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SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS        Wright,J.A., Young,A.H. and Dugourd,D.
TITLE          Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms
JOURNAL        Patent: WO 0136625-A 354 25-MAY-2001;
GeneSense Technologies Inc. (CA)
FEATURES       Location/Qualifiers
               source
               1..19
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Antisense oligonucleotide"

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      567 TTTTAAATACCTTTATA 583
        ||||| ||||| |||||
Db       18 TTTTAAAACCTTTAGA 2

RESULT 210
BD012154
LOCUS          BD012154      19 bp      DNA          linear      PAT 02-AUG-2002
DEFINITION     Polypeptide.
ACCESSION      BD012154
VERSION        BD012154.1  GI:22092343
KEYWORDS       WO 0109348-A/7.
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1 (bases 1 to 19)
AUTHORS        Koyama,N., Okui,T., Takakura,H., Asada,K. and Kato,I.
TITLE          Polypeptide
JOURNAL        Patent: WO 0109348-A 7 08-FEB-2001;
TAKARA SHUZO CO LTD,NOBUTO KOYAMA,TOSHITAKE OKUI,HIKARU TAKAKURA,
KIYOZO ASADA,IKUNOSHIN KATO
COMMENT        OS Artificial Sequence
                PN WO 0109348-A/7
                PD 08-FEB-2001
                PF 26-JUL-2000 WO 2000JP004956
                PR 02-AUG-1999 JP 99P 218778
                PI NOBUTO KOYAMA,TOSHITAKE OKUI,HIKARU TAKAKURA,KIYOZO ASADA, PI
                IKUNOSHIN KATO
                PC C12N15/56,C12N9/26,C12P19/14,C12N1/15,C12N1/19,C12N1/21, PC
                CC PCR primer R4.
                FH Key
                Location/Qualifiers
                source
                1..19
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      857 TCTTTGTGTTGTAGTCC 873
        ||||| ||||| |||||
Db       3 TCCATGTGTTGTAGTCC 19

RESULT 211
AX348064/c
LOCUS          AX348064      15 bp      DNA          linear      PAT 06-FEB-2002
DEFINITION     Sequence 2 from Patent EP1172445.
ACCESSION      AX348064
VERSION        AX348064.1  GI:18614174
KEYWORDS

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Fri Aug 19 10:59:59 2005

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
TITLE
JOURNAL
Wiebusch,H., Schmitt-John,T. and Weidner,J.
A method for direct genetic analysis of target cells by using
fluorescence probes
Patent: EP 1172445-A 2 16-JAN-2002;
Praenadia GmbH (DE)
Location/Qualifiers
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer for beta-actin, upstream"
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 42 GAAGCAGCGCGGCC 56
Db 15 GAAGCAGCGCGGCC 1
RESULT 212
AX540329/c 15 bp DNA linear PAT 23-NOV-2002
LOCUS
DEFINITION
Sequence 3 from Patent WO0206524.
AX540329
ACCESSION
AX540329.1 GI:25273335
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
Wiebusch,H., Schmitt-John,T. and Weidner,J.
A method for direct genetic analysis of target cells by using
fluorescence probes
Patent: WO 0206524-A 3 24-JAN-2002;
Praenadia GmbH (DE)
Location/Qualifiers
FEATURES
source
1. .15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 42 GAAGCAGCGCGGCC 56
Db 15 GAAGCAGCGCGGCC 1
RESULT 213
I35386/c 16 bp DNA linear PAT 13-MAY-1997
LOCUS
DEFINITION
Sequence 354 from patent US 5599706.
I35386
ACCESSION
I35386.1 GI:2088354
KEYWORDS
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE
Ribozymes targeted to apo(a) mRNA
JOURNAL
Patent: US 5599706-A 354 04-FEB-1997;
Location/Qualifiers
FEATURES
source

source 1. .16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 448 TAGCTGGGACAGTG 462
Db 16 TAGCTGGGACAGTG 2
RESULT 214
AR047122/c 17 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION
Sequence 1915 from patent US 5817796.
AR047122
ACCESSION
AR047122
VERSION
AR047122.1 GI:5968587
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE
C-myc ribozymes having 2'-5'-linked adenylyate residues
JOURNAL
Patent: US 5817796-A 1915 06-OCT-1998;
Location/Qualifiers
FEATURES
source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 274 ACTGGCATATTCCT 288
Db 16 ACTGGCATATTCCT 2
RESULT 215
BD232102 17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Complex formed of major histocompatibility antigen gene complex
product on the phage surface and peptide.
BD232102
ACCESSION
BD232102.1 GI:33041872
VERSION
JP 2002514431-A/20.
KEYWORDS
unidentified
SOURCE
unclassified.
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Gorochoy,G., Piqueras,B., Doussal,J.M.L. and Debre,P.
TITLE
Complex formed of major histocompatibility antigen gene complex
product on the phage surface and peptide
JOURNAL
Patent: JP 2002514431-A 20 21-MAY-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE CNRS
COMMENT
OS Unidentified
PN JP 2002514431-A/20
PD 21-MAY-2002
PF 12-MAY-1999 JP 2000548484
PR 14-MAY-1998 FR 98/06213
PI GUY GOROCHOV,BERNARD PIQUERAS,JEAN MARC LE DOUSSAL,PATRICE PI
DEBRE
PC C12N15/09,A61K38/00,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC G01N33/68,C12N15/00,A61K37/02,C12N5/00
CC Sequence Figure 1A
FH Key Location/Qualifiers
FT misc feature (1)..(17).
Location/Qualifiers
FEATURES
source
1. .17

[illegible]

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/db_xref="taxon:32644"

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 851 GATCCCTCTTTGTGT 865
    ||| ||||| ||||| |||
Db 2 GATACCTCTTTGTGT 16

RESULT 219
BD256865      17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256865
VERSION BD256865.1 GI:33066635
KEYWORDS JP 2002541795-A/4658.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4658 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/4658
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT 1..17 /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 851 GATCCCTCTTTGTGT 865
    ||| ||||| ||||| |||
Db 2 GATACCTCTTTGTGT 16

RESULT 221
CQ617827/C
LOCUS
DEFINITION Sequence 2567 from Patent WO0192524.
ACCESSION CQ617827
VERSION CQ617827.1 GI:41668045
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2567 06-DEC-2001;
FEATURES
source
1..17
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCT 757
    ||| ||||| ||||| |||
Db 15 AGGCAGCTGCCACCT 1

RESULT 222
CQ621547
LOCUS
DEFINITION Sequence 6287 from Patent WO0192524.
ACCESSION CQ621547
VERSION CQ621547.1 GI:41671765
KEYWORDS

COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/4796
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61P43/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT 1..17 /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 TTTTCCTTACAATTC 410
    ||| ||||| ||||| |||
Db 2 TTTTCCTTACAATTC 16

RESULT 220
BD257003      17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD257003
VERSION BD257003.1 GI:33066773
KEYWORDS JP 2002541795-A/4796.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4796 10-DEC-2002;

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SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
JOURNAL     Shannon,M.E.
            Myosin-like gene expressed in human heart and muscle
            Patent: WO 0192524-A 6287 06-DEC-2001;
FEATURES     Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21  CCGGGCCGTGGCAGG 35
         ||||| |||||
Db      3  CCGGGCTGTGGCAGG 17

RESULT 223
LOCUS      CQ621548              17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 6288 from Patent WO0192524.
ACCESSION  CQ621548
VERSION     CQ621548.1  GI:41671766
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
JOURNAL   Shannon,M.E.
            Myosin-like gene expressed in human heart and muscle
            Patent: WO 0192524-A 6288 06-DEC-2001;
FEATURES   Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21  CCGGGCCGTGGCAGG 35
         ||||| |||||
Db      2  CCGGGCTGTGGCAGG 16

RESULT 224
LOCUS      CQ621549              17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 6289 from Patent WO0192524.
ACCESSION  CQ621549
VERSION     CQ621549.1  GI:41671767
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
JOURNAL   Shannon,M.E.
            Myosin-like gene expressed in human heart and muscle
            Patent: WO 0192524-A 6289 06-DEC-2001;
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FEATURES     Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21  CCGGGCCGTGGCAGG 35
         ||||| |||||
Db      1  CCGGGCTGTGGCAGG 15

RESULT 225
LOCUS      I54174              17 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 1915 from patent US 5646042.
ACCESSION  I54174
VERSION     I54174.1  GI:2475377
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE     C-myb targeted ribozymes
JOURNAL    Patent: US 5646042-A 1915 08-JUL-1997;
FEATURES   Location/Qualifiers
            source
              1..17
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      274  ACTGGCATATTTCTT 288
         ||||| |||||
Db      16  ACTGGCATATTTCTT 2

RESULT 226
LOCUS      AR327041              17 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 4443 from patent US 6566127.
ACCESSION  AR327041
VERSION     AR327041.1  GI:33712849
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 4443 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
              1..17
                /organism="unknown"
                /mol_type="unassigned RNA"

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626  GTTTTATTCTCAGCA 640
         ||||| |||||
Db      15  GTTTTATGCTCAGCA 1
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RESULT 227
AR458890/c LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2567 from patent US 6686188.
ACCESSION AR458890
VERSION AR458890.1 GI:42693947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2567 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1..2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 743 AGGCAGCTGCCACT 757
Db 15 AGGCAGCTGCCCT 1

RESULT 228
AR462610 LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6287 from patent US 6686188.
ACCESSION AR462610
VERSION AR462610.1 GI:42697667
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6287 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1..2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 743 AGGCAGCTGCCACT 757
Db 15 AGGCAGCTGCCCT 1

RESULT 229
AR462611 LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6288 from patent US 6686188.
ACCESSION AR462611
VERSION AR462611.1 GI:42697668
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.

RESULT 230
AR462612 LOCUS 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6289 from patent US 6686188.
ACCESSION AR462612
VERSION AR462612.1 GI:42697669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6289 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1..2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 21 CCGGGCCGTGGCAGG 35
Db 2 CCGGGCTGTGGCAGG 16

RESULT 231
AR462612 LOCUS 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 818 from Patent WO0159103.
ACCESSION AR462612
VERSION AR462612.1 GI:15525419
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 818 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1..2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 CCGCGGCCCGAGTTC 63
 Db 2 CCGCGGCCCGAGTGC 16

RESULT 232
 AX215377
 LOCUS AX215377 17 bp RNA linear PAT 07-SEP-2001
 DEFINITION Sequence 819 from Patent WO0159103.
 ACCESSION AX215377
 VERSION AX215377.1 GI:15525420
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 PATENT: WO 0159103-A 819 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
 source
 1..17
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 CCGCGGCCCGAGTTC 63
 Db 1 CCGCGGCCCGAGTGC 15

RESULT 233
 AX217124/C
 LOCUS AX217124 17 bp RNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2566 from Patent WO0159103.
 ACCESSION AX217124
 VERSION AX217124.1 GI:15527185
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 PATENT: WO 0159103-A 2566 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
 source
 1..17
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 415 GTTTTCCTTATTT 429
 Db 16 GTTTTCCTTATTT 2

RESULT 234
 AX422711
 LOCUS AX422711 17 bp RNA linear PAT 18-JUN-2002
 DEFINITION Sequence 1047 from Patent WO0188124.
 ACCESSION AX422711
 VERSION AX422711.1 GI:21526093
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, P.G. and
 Randi, A.M.
 TITLE Method and reagent for the inhibition of erg
 JOURNAL PATENT: WO 0188124-A 1047 22-NOV-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)

FEATURES
 source
 1..17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned RNA"
 /db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 958 CTGGACCCAGGACAT 972
 Db 3 CTGGACTCAGGACAT 17

RESULT 235
 AX502937
 LOCUS AX502937 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 4244 from Patent EP1229046.
 ACCESSION AX502937
 VERSION AX502937.1 GI:23385230
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Zhan, J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 4244 07-AUG-2002;
 Aeomica, Inc. (US)

FEATURES
 source
 1..17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 675 ATTATGTTACTTGT 689
 Db 2 ATTATGTTCTTGT 16

RESULT 236
 AX502938
 LOCUS AX502938 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 4245 from Patent EP1229046.
 ACCESSION AX502938
 VERSION AX502938.1 GI:23385231
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

892 CCCACAGACCAAGAG 906

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Db      1  ||||| ||||| ||||| |||||
          CCCAGAGACCAGAG 15

RESULT 241
AX723809 LOCUS AX723809 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1496 from Patent WO03025176.
ACCESSION AX723809
VERSION AX723809.1 GI:30503152
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1496 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 621 GATGAGTTTATTCT 635
Db 1 GATCAGTTTATTCT 15

RESULT 242
AX728020/c LOCUS AX728020 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5707 from Patent WO03025176.
ACCESSION AX728020
VERSION AX728020.1 GI:30507363
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5707 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 606 ACTTCATAGTAGGA 620
Db 17 ACTTCATCAGTAGGA 3

RESULT 243
AX729829 LOCUS AX729829 17 bp DNA linear PAT 08-MAY-2003

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DEFINITION Sequence 1463 from Patent WO03025175.
ACCESSION AX729829
VERSION AX729829.1 GI:30509172
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 1463 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTG 527
Db 2 ATCTGTATACATATG 16

RESULT 244
AX733736/c LOCUS AX733736 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5370 from Patent WO03025175.
ACCESSION AX733736
VERSION AX733736.1 GI:30513079
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5370 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 588 ATGTTCACTTTAAGA 602
Db 17 ATGTTCACTTGAAGA 3

RESULT 245
AX736422 LOCUS AX736422 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2012 from Patent WO03025177.
ACCESSION AX736422
VERSION AX736422.1 GI:30515710
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2012 27-MAR-2003;
Molecular Engines Laboratories (PR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 ATATGCTGGGTTTTT 570
||| ||||| ||||| |||||
Db 2 ATCTGCTGGGTTTTT 16

RESULT 246
AX738575/c 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 4165 from Patent WO03025177.
ACCESSION AX738575
VERSION AX738575.1 GI:30517865
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4165 27-MAR-2003;
Molecular Engines Laboratories (PR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
||| ||||| ||||| |||||
Db 17 ATGTTCACTTTGAAGA 3

RESULT 247
AX754465/c 17 bp DNA linear PAT 23-JUN-2003
LOCUS
DEFINITION Sequence 812 from Patent WO03037931.
ACCESSION AX754465
VERSION AX754465.1 GI:32167162
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 812 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
||| ||||| ||||| |||||
Db 17 TCATTTTCCTTCAAA 3

RESULT 248
AX754466/c 17 bp DNA linear PAT 23-JUN-2003
LOCUS
DEFINITION Sequence 813 from Patent WO03037931.
ACCESSION AX754466
VERSION AX754466.1 GI:32167163
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 813 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
||| ||||| ||||| |||||
Db 17 TCATTTTCCTTCAAA 3

RESULT 249
AX754467/c 17 bp DNA linear PAT 23-JUN-2003
LOCUS
DEFINITION Sequence 814 from Patent WO03037931.
ACCESSION AX754467
VERSION AX754467.1 GI:32167164
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 814 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
||| ||||| ||||| |||||
Db 16 TCATTTTCCTTCAAA 2

RESULT 250
AX754468/c 17 bp DNA linear PAT 23-JUN-2003
LOCUS
DEFINITION Sequence 815 from Patent WO03037931.
ACCESSION AX754468
VERSION AX754468.1 GI:32167165
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 815 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
||| ||||| ||||| |||||
Db 17 TCATTTTCCTTCAAA 3

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Db      15 TCATTTTCCTTTCAA 1
RESULT 250
AX759999/c
LOCUS   AX759999          17 bp    DNA          linear    PAT 25-JUN-2003
DEFINITION
Sequence 3320 from Patent WO03040369.
ACCESSION
AX759999
VERSION  AX759999.1  GI:32254615
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS  Telerman,A., Anson,R. and Tuijnder,M.
TITLE    Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL  Patent: WO 03040369-A 3320 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source   1..17
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match      1..2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      588 ATGTTCACTTTAAGA 602
Db      17 ATGTTCACTTTGAAGA 3

RESULT 251
AX762004
LOCUS   AX762004          17 bp    DNA          linear    PAT 25-JUN-2003
DEFINITION
Sequence 5325 from Patent WO03040369.
ACCESSION
AX762004
VERSION  AX762004.1  GI:32256620
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS  Telerman,A., Anson,R. and Tuijnder,M.
TITLE    Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL  Patent: WO 03040369-A 5325 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source   1..17
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      851 GATCCCTCTTGTGT 865
Db      1 GATCCCTCTTGTGT 15

RESULT 252
AR119278
LOCUS   AR119278          18 bp    DNA          linear    PAT 16-MAY-2001
DEFINITION
Sequence 41 from patent US 6150104.

ACCESSION
AR119278
VERSION  AR119278.1  GI:14101188
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS  Splawski,I. and Keating,M.T.
TITLE    Homozygous mutation in KVLQT1 which causes Jervell and Lange
Nielsen syndrome
JOURNAL  Patent: US 6150104-A 41 21-NOV-2000;
Location/Qualifiers
FEATURES
source   1..18
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      48 GCCGCGCCCCCAGTT 62
Db      2 GCCGCGCCCCCAGTT 16

RESULT 253
AR164732
LOCUS   AR164732          18 bp    DNA          linear    PAT 17-OCT-2001
DEFINITION
Sequence 43 from patent US 6274332.
ACCESSION
AR164732
VERSION  AR164732.1  GI:16237874
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS  Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE    Mutations in the KCNE1 gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL  Patent: US 6274332-A 43 14-AUG-2001;
Location/Qualifiers
FEATURES
source   1..18
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
Query Match      1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      48 GCCGCGCCCCCAGTT 62
Db      2 GCCGCGCCCCCAGTT 16

RESULT 254
BD222843
LOCUS   BD222843          18 bp    DNA          linear    PAT 17-JUL-2003
DEFINITION
KVLQT1-OT extension syndrome.
ACCESSION
BD222843
VERSION  BD222843.1  GI:33032613
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS  Keating,M.T., Sanguinetti,M.C., Karan,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
TITLE    KVLQT1-OT extension syndrome
JOURNAL  Patent: JP 2002521045-A 41 16-JUL-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION, GENZYME CORP
COMMENT   OS Homo sapiens (human)
PN JP 2002521045-A/41
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PD 16-JUL-2002
DP 12-MAY-1999 JP 2000562052
PR 29-JUL-1998 US 60/094477,17-AUG-1998 US 09/135010 PI
MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KAFAN,GREGORY M PI
LANDES,
PI TIMOTHY D CONNORS,TIMOTHY C BURN,IGOR SPLAWSKI PC
C12N15/09,A01K67/027,C07K14/46,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/ PC
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PC G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68,
PC C12N15/00,
PC C12N5/00
CC KVLQTL-QT extension syndrome
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGAGTT 62
Db 2 GCCGCGGCCCGAGTT 16

RESULT 255
BD230253 18 bp DNA linear PAT 17-JUL-2003
LOCUS Total genome radiation hybrid map of canine genome and its use for
DEFINITION identification of interesting genes.
ACCESSION BD230253
VERSION BD230253.1 GI:33040023
KEYWORDS JP 2002530091-A/122.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galibert,F. and Andre,C.
TITLE Total genome radiation hybrid map of canine genome and its use for
JOURNAL identification of interesting genes
Patent: JP 2002530091-A 122 17-SEP-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT OS Canis familiaris (dog)
PN JP 2002530091-A/122
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT,CATHERINE ANDRE
PC C12N15/09,C12Q1/68,C12N15/00
CC A0076
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
1..18
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 523 ATGTGCACATGCGGC 537

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Db 17 ATGTGCACATGCGGC 3
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CO774947 18 bp DNA linear PAT 06-MAR-2004
LOCUS Sequence 16 from Patent WO2004012817.
DEFINITION CO774947
ACCESSION CO774947
VERSION CO774947.1 GI:45238085
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS van Lohuizen,M.M., Berns,A.J., Martins,C.P., Mikkers,H.M.,
Lenz,J.R., Lund,A.H. and de Koning,J.P.
TITLE Use of genes identified to be involved in tumor development for the
JOURNAL development of anti-cancer drugs
Patent: WO 2004012817-A 16 12-FEB-2004;
Kylix B.V. (NL)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide PSK RV"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 896 CAGACCAAGAGCCTC 910
|||||
Db 15 CAGCCCCAAGAGCCTC 1

RESULT 257
CO799841 18 bp DNA linear PAT 28-APR-2004
LOCUS Sequence 491 from Patent WO2004031413.
DEFINITION CO799841
ACCESSION CO799841
VERSION CO799841.1 GI:46848788
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,Y., Daigo,Y. and Nakatsuru,S.
TITLE Method for diagnosing non-small cell lung cancers
JOURNAL Patent: WO 2004031413-A 491 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized S-oligonucleotide sequence
for antisense method"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 196 CGCCATCTCCCAT 210
|||||
Db 16 CGCCATCTCCCAT 2

RESULT 258
CO807850 18 bp DNA linear PAT 10-MAY-2004
LOCUS CQ807850

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Sequence 1300 from Patent WO2004035803.
 CQ807850
 CQ807850.1 GI:47113244
 .
 synthetic construct
 other sequences; artificial sequences.
 1
 Fockens,J., Hatbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
 Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
 Marx,A.
 Method and nucleic acids for the improved treatment of breast cell
 proliferative disorders
 Patent: WO 2004035803-A 1300 29-APR-2004;
 Epigenomics AG (DE)
 FEATURES
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 1. .18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Detection oligonucleotide for X51730 PGR"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 TAGGAGATGAGTTT 630
 |||||
 Db 3 TAGGAGATGAGTTT 17

RESULT 259
 AR218558
 LOCUS AR218558 18 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 6 from patent US 6420117.
 ACCESSION AR218558
 VERSION AR218558.1 GI:23319338
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 18)
 REFERENCE Wessler,S.R. and Casa,A.M.
 AUTHORS Miniature inverted repeat transposable elements and methods of use
 TITLE Patent: US 6420117-A 6 16-JUL-2002;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1. .18
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 909 TCAACATTTCTTAGA 923
 |||||
 Db 1 TCAACGTTTCTTAGA 15

RESULT 260
 AR218696
 LOCUS AR218696 18 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 43 from patent US 6420124.
 ACCESSION AR218696
 VERSION AR218696.1 GI:23319591
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 18)
 REFERENCE Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
 AUTHORS Connors,T.D., Burn,T.C. and Splawski,I.
 TITLE KVLQT1--a long qt syndrome gene

Sequence 1300 from Patent WO2004035803.
 CQ807850
 CQ807850.1 GI:47113244
 .
 synthetic construct
 other sequences; artificial sequences.
 1
 Fockens,J., Hatbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
 Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
 Marx,A.
 Method and nucleic acids for the improved treatment of breast cell
 proliferative disorders
 Patent: WO 2004035803-A 1300 29-APR-2004;
 Epigenomics AG (DE)
 FEATURES
 source
 1. .18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Detection oligonucleotide for X51730 PGR"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 TAGGAGATGAGTTT 630
 |||||
 Db 3 TAGGAGATGAGTTT 17

RESULT 259
 AR218558
 LOCUS AR218558 18 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 6 from patent US 6420117.
 ACCESSION AR218558
 VERSION AR218558.1 GI:23319338
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 18)
 REFERENCE Wessler,S.R. and Casa,A.M.
 AUTHORS Miniature inverted repeat transposable elements and methods of use
 TITLE Patent: US 6420117-A 6 16-JUL-2002;
 JOURNAL Location/Qualifiers
 FEATURES
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 1. .18
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 909 TCAACATTTCTTAGA 923
 |||||
 Db 1 TCAACGTTTCTTAGA 15

RESULT 260
 AR218696
 LOCUS AR218696 18 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 43 from patent US 6420124.
 ACCESSION AR218696
 VERSION AR218696.1 GI:23319591
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 18)
 REFERENCE Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
 AUTHORS Connors,T.D., Burn,T.C. and Splawski,I.
 TITLE KVLQT1--a long qt syndrome gene

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RESULT 263
LOCUS AR262129 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 43 from patent US 6323026.
ACCESSION AR262129
VERSION AR262129.1 GI:28073490
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6323026-A 43 27-NOV-2001;
FEATURES
source
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGCAGTT 62
Db 2 GCCGCGGCCCGCAGTT 16

RESULT 264
LOCUS AR293760 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5495 from patent US 6537751.
ACCESSION AR293760
VERSION AR293760.1 GI:31681044
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 5495 25-MAR-2003;
FEATURES
source
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1060 CTTCCAGTGGCTAA 1074
Db 18 CTTACCAAGTGGCTAA 4

RESULT 265
LOCUS AR294009 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5744 from patent US 6537751.
ACCESSION AR294009
VERSION AR294009.1 GI:31681293
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 5744 25-MAR-2003;
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FEATURES
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Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 612 TAAGTAGGAGATGAG 626
Db 3 TAAAGTAAGAGATGAG 17

RESULT 266
LOCUS AR344567 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 43 from patent US 6582913.
ACCESSION AR344567
VERSION AR344567.1 GI:33740636
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 43 24-JUN-2003;
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGCAGTT 62
Db 2 GCCGCGGCCCGCAGTT 16

RESULT 267
LOCUS AX119482 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 139 from Patent WO0129251.
ACCESSION AX119482
VERSION AX119482.1 GI:14036401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nrl gene
JOURNAL Patent: WO 0129251-A 139 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
source
1..18
/organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 416 TTTTTCCTTATATT 430
Db 18 TTTTTCCTTATAGTT 4
```

REFERENCE 1
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nrl gene
JOURNAL Patent: WO 0129251-A 139 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT	268	AX119538	18 bp	DNA	linear	PAT 11-MAY-2001
LOCUS		Sequence 195 from Patent WO0129251.				
DEFINITION		AX119538				
ACCESSION		AX119538				
VERSION		AX119538.1	GI:14036457			
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS		Messiaen,L. and Callens,T.				
TITLE		Improved mutation analysis of the nfi gene				
JOURNAL		Patent: WO 0129251-A 195 26-APR-2001;				
FEATURES		UNIVERSITEIT GENT (BE)				
source		Location/Qualifiers				
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		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		1.2%; Score 13.4; DB 1; Length 18;				
Best Local Similarity		93.3%; Pred. No. 1.3e+02;				
Matches		14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	416	TTTTTCCTTATATT 430				
Db	18	TTTTTCCTTATAGTT 4				
RESULT	269	BD196757	19 bp	DNA	linear	PAT 17-JUL-2003
LOCUS		Prostatic cancer gene.				
DEFINITION		BD196757				
ACCESSION		BD196757				
VERSION		BD196757.1	GI:33006527			
KEYWORDS		JP 2002516657-A/346.				
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS		1 (bases 1 to 19)				
TITLE		Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.				
JOURNAL		Prostatic cancer gene				
COMMENT		Patent: JP 2002516657-A 346 11-JUN-2002;				
		GENSET				
		OS Homo sapiens (human)				
		PN JP 2002516657-A/346				
		PD 11-JUN-2002				
		PF 22-DEC-1998 JP 2000525562				
		PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PT				
		DANIEL COHEN, MARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC				
		C12N15/09, C12N15/09, A01K67/027, C07K14/47, C07K16/18, C12N1/15, PC				
		C12N1/19.				
		PC C12N1/21, C12N5/10, C12N5/10, C12P21/08, C12Q1/68, G01N33/50 PC				
		, C12N15/00, C12N5/00,				
		PC C12N5/00, C12N15/00				
		CC upstream amplification primer for SEQ 251, SEQ 328 FH Key				
		Location/Qualifiers				
		FT primer bind 1..19.				
FEATURES		Location/Qualifiers				
source		1..19				
		/organism="Homo sapiens"				
		/mol_type="genomic DNA"				
		/db_xref="taxon:9606"				
Query Match		1.2%; Score 13.4; DB 1; Length 19;				
Best Local Similarity		93.3%; Pred. No. 1.3e+02;				
Matches		14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	351	TCAAATGGGAGCCT 365				

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1100 CTGCTCATTTGTTTA 1114
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 Db 19 CTGCTCATTTTITTA 5

RESULT 272
 AR211777 AR211777 19 bp DNA linear PAT 20-JUN-2002
 LOCUS Sequence 23 from patent US 6399370.
 DEFINITION AR211777
 ACCESSION AR211777 GI:21515190
 VERSION AR211777.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Wilson J.M., Goldman M., Bals R., Stolzenberg E.D., Anderson M.,
 Zasloff M. and Kari P.
 TITLE Compositions and methods for use of defensin
 JOURNAL Patent: US 6399370-A 23 04-JUN-2002;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 954 CACTCTGACCCAGG 968
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 Db 3 CACTCTGACCCCTGG 17

RESULT 273
 AR292652/c AR292652 19 bp DNA linear PAT 12-JUN-2003
 LOCUS Sequence 4387 from patent US 6537751.
 DEFINITION AR292652
 ACCESSION AR292652 GI:31679936
 VERSION AR292652.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen D., Chumakov I. and Blumenfeld M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 4387 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAATGGGGAGCCT 365
 |||||
 Db 15 TCAAAAGGGGAGCCT 1

RESULT 274
 AR299591 AR299591 19 bp DNA linear PAT 12-JUN-2003
 LOCUS Sequence 11326 from patent US 6537751.
 DEFINITION AR299591
 ACCESSION AR299591

VERSION AR299591.1 GI:31686875
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen D., Chumakov I. and Blumenfeld M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 11326 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 CATTTCCTTACAAT 408
 |||||
 Db 4 CATTTCCTTACAAT 18

RESULT 275
 AR452230/c AR452230 19 bp DNA linear PAT 20-FEB-2004
 LOCUS Sequence 80 from patent US 6677146.
 DEFINITION AR452230
 ACCESSION AR452230
 VERSION AR452230.1 GI:42683776
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Janjic N., Bullard J.M., McHenry C.S. and Kery V.
 TITLE Thermophilic polymerase III holoenzyme
 JOURNAL Patent: US 6677146-A 80 13-JAN-2004;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAAGCGCGGGT 849
 |||||
 Db 15 CTGGAAGCGCGGGT 1

RESULT 276
 AX132453 AX132453 19 bp DNA linear PAT 15-MAY-2001
 LOCUS Sequence 3671 from Patent WO0130362.
 DEFINITION AX132453
 ACCESSION AX132453
 VERSION AX132453.1 GI:14138758
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Robbins J.M. and Tritz R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye
 diseases
 JOURNAL Patent: WO 0130362-A 3671 03-MAY-2001;
 FEATURES INMUSOL, INC. (US)
 source 1..19
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"

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/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 238 CTATGACTCAGATGC 252
    |||||
Db 2 CTATCACTCAGATGC 16

RESULT 277
LOCUS AX262324 19 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 80 from Patent WO0173052.
ACCESSION AX262324
VERSION AX262324.1 GI:16511266
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS McHenry, C.S.
TITLE Thermophilic polymerase III holoenzyme
JOURNAL Patent: WO 0173052-A 80 04-OCT-2001;
McHenry, Charles S. (US)
FEATURES
    source
        1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="reverse/antisense ATG primer #P133-A1237"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAAGCGCGGGT 849
    |||||
Db 15 CTGGAAGCGCGGGT 1

RESULT 278
LOCUS BD009904 19 bp DNA linear PAT 31-JAN-2002
DEFINITION Compositions and methods for use of defensin.
ACCESSION BD009904
VERSION BD009904.1 GI:18638277
KEYWORDS JP 2001502891-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Wilson, J.M., Goldman, M., Bals, R., Stolzenberg, E.D., Anderson, M.,
Zaslouff, M., and Kari, P.
TITLE Compositions and methods for use of defensin
JOURNAL Patent: JP 2001502891-A 13 06-MAR-2001;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA, AGAININ
PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2001502891-A/13
PD 06-MAR-2001
PR 20-AUG-1997 JP 1998510921
PR 22-AUG-1996 US 60/023424, 01-OCT-1996 US 60/027334 PR
18-FEB-1997 US 60/038685
PI JAMES M WILSON, MITCHELL GOLDMAN, ROBERT BALS,
PI ETHAN D STOLZENBERG,
PI MARK ANDERSON, MICHAEL ZASLOFF, PRASAD KARI
PC C12N5/00, C12N15/00, C07H21/04, A61K38/00, A61K48/00, C07K2/00, PC
A01N37/18
CC
FH Key Location/Qualifiers

FT source 1..19
FT /organism="Artificial Sequence".
FEATURES
    source
        1..19
        Location/Qualifiers
        1..19
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 954 CACTCTGACCCAGG 968
    |||||
Db 3 CACTCTGGACCCCTGG 17

RESULT 279
LOCUS BD088340/c 19 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088340
VERSION BD088340.1 GI:22633950
KEYWORDS JP 2001321190-A/584.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda, E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 584 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT OS Artificial Sequence
PN JP 2001321190-A/584
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
C12N15/00,
CC Description of Artificial Sequence: Synthetic DNA FH Key
FT source 1..19
FT Location/Qualifiers
    1..19
    /organism="Artificial Sequence".
FEATURES
    source
        1..19
        Location/Qualifiers
        1..19
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 406 AATTCAGGGTTT 420
    |||||
Db 16 AATTCAGGGTTATT 2

RESULT 280
LOCUS AB068097/c 19 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-stSG4211
at 1p36.
ACCESSION AB068097
VERSION AB068097.1 GI:15128901
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K.,

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QY 192 TCCACGCCATCTCCCA 209
Db 1 TCCCGGCATCTCCACCA 18

RESULT 285
AR039068/c
LOCUS AR039068 18 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 34 from patent US 5807730.
ACCESSION AR039068
VERSION AR039068.1 GI:5958431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ito, K., Yamaki, T., Arii, T., Tsuruoka, M. and Nakamura, T.
TITLE Nitrite hydratase
JOURNAL Patent: US 5807730-A 34 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 CTGCGCGCGCGTGGCAG 34
Db 18 CTGCTCGTGGCGGGCAG 1

RESULT 286
AR071248/c
LOCUS AR071248 18 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5910432.
ACCESSION AR071248
VERSION AR071248.1 GI:7222136
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ito, K., Yamaki, T., Arii, T., Tsuruoka, M. and Nakamura, T.
TITLE Nitrite hydratase
JOURNAL Patent: US 5910432-A 34 08-JUN-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 CTGCGCGCGCGTGGCAG 34
Db 18 CTGCTCGTGGCGGGCAG 1

RESULT 287
AR076370/c
LOCUS AR076370 18 bp DNA PAT 30-AUG-2000
DEFINITION Sequence 37 from patent US 5958772.
ACCESSION AR076370
VERSION AR076370.1 GI:10003116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)

AUTHORS Bennett, C. Frank., Ackermann, E. J. and Cowsert, L. M.
TITLE Antisense inhibition of cellular inhibitor of apoptosis-1 expression
JOURNAL Patent: US 5958772-A 37 28-SEP-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 TTGATGAGATCCAAAGGA 991
Db 18 TTGATGAGATTCAGGTA 1

RESULT 288
AR107284
LOCUS AR107284 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107478.
ACCESSION AR107284
VERSION AR107284.1 GI:12821814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pedersen, F. Skou., Lund, A. Henrik., Lovmand, J., J. O. slashed. xgensen, P. and Duch, M.
TITLE Retroviral vector, a replication system for said vector and avian or mammalian cells transfected with said vector
JOURNAL Patent: US 6107478-A 3 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 192 TCCACGCCATCTCCCA 209
Db 1 TCCCGGCATCTCCACCA 18

RESULT 289
AR11390/c
LOCUS AR11390 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6127133.
ACCESSION AR11390
VERSION AR11390.1 GI:12828238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Akong, M. Anthony., Harpold, M. Miller., Velicelebi, G. and Brust, P.
TITLE Automated analysis equipment and assay method for detecting cell surface protein function using same
JOURNAL Patent: US 6127133-A 2 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 695 GTTCATGTAGTCACGGTG 712

Fri Aug 19 10:59:59 2005

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CC Methods and products related to genotyping and DNA analysis FH
Key Location/Qualifiers
FT source 1..18 /organism='Homo sapiens (human)'.
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FEATURES
source
1..18 Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 568 TTTTAAATACCTTTATATA 585
Db 18 TTTTATACCTTCATAAA 1

RESULT 292
BD266398/c LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Universal arrays.
ACCESSION BD266398
VERSION BD266398.1 GI:33076166
KEYWORDS JP 2002539849-A/398.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S.,
Lockhart, D.J., Ryder, T. and Sklar, P.
TITLE Universal arrays
JOURNAL Patent: JP 2002539849-A 398 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
COMMENT OS Artificial Sequence
PN JP 2002539849-A/398
PD 26-NOV-2002
PF 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359
JIAN BING FAN, JOEL N HIRSCHHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
PI S LANDER,
PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
CC Primer
FH Key
FT source 1..18 Location/Qualifiers
FT

FEATURES
source
1..18 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 93 TGGCATTATCCTTCAGTG 110
Db 18 TGGCCTTCCTCCTCAGTG 1

RESULT 293
E14118/c LOCUS 18 bp DNA linear PAT 28-JUL-1999
DEFINITION PCR primer for producing mutated Pseudonocardia nitrolydratase.
ACCESSION E14118
VERSION E14118.1 GI:5708801
KEYWORDS JP 1997275978-A/32.

CC Methods and products related to genotyping and DNA analysis FH
Key Location/Qualifiers
FT source 1..18 /organism='Homo sapiens (human)'.
FT

FEATURES
source
1..18 Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 974 TTGATGAGATCCAAAGGA 991
Db 18 TTGATGAGATCCAAAGGA 1

RESULT 291
BD241069/c LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241069
VERSION BD241069.1 GI:33050839
KEYWORDS JP 2002525127-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 18)
Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 16 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/16
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST
PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
G01N37/00,
PC C12N15/00

RESULT 290
BD234313/c LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of expression of cellular inhibitor of
apoptosis-1.
ACCESSION BD234313
VERSION BD234313.1 GI:33044083
KEYWORDS JP 2002531469-A/37.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, F.C., Ackermann, E.A. and Cowse, L.M.
TITLE Antisense modulation of expression of cellular inhibitor of
JOURNAL Patent: JP 2002531469-A 37 24-SEP-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002531469-A/37
PD 24-SEP-2002
PF 16-JUN-1999 JP 2000585447
PR 03-DEC-1998 US 09/205204
PI FRANK C BENNETT, ELIZABETH A ACKERMANN, LEX M COWSE, PC
A61K48/00, A61K31/7115, A61K31/712, A61K31/7125, A61P29/00
PC A61P31/00, A61P35/00,
PC A61P37/02, A61P43/00, C12N15/09, C12N15/00
CC Synthetic
FH Key
FT source 1..18 Location/Qualifiers
FT

FEATURES
source
1..18 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 974 TTGATGAGATCCAAAGGA 991
Db 18 TTGATGAGATCCAAAGGA 1

RESULT 291
BD241069/c LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241069
VERSION BD241069.1 GI:33050839
KEYWORDS JP 2002525127-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 18)
Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 16 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/16
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST
PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
G01N37/00,
PC C12N15/00

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SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 18)
AUTHORS     Ito, K., Yamaki, T., Arii, T., Tsuruoka, M. and Nakamura, T.
TITLE       NEW NITRILE-HYDRATASE
JOURNAL     Patent: JP 1997275978-A 32 28-OCT-1997;
            MITSUI TOATSU CHEM INC
COMMENT     OS None
            OC Artificial sequences.
            PN JP 1997275978-A/32
            PD 28-OCT-1997
            PF 29-JAN-1997 JP 1997015295
            PR 14-FEB-1996 JP 96P 27004
            PI ITO KIYOSHI, YAMAKI TOSHIBUMI, ARII TERUO, TSURUOKA MIYUKI, PI
              NAKAMURA TAKESHI
            PC C12N9/88,C12N1/21,C12N15/09,(C12N9/88,C12R1:19),(C12N1/21,PC
              C12R1:19),
            CC (C12N15/09,C12R1:01);
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: No;
            FH Key
            FH Location/Qualifiers
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            Location/Qualifiers
            /organism="Artificial sequences".
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 17 CTGCCCCGGCCCTGGCAG 34
    |||||
DB 18 CTGCTCGTCCGGGGCAG 1
    |||||
RESULT 294
E54096      18 bp DNA linear PAT 31-JAN-2002
LOCUS       Novel gene regulated and decreased in metastatic human melanoma
DEFINITION cell and protein thereof, process for producing the same and
            utilization of the same.
E54096
ACCESSION   E54096.1 GI:18629688
VERSION     JP 2000217585-A/5.
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 18)
REFERENCE   1 (bases 1 to 18)
AUTHORS     Myiuen,H.N.P.F. and Zandoman,A.I.W.
TITLE       Novel gene regulated and decreased in metastatic human melanoma
            cell and protein thereof, process for producing the same and
            utilization of the same
JOURNAL     Patent: JP 2000217585-A 5 08-AUG-2000;
            F HOFFMANN LA ROCHE AG
COMMENT     OS Artificial Sequence
            PN JP 2000217585-A/5
            PD 08-AUG-2000
            PF 31-JAN-2000 JP 2000021873
            PR 29-JAN-1999 EP 99101925.8
            PI HOSEN N P FAN MYUIEN,ALBERT IE W ZENDOMAN
            PC C12N15/09,C07K14/82,C07K16/32,C12P21/02,C12Q1/68,G01N33/566,
            G01N33/574,
            PC G01N33/577,C12N15/00
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            FH Key
            FH Location/Qualifiers
FEATURES    FT source
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            Location/Qualifiers
            /organism="Artificial sequences".
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 17 CTGCCCCGGCCCTGGCAG 34
    |||||
DB 18 CTGCTCGTCCGGGGCAG 1
    |||||
RESULT 294
E54096      18 bp DNA linear PAT 31-JAN-2002
LOCUS       Novel gene regulated and decreased in metastatic human melanoma
DEFINITION cell and protein thereof, process for producing the same and
            utilization of the same.
E54096
ACCESSION   E54096.1 GI:18629688
VERSION     JP 2000217585-A/5.
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 18)
REFERENCE   1 (bases 1 to 18)
AUTHORS     Myiuen,H.N.P.F. and Zandoman,A.I.W.
TITLE       Novel gene regulated and decreased in metastatic human melanoma
            cell and protein thereof, process for producing the same and
            utilization of the same
JOURNAL     Patent: JP 2000217585-A 5 08-AUG-2000;
            F HOFFMANN LA ROCHE AG
COMMENT     OS Artificial Sequence
            PN JP 2000217585-A/5
            PD 08-AUG-2000
            PF 31-JAN-2000 JP 2000021873
            PR 29-JAN-1999 EP 99101925.8
            PI HOSEN N P FAN MYUIEN,ALBERT IE W ZENDOMAN
            PC C12N15/09,C07K14/82,C07K16/32,C12P21/02,C12Q1/68,G01N33/566,
            G01N33/574,
            PC G01N33/577,C12N15/00
            CC
            FH Key
            FH Location/Qualifiers
FEATURES    FT source
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            /organism="Artificial sequences".
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

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FEATURES    FT source
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            Location/Qualifiers
            /organism="Artificial Sequence".
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 349 GATCAAAATGGGGAGCCTG 366
    |||||
DB 1 GAGCTGATGGGGAGCCTG 18
    |||||
RESULT 295
AR210385    18 bp DNA linear PAT 20-JUN-2002
LOCUS       AR210385
DEFINITION Sequence 131 from patent US 6387657.
ACCESSION   AR210385
VERSION     AR210385.1 GI:21512603
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
            Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
TITLE       WISP polypeptides and nucleic acids encoding same
JOURNAL     Patent: US 6387657-A 131 14-MAY-2002;
            Location/Qualifiers
FEATURES    1..18
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            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 897 AGACCAAGAGCTCAACA 914
    |||||
DB 1 AGTCCAAGAGTCTCAGCA 18
    |||||
RESULT 296
AR293973    18 bp DNA linear PAT 12-JUN-2003
LOCUS       AR293973
DEFINITION Sequence 5708 from patent US 6537751.
ACCESSION   AR293973
VERSION     AR293973.1 GI:31681257
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 5708 25-MAR-2003;
            Location/Qualifiers
FEATURES    1..18
            source
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 871 TCCATGCTATTAAAGTG 888
    |||||
DB 1 TCCATGCTCTTACCAGTG 18
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RESULT 297
AR298224          18 bp  DNA          linear          PAT 12-JUN-2003
LOCUS
DEFINITION      Sequence 9959 from patent US 6537751.
ACCESSION      AR298224
VERSION        AR298224.1  GI:31685508
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS      Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE        Biallelic markers for use in constructing a high density
              disequilibrium map of the human genome
JOURNAL       Patent: US 6537751-A 9959 25-MAR-2003;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      209 ATCCCCCATTCATTGCC 226
Db      1 ATCCCCCTCTTCATTGCC 18

RESULT 298
AR351536/c
LOCUS
DEFINITION      Sequence 29 from patent US 6586581.
ACCESSION      AR351536
VERSION        AR351536.1  GI:33753313
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS      Bancroft,F.C., Fliss,M. and Clelland,C.L.
TITLE        Prolactin regulatory element binding protein and uses thereof
JOURNAL       Patent: US 6586581-A 29 01-JUL-2003;
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      279 CATATTCTCTCACTACTG 296
Db      18 CACATTCTCTCTCTGCTG 1

RESULT 299
AR364672/c
LOCUS
DEFINITION      Sequence 3 from patent US 5401629.
ACCESSION      AR364672
VERSION        AR364672.1  GI:34427596
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS      Harpold,M.M. and Brust,P.
TITLE        Assay methods and compositions useful for measuring the
              transduction of an intracellular signal
JOURNAL       Patent: US 5401629-A 3 28-MAR-1995;

FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notice="Description of Combined DNA/RNA Molecule:
Endonuclease protected sequence-detection oligonucleotide"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1056 TTATCTTTCAGTCGCTA 1073
Db      1 TTCTCCTTCCAGTTGCTA 18
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FEATURES
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/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      695 GTTCATGTAGTCACGGTG 712
Db      18 GTTCATGATTCAGGTG 1

RESULT 300
AR482570/c
LOCUS
DEFINITION      Sequence 16 from patent US 6703228.
ACCESSION      AR482570
VERSION        AR482570.1  GI:47245093
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS      Landers,J., Jordan,B., Housman,D.E. and Charest,A.
TITLE        Methods and products related to genotyping and DNA analysis
JOURNAL       Patent: US 6703228-A 16 09-MAR-2004;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      568 TTTTAATACCTTTATATA 585
Db      18 TTTTATACCTTCATAAA 1

RESULT 301
AX035247
LOCUS
DEFINITION      Sequence 4 from Patent WO055365.
ACCESSION      AX035247
VERSION        AX035247.1  GI:11190994
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS      Mulrooney,C. and Oultram,J.D.
TITLE        Enzymatically catalysed signal amplification
JOURNAL       Patent: WO 0055365-A 4 21-SEP-2000;
              MULROONEY CONOR (GB) ; OULTRAM JOHN DOUGLAS (GB) ; TEPNEL MEDICAL
              LTD (GB)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notice="Description of Combined DNA/RNA Molecule:
Endonuclease protected sequence-detection oligonucleotide"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1056 TTATCTTTCAGTCGCTA 1073
Db      1 TTCTCCTTCCAGTTGCTA 18
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RESULT 302
AX078863/c
LOCUS AX078863 18 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 37 from Patent WO0105963.
ACCESSION AX078863
VERSION AX078863.1 GI:13158480
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1
JOURNAL Fundytus, M.E., Coderre, T.J., Cohen, S.R., Henry, J.L. and Vainio, A.
Antisense oligonucleotides for metabotropic glutamate receptor type
1 (mglur1)
PATENT: WO 0105963-A 37 25-JAN-2001;
McGill University (CA)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 901 CAAGAGCCTCACATTTC 918
Db 18 CAAGAGCCTGACCTTTC 1
RESULT 303
AX348093
LOCUS AX348093 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 10 from Patent WO0202630.
ACCESSION AX348093
VERSION AX348093.1 GI:18614197
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1
JOURNAL Strijbos, P.J., Bates, S.G., Gloger, I.G. and Davies, C.G.
New use
PATENT: WO 0202630-A 10 10-JAN-2002;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 144 GTGCTTTAGAGGATTATG 161
Db 1 GTGCTTTCGGGATGATG 18
RESULT 304
AX398208
LOCUS AX398208 18 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 13 from Patent WO0220790.
ACCESSION AX398208
VERSION AX398208.1 GI:21261023
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Geraci, D., Colombo, P., Duro, G., Izzo, V. and Costa, M.A.
AUTHORS Parietaria judaica ns-ltp antigen variants, uses thereof and
TITLES compositions comprising them
JOURNAL Patent: WO 020790-A 13 14-MAR-2002;
CONSIGLIO NAZIONALE DELLE RICERCHE (IT)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
4
/misc_feature
/note="Residue mutated with respect to the corresponding
position in Par j1.0102"
6
/misc_feature
/note="Residue mutated with respect to the corresponding
position in Par j1.0102"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 41 GGAAGCAGCCCGCGGCC 58
Db 1 GGGAGCAGCAGCGCGGCC 18
RESULT 305
AX599791/c
LOCUS AX599791 18 bp DNA linear PAT 14-FEB-2003
DEFINITION. Sequence 1131 from Patent WO02077272.
ACCESSION AX599791
VERSION AX599791.1 GI:28399939
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E.,
Lewin, A., Lipschroter, B., Maier, S., Model, F., Mueller, V., Otto, T.,
Pellet, C. and Ziebarth, H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
PATENT: WO 02077272-A 1131 03-OCT-2002;
Epigenomics AG (DE)
JOURNAL Location/Qualifiers
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for Me491/TD63"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1071 CTAACCACTTAACCTCT 1088
Db 18 CAAACCACTTAACCTCT 1
RESULT 306
AX599792/c
LOCUS AX599792 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1132 from Patent WO02077272.
ACCESSION AX599792
VERSION AX599792.1 GI:28399940
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Geraci, D., Colombo, P., Duro, G., Izzo, V. and Costa, M.A.
AUTHORS Parietaria judaica ns-ltp antigen variants, uses thereof and
TITLES compositions comprising them
JOURNAL Patent: WO 020790-A 13 14-MAR-2002;
CONSIGLIO NAZIONALE DELLE RICERCHE (IT)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
4
/misc_feature
/note="Residue mutated with respect to the corresponding
position in Par j1.0102"
6
/misc_feature
/note="Residue mutated with respect to the corresponding
position in Par j1.0102"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1071 CTAACCACTTAACCTCT 1088
Db 18 CAAACCACTTAACCTCT 1
RESULT 306
AX599792/c
LOCUS AX599792 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1132 from Patent WO02077272.
ACCESSION AX599792
VERSION AX599792.1 GI:28399940
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Geraci, D., Colombo, P., Duro, G., Izzo, V. and Costa, M.A.
AUTHORS Parietaria judaica ns-ltp antigen variants, uses thereof and
TITLES compositions comprising them
JOURNAL Patent: WO 020790-A 13 14-MAR-2002;
CONSIGLIO NAZIONALE DELLE RICERCHE (IT)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
4
/misc_feature
/note="Residue mutated with respect to the corresponding
position in Par j1.0102"
6
/misc_feature
/note="Residue mutated with respect to the corresponding
position in Par j1.0102"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1071 CTAACCACTTAACCTCT 1088
Db 18 CAAACCACTTAACCTCT 1

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ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS      Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorian,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pellet,C. and Ziebarth,H.
TITLE        Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL      Patent: WO 02077272-A 1132 03-OCT-2002;
Epigenomics AG (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for Me491/TD63"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1071 CTAACACACTTAACCTCT 1088
Db      18 CAAACACATAACCCCT 1

RESULT 307
AX815835      18 bp DNA linear PAT 09-DEC-2003
LOCUS
DEFINITION    Sequence 90 from Patent WO03066891.
ACCESSION     AX815835
VERSION       AX815835.1 GI:39646515
KEYWORDS      Sus scrofa (pig)
SOURCE        Sus scrofa
ORGANISM      Sus scrofa
REFERENCE
1
AUTHORS      Hardge,T., Schellander,K. and Wimmers,K.
TITLE        Genetic markers for the diagnosis of the expression of inverted
nipples in pets, breeding animals and domestic cattle
JOURNAL      Patent: WO 03066891-A 90 14-AUG-2003;
Foerderverein Biotechnologieforschung der deutschen
Schweineproduktion e.V. (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="Sus scrofa"
/mol_type="unassigned DNA"
/db_xref="taxon:9823"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      300 TTGTTGTTTCGCTTTG 317
Db      1 TTGCTGCTTGTCCTTTG 18

RESULT 308
AX837801/c
LOCUS
DEFINITION    Sequence 4925 from Patent EP1347046.
ACCESSION     AX837801
VERSION       AX837801.1 GI:39921493
KEYWORDS      unidentified
SOURCE        unidentified
ORGANISM      unidentified.
REFERENCE
1
AUTHORS      Isogai,T., Sugiyama,T., Otsuka,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Negai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuko,Y.
Full-length cDNA sequences
Patent: EP 1347046-A 4925 24-SEP-2003;
Research Association for Biotechnology (JP)
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of Artificial Sequence: an artificially
synthesized primer se q"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      314 TTGGATTTCCTGTATT 331
Db      18 TCTGGAGTTGCTGTATT 1

RESULT 309
BD065371/c
LOCUS
DEFINITION    An antisense oligonucleotide preparation method.
ACCESSION     BD065371
VERSION       BD065371.1 GI:22610974
KEYWORDS      JP 2001511000-A/6.
SOURCE        unidentified
ORGANISM      unidentified
REFERENCE
1 (bases 1 to 18)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 2001511000-A 6 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/6
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method PH Key
Location/Qualifiers
FT source 1..18
FT /organism='Unknown'.

FEATURES
source
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      196 CGCCATCTCCCATCCC 213
Db      18 CGCGGCTCCCATGCC 1

RESULT 310
AR028977/c
LOCUS
DEFINITION    Sequence 16 from patent US 5858981.
ACCESSION     AR028977
VERSION       AR028977.1 GI:5940950
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.

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REFERENCE 1 (bases 1 to 16)
AUTHORS Schreiber,A.D. and Park,J.-G.
TITLE Method of inhibiting phagocytosis
JOURNAL Patent: US 5858981-A 16 12-JAN-1999;
FEATURES
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        Location/Qualifiers
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 1.2%; Score 13; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGC 79
DB 16 AGACATGGCGGC 4

RESULT 311
AR156859/c
LOCUS AR156859 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 16 from patent US 6242427.
ACCESSION AR156859
VERSION AR156859.1 GI:15125563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schreiber,A.D. and Park,J.-G.
TITLE Methods of inhibiting phagocytosis
JOURNAL Patent: US 6242427-A 16 05-JUN-2001;
FEATURES
    source
        Location/Qualifiers
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 1.2%; Score 13; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGC 79
DB 16 AGACATGGCGGC 4

RESULT 312
AR412057/c
LOCUS AR412057 16 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6638764.
ACCESSION AR412057
VERSION AR412057.1 GI:40164606
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schreiber,A.D. and Park,J.-G.
TITLE Methods of inhibiting phagocytosis
JOURNAL Patent: US 6638764-A 16 28-OCT-2003;
FEATURES
    source
        Location/Qualifiers
            1..16
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
Best Local Similarity 1.2%; Score 13; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGC 79
DB 16 AGACATGGCGGC 4

RESULT 313
BD258394/c
LOCUS BD258394 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258394
VERSION BD258394.1 GI:33068164
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6187 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/6187
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
FEATURES
    source
        Location/Qualifiers
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            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match
Best Local Similarity 1.2%; Score 13; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCAGGCAATGCAG 392
DB 15 GCAGGCAATGCAG 3

RESULT 314
AX216369
LOCUS AX216369 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1811 from Patent WO0159103.
ACCESSION AX216369
VERSION AX216369.1 GI:15526430
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1811 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
MCSWIGGEN, James (US) ; Chowrira, Bharat M. (US)
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"

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Query Match          1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCAGT 61
   |||||
Db 4 CCGCGGCCCCAGT 16

RESULT 315
AX216945          17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 2387 from Patent WO0159103.
ACCESSION
AX216945
VERSION
AX216945.1 GI:15527006
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
1
REFERENCE
Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
AUTHORS
Method and reagent for the modulation and diagnosis of cd20 and
TITLE
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2387 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match          1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCAGT 61
   |||||
Db 5 CCGCGGCCCCAGT 17

RESULT 316
AX226887/c
LOCUS
DEFINITION
Sequence 259 from Patent WO0157206.
ACCESSION
AX226887
VERSION
AX226887.1 GI:15556028
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
1
REFERENCE
Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
AUTHORS
Method and reagent for the inhibition of checkpoint kinase-1 (chk
TITLE
1) enzyme
JOURNAL
Patent: WO 0157206-A 259 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match          1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAGGCC 40
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Db 17 GTGGCAGGAGGCC 5

RESULT 317
AX226888/c
LOCUS
DEFINITION
Sequence 260 from Patent WO0157206.
ACCESSION
AX226888
VERSION
AX226888.1 GI:15556029
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
1
REFERENCE
Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
AUTHORS
Method and reagent for the inhibition of checkpoint kinase-1 (chk
TITLE
1) enzyme
JOURNAL
Patent: WO 0157206-A 260 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match          1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAGGCC 40
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Db 16 GTGGCAGGAGGCC 4

RESULT 318
AX227245/c
LOCUS
DEFINITION
Sequence 617 from Patent WO0157206.
ACCESSION
AX227245
VERSION
AX227245.1 GI:15556386
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
1
REFERENCE
Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
AUTHORS
Method and reagent for the inhibition of checkpoint kinase-1 (chk
TITLE
1) enzyme
JOURNAL
Patent: WO 0157206-A 617 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match          1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAGGCC 40
   |||||
Db 15 GTGGCAGGAGGCC 3

RESULT 319
AX227246/c
LOCUS
DEFINITION
Sequence 618 from Patent WO0157206.
ACCESSION
AX227246
VERSION
AX227246.1 GI:15556387
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
1
REFERENCE

```

AUTHORS Fattaey,A.R., Jarvis,T., Meswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 618 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAAGCC 40
Db 14 GTGGCAGGAAGCC 2

RESULT 320
AX227395/c
LOCUS AX227395 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 767 from Patent WO0157206.
ACCESSION AX227395
VERSION AX227395.1 GI:15556536
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Fattaey,A.R., Jarvis,T., Meswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 767 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAAGCC 40
Db 13 GTGGCAGGAAGCC 1

RESULT 321
AX735823
LOCUS AX735823 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1413 from Patent WO03025177.
ACCESSION AX735823
VERSION AX735823.1 GI:30515100
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Telerman,A., Anson,R. and Tuijnder,M.
SEQUENCES involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 1413 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGT 993
Db 1 GATCCAAAGGAGT 13

RESULT 322
AX758667/c
LOCUS AX758667 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1988 from Patent WO03040369.
ACCESSION AX758667
VERSION AX758667.1 GI:32253283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Telerman,A., Anson,R. and Tuijnder,M.
SEQUENCES involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 1988 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 796 TGGAGAGGCAGAT 808
Db 14 TGGAGAGGCAGAT 2

RESULT 323
AX760253
LOCUS AX760253 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3574 from Patent WO03040369.
ACCESSION AX760253
VERSION AX760253.1 GI:32254869
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Telerman,A., Anson,R. and Tuijnder,M.
SEQUENCES involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3574 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Aug 19 10:59:59 2005

DEFINITION Sequence 4476 from Patent WO03025176.
 ACCESSION AX726789
 VERSION AX726789.1 GI:30506132
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversal, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025176-A 4476 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Mus musculus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"
 Query Match 1.1%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 522 CATGTGCACATG 533
 Db 16 CATGTGCACATG 5
 Search completed: August 19, 2005, 10:52:32
 Job time : 7 secs

Db 4 CTTATATTGGAA 16
 |||||
 RESULT 324
 AX822240/c
 LOCUS AX822240 18 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 132 from Patent EP1340818.
 ACCESSION AX822240
 VERSION AX822240.1 GI:39748868
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Adorjan,P., Burger,M., Maier,S., Nimrich,I., Becker,E., Lesche,R.,
 Rujan,T. and Schmitt,A.
 TITLE Method and nucleic acids for the analysis of a colon cell
 proliferative disorder
 JOURNAL Patent: EP 1340818-A 132 03-SEP-2003;
 FEATURES Epigenomics AG (DE)
 source Location/Qualifiers
 1.18
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 1.2%; Score 13; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AGCCGGAAGCAGC 49
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 Db 13 AGCCGGAAGCAGC 1
 RESULT 325
 AX825880/c
 LOCUS AX825880 18 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 132 from Patent WO03072821.
 ACCESSION AX825880
 VERSION AX825880.1 GI:39751394
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Adorjan,P., Burger,M., Maier,S., Nimrich,I., Becker,E., Lesche,R.,
 Rujan,T. and Schmitt,A.
 TITLE Method and nucleic acids for the analysis of a colon cell
 proliferative disorder
 JOURNAL Patent: WO 03072821-A 132 04-SEP-2003;
 FEATURES Epigenomics AG (DE)
 source Location/Qualifiers
 1.18
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 1.2%; Score 13; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AGCCGGAAGCAGC 49
 |||||
 Db 13 AGCCGGAAGCAGC 1
 RESULT 326
 AX726789/c
 LOCUS AX726789 17 bp DNA linear PAT 08-MAY-2003

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:37:46 ; Search time 0.001 Seconds
(without alignments)
352.024 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gctcgttggcaggctgc.....gttacctgtcattgttta 1114

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 9 seqs, 158 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 9 summaries

Database : estdb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	15.6	1.4	22	1	AZ457101
c 2	14.8	1.3	19	1	D44776
c 3	14.8	1.3	19	1	AZ579189
c 4	14.8	1.3	20	1	AU060353
c 5	12.8	1.1	16	1	AI446372
c 6	12.8	1.1	18	1	AJ588273
c 7	12.4	1.1	14	1	BH169716
c 8	12.4	1.1	15	1	CA851710
c 9	12	1.1	15	1	AJ727978

ALIGNMENTS

RESULT 1
AZ457101/c
LOCUS
DEFINITION 1M0260J17F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0260J17 F, genomic survey sequence.
ACCESSION AZ457101
VERSION AZ457101.1 GI:10615226
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5066
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0260 row: J column: 17
Seq primer: GGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0260J17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 920 TAGAGCCTTATTAGAAATGCAG 941
Db 22 TGGAGGCTTTTGAGAAATGCAG 1

RESULT 2
D44776/c

LOCUS
DEFINITION HUMSUPY214 Human brain cDNA Homo sapiens cDNA clone MF51-S-2, mRNA
sequence.
ACCESSION D44776
VERSION D44776.1 GI:1572251
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

Hadano, S., Ishida, Y., Tomiyasu, H., Yamamoto, K., Bates, G.P. and

Ikedo, J.

Transcript map of the human chromosome 4p16.3 consisting of 627

cDNA clones derived from 1 Mb of the Huntington's disease locus

DNA Res. 3 (4), 239-255 (1996)

97101646

PUBMED

8946164

est.res

Fri Aug 19 10:59:58 2005

COMMENT
Contact: Shinji Hadano
Japan Science and Technology Corporation, NeuroGenes Project, ICORP
Univ. of Tokai School of Med.
Boheidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-5095
Fax: 81-463-91-4993
Email: shinji@nga.med.u-tokai.ac.jp.

FEATURES
source

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Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 390 CAGTCATTTTCCTTACAA 407
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DB 19 CAGTCATTTTCCCAACA 2

RESULT 3
AZ579189 19 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
IM0363112P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0363112 F, genomic survey sequence.

ACCESSION
AZ579189
VERSION
KEYWORDS
SOURCE
GSS.

ORGANISM
Mus musculus
(house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: I column: 12
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends

FEATURES
source

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Location/Qualifiers
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/clone="UUGC1M0363112"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 198 CCATCTCCCCCATCCCCC 215
|||||
DB 2 CCCTCTCCCCCTCCCCC 19

RESULT 4
AU060353

LOCUS
DEFINITION
AU060353 Dictyostelium discoideum SL (H. Urushihara) Dictyostelium
discoideum cDNA clone SLJ384, mRNA sequence.

ACCESSION
AU060353
VERSION
KEYWORDS
SOURCE
GI:4881457

ORGANISM
Dictyostelium discoideum
Dictyostelium discoideum

REFERENCE
AUTHORS
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 20)

TITLE
JOURNAL
COMMENT
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.

FEATURES
source

1.20
Location/Qualifiers
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
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/db_xref="taxon:44689"
/clone="SLJ384"
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/clone_lib="Dictyostelium discoideum SL (H. Urushihara)"

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Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 TTGTTGGCTGTTTCATGT 702
|||||
DB 3 TTGTTGGCTGTTGAATGT 20

RESULT 5
AI446372

LOCUS
DEFINITION
AI446372 NCI_CGAP Gas4 Homo sapiens cDNA clone IMAGE:2141098 3',
tj10C06.x1 similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B.; contains

element MSRI repetitive element ;, mRNA sequence.
 A1446372 1 GI:4294748
 VERSION
 EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 16)
 REFERENCE
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
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 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2141098"
 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_hosts="DH10B"
 /clone_lib="NCI_CGAP Gas4"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
 Query Match 1.1%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3.4;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 204 CCCCCATCCCCCATTT 219
 Db 1 CCCCCCCCCCCCCCATTT 16
 RESULT 6
 AJ588273/c 18 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
 DEFINITION 529E06, genomic survey sequence.
 ACCESSION AJ588273
 VERSION AJ588273.1 GI:37937897
 KEYWORDS GSS; right border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 14)
 REFERENCE
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535
 element MSRI repetitive element ;, mRNA sequence.
 A1446372 1 GI:4294748
 VERSION
 EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 16)
 REFERENCE
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Insert Length: 1948 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 FEATURES
 source Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2141098"
 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_hosts="DH10B"
 /clone_lib="NCI_CGAP Gas4"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
 Query Match 1.1%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3.4;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 204 CCCCCATCCCCCATTT 219
 Db 1 CCCCCCCCCCCCCCATTT 16
 RESULT 6
 AJ588273/c 18 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
 DEFINITION 529E06, genomic survey sequence.
 ACCESSION AJ588273
 VERSION AJ588273.1 GI:37937897
 KEYWORDS GSS; right border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 14)
 REFERENCE
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535

12445565
 PUBMED 2 (bases 1 to 18)
 REFERENCE Balzergue, S.
 AUTHORS Direct Submission
 TITLE Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment (8) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassiliewskaja"
 /db_xref="taxon:3702"
 /clone="529E06"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 misc_feature
 1..18
 /note="T-DNA flanking sequence
 right border"
 Query Match 1.1%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 18 TGCCCCGGCGCGTGGCAGG 35
 Db 18 TGCCCCGGCGCGGAGG 1
 RESULT 7
 BH169716 14 bp DNA linear GSS 03-OCT-2001
 LOCUS Arabidopsis thaliana T-DNA insertion lines Arabidopsis
 DEFINITION SALK_001788 Arabidopsis thaliana T-DNA insertion lines Arabidopsis
 thaliana genomic clone SALK_001788, genomic survey sequence.
 ACCESSION BH169716
 VERSION BH169716.1 GI:15905091
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 14)
 REFERENCE
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmermann, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 CONTACT: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salik.edu
 This is single pass sequence recovered from the left border of
 T-DNA.
 Class: T-DNA tagged.
 FEATURES
 source Location/Qualifiers
 1..14
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"

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/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match      1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.5;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GCTGCCCGGGCCGT 29
DB 1 GCAGCCCGGGCCGT 14

RESULT 8
CA851710      15 bp mRNA linear EST 01-AUG-2003
LOCUS D16F12.124 12.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D16F12 5', mRNA sequence.
ACCESSION CA851710
VERSION CA851710.1 GI:33388503
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 15)
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
Location/Qualifiers
FEATURES
source
1..15
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D16F12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match      1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.8;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1046 CCCACTTCCTTAT 1059
DB 2 CCCACTTCCTTAT 15

RESULT 9
AJ727978/c
LOCUS AJ727978 15 bp mRNA linear EST 07-OCT-2004
DEFINITION AJ727978 riken1 Gallus gallus cDNA clone 32b1389, mRNA sequence.
ACCESSION AJ727978

```

```

VERSION AJ727978.1 GI:53893388
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 15)
AUTHORS Caldwell, R.B., Kierzek, A.M., Atakawa, H., Bezubov, Y., Zaim, J.,
Fiedler, P., Kuter, S., Blagodatski, A., Kostovska, D., Koter, M.,
Plachy, J., Carninci, P., Hayashizaki, Y., and Buerstedde, J.M.
Full-length cDNAs from bursal lymphocytes to facilitate gene
function analysis
JOURNAL Unpublished (2004)
COMMENT Contact: Caldwell, R.B.
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
Location/Qualifiers
FEATURES
source
1..15
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="32b1389"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="riken1"
/note="CB inbred strain"

Query Match      1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 AGGACATTGTGA 977
DB 13 AGGACATTGTGA 2

Search completed: August 19, 2005, 10:37:47
Job time : 0.001 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:56:24 ; Search time 8 Seconds
(without alignments)
2.891 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gctggcttggcagcgtgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY NUC
Gap 10.0 , Gapext 0.5

Searched: 536 seqs, 10381 residues

Total number of hits satisfying chosen parameters: 1072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 537 summaries

Database : ngsdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	60	5.4	60	1 ACA56897
2	51	4.6	51	1 AAH90177
3	49.4	4.4	51	1 AAH90178
4	22	2.0	22	1 ADR27689
5	21	1.9	21	1 ADT71352
6	20.2	1.8	25	1 ACK10810
7	20	1.8	20	1 AAV17684
8	20	1.8	20	1 AAV17685
9	20	1.8	20	1 AAK95054
10	20	1.8	20	1 ADJ32266
11	20	1.8	20	1 ADR27690
12	20	1.8	20	1 ADR27680
13	20	1.8	20	1 ADR27685
14	20	1.8	20	1 ADR27653
15	20	1.8	20	1 ADR27682
16	20	1.8	20	1 ADR27688
17	20	1.8	20	1 ADR27681
18	20	1.8	20	1 ADR27687
19	20	1.8	20	1 ADR27679
20	20	1.8	20	1 ADR27692
21	20	1.8	20	1 ADR27683
22	20	1.8	20	1 ADR27686
23	20	1.8	20	1 ADR27684
24	20	1.8	20	1 ADR27691
25	20	1.8	20	1 ADT71351
26	19.8	1.8	25	1 ABK39905
27	19	1.7	19	1 AAT64982
28	18.6	1.7	25	1 ACK10811
29	18.2	1.6	25	1 ACI63081
30	18	1.6	18	1 AAT64981
31	18	1.6	18	1 AAT85600
32	18	1.6	18	1 AAT85601
33	18	1.6	18	1 ACA75490

34	18	1.6	18	1 ACA75491	Human WSX receptor
35	18	1.6	18	1 ACH66797	Human WSX receptor
c 36	18	1.6	18	1 ACH66796	Human WSX receptor
c 37	18	1.6	18	1 ADC08932	Human WSX receptor
c 38	18	1.6	18	1 ADC08931	Human WSX receptor
c 39	17.6	1.6	24	1 AAD38375	Human BAT-25 locus
c 40	17.6	1.6	24	1 AET03742	Human Phox2b gene
c 41	17.6	1.6	24	1 AAD36414	Human BAT-25 loci
c 42	17.6	1.6	24	1 AAD31191	Human microarray D
c 43	17.6	1.6	25	1 ACI87101	Human microarray D
c 44	17	1.5	17	1 ADI51286	Human tumour suppressor
c 45	16.8	1.5	20	1 ADJ25095	Human endothelial
c 46	16.8	1.5	20	1 ADJ25250	Human endothelial
c 47	16.8	1.5	20	1 AAAS0752	PCR primer 1F used
c 48	16.8	1.5	24	1 AAT89716	PCR primer used for
c 49	16.8	1.5	24	1 ABA9037	PCR primer correspond
c 50	16.6	1.5	23	1 AAS03279	Rat PDGF-associate
c 51	16.6	1.5	23	1 ABZ30445	Candida albicans G
c 52	16.6	1.5	23	1 ABZ30445	Murine fangc/xrcc9
c 53	16.2	1.5	23	1 ADK67738	Chromosome 11 (loc
c 54	16.2	1.5	21	1 AAQ82600	Primer #2 to ampl
c 55	16.2	1.5	21	1 AAT65977	Human multidrug re
c 56	16.2	1.5	23	1 ABK86295	Human TGR342 RT-PC
c 57	16.2	1.5	23	1 ADB15943	EKX1-IR human-sp
c 58	16	1.4	16	1 ADR27674	Leptin receptor re
c 59	16	1.4	17	1 ADI52070	Human tumour suppressor
c 60	16	1.4	20	1 AAS97676	Human SAC1 gene-9p
c 61	16	1.4	20	1 AAS97674	Human SAC1 gene-9p
c 62	16	1.4	20	1 ADJ93118	Human G-coupled re
c 63	16	1.4	20	1 ADM16016	Human SAC1 DNA PCR
c 64	16	1.4	20	1 ADM16014	Human SAC1 DNA PCR
c 65	15.8	1.4	19	1 ADE78595	Endogenous caroten
c 66	15.8	1.4	19	1 ADF50077	Human BCL2 siNA up
c 67	15.8	1.4	19	1 ADF49663	Human BCL2 siNA up
c 68	15.8	1.4	20	1 AAT36558	Campylobacter fetu
c 69	15.8	1.4	20	1 ADG37263	Fox specific PCR p
c 70	15.8	1.4	20	1 ADG86812	Human PPAR antisense
c 71	15.8	1.4	20	1 ADG86960	Human PPAR antisense
c 72	15.8	1.4	20	1 ADJ61530	Oligonucleotide as
c 73	15.8	1.4	20	1 ADJ24889	Human endothelial
c 74	15.8	1.4	20	1 ADJ23864	Human endothelial
c 75	15.8	1.4	20	1 ADL34750	Antisense oligonuc
c 76	15.8	1.4	20	1 ADL34898	Human PPAR-delta t
c 77	15.8	1.4	20	1 ADO46920	Human oligonucleot
c 78	15.8	1.4	21	1 ABV76832	Control PCR primer
c 79	15.8	1.4	21	1 ADA73990	PCR primer #1 for
c 80	15.8	1.4	22	1 AAS23701	Primer A #15 used
c 81	15.8	1.4	22	1 ABZ29880	Candida albicans G
c 82	15.6	1.4	20	1 AAV75536	H. pylori vaca pro
c 83	15.6	1.4	22	1 ADH42586	Novel human nuclei
c 84	15.6	1.4	22	1 ADS75784	DNA molecule prepa
c 85	15.6	1.4	22	1 ADS08410	STS marker seconda
c 86	15.4	1.4	17	1 ABK18401	Human ERG hamme
c 87	15.4	1.4	17	1 ABT38549	Tumour suppression
c 88	15.4	1.4	17	1 ADB42880	Tumour suppression
c 89	15.4	1.4	17	1 AAZ77304	Human biallelic ma
c 90	15.4	1.4	18	1 ADJ24780	Human CYP2D6 C100T
c 91	15.4	1.4	19	1 AAQ81302	Ribozyme target se
c 92	15.4	1.4	19	1 AA85723	Cyclin B1 ribozyme
c 93	15.4	1.4	19	1 AA85723	Cyclin B1 ribozyme
c 94	15.4	1.4	20	1 AAT50899	Probe #13 for inc
c 95	15.4	1.4	20	1 AAAS97050	Mouse anti-human D
c 96	15.4	1.4	20	1 AAL60465	Single nucleotide
c 97	15.4	1.4	20	1 ADF87587	TRA-8 antibody PCR
c 98	15.4	1.4	20	1 ADJ79773	Human endothelial
c 99	15.4	1.4	20	1 ADJ25296	Human endothelial
100	15.4	1.4	20	1 ADJ24880	Chimeric phosphor
101	15.4	1.4	20	1 ADP78840	Chimeric phosphor
102	15.4	1.4	20	1 ADP78598	Chimeric phosphor
103	15.4	1.4	20	1 ADP78693	Chimeric phosphor
104	15.4	1.4	21	1 ADP78666	Chimeric phosphor
c 105	15.4	1.4	21	1 ADK53793	DMS:acceptor oxido
c 106	15.2	1.4	20	1 AAX96738	PCR primer used to

C 107	15.2	1.4	20	1	AAC67691	Oligonucleotide #2
C 108	15.2	1.4	20	1	AAF23345	Oligonucleotide fo
C 109	15.2	1.4	20	1	AAD20131	Human histone deac
C 110	15.2	1.4	20	1	AAF23365	PCR primer specifi
C 111	15.2	1.4	20	1	ABV73091	Human HDAC-8 mRNA
C 112	15.2	1.4	20	1	ABV73053	Capture oligonucle
C 113	15.2	1.4	20	1	ABX87739	Human histone deac
C 114	15.2	1.4	20	1	ABV74507	Human histone deac
C 115	15.2	1.4	20	1	ABK87739	Human HDAC-8 antis
C 116	15.2	1.4	20	1	ADG79289	5'-RACE primer for
C 117	15.2	1.4	20	1	ADG76492	Human HDAC8 mRNA t
C 118	15.2	1.4	20	1	ADH50696	Human IRAK-1 DNA t
C 119	15.2	1.4	20	1	ADH50625	Hepatoma-derived g
C 120	15.2	1.4	20	1	ADJ45254	Hepatoma-derived g
C 121	15.2	1.4	20	1	ADJ45325	Human HDAC8-specif
C 122	15.2	1.4	20	1	ADJ34745	Human breast cance
C 123	15.2	1.4	20	1	ADJ96374	Human breast cance
C 124	15.2	1.4	20	1	ADJ96440	Human endothelial
C 125	15.2	1.4	20	1	ADJ23337	Human endothelial
C 126	15.2	1.4	20	1	ADJ23394	Human histone deac
C 127	15.2	1.4	20	1	ADO07539	Human histone deac
C 128	15.2	1.4	20	1	ADR20736	Asialoglycoprotein
C 129	15.2	1.4	21	1	AAT66953	Human gene single
C 130	15.2	1.4	21	1	AAF95925	Human gene single
C 131	15.2	1.4	21	1	ABK62248	Human ATP-binding
C 132	15.2	1.4	21	1	ABS98518	Human acetyl choli
C 133	15.2	1.4	21	1	ADH68383	Rosa sp forward PC
C 134	15.2	1.4	21	1	ADRG68090	BAFF siRNA sense s
C 135	15.2	1.4	21	1	AAJ79744	PCR primer H528 f
C 136	15	1.3	20	1	ADJ33553	PCR primer used to
C 137	15	1.3	20	1	AAH73748	Mitogen activated
C 138	14.8	1.3	18	1	ADE29652	Mitogen activated
C 139	14.8	1.3	19	1	ADQ27277	RNA interference t
C 140	14.8	1.3	19	1	ADR27528	Human single nucle
C 141	14.8	1.3	19	1	AAQ27277	PCR primer for det
C 142	14.8	1.3	19	1	AAQ27277	Human Int6 exon 3
C 143	14.8	1.3	20	1	AAI72504	PCR primer used to
C 144	14.8	1.3	20	1	AAZ03074	Mouse IL-5R antis
C 145	14.8	1.3	20	1	AAZ03074	Mouse IL-5R antis
C 146	14.8	1.3	20	1	AAZ03074	Mouse IL-5R antis
C 147	14.8	1.3	20	1	AAZ03074	Mouse IL-5R antis
C 148	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 149	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 150	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 151	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 152	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 153	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 154	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 155	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 156	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 157	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 158	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 159	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 160	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 161	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 162	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 163	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 164	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 165	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 166	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 167	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 168	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 169	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 170	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 171	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 172	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 173	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 174	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 175	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 176	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 177	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 178	14.8	1.3	20	1	AAZ03074	Human chromosome 2
C 179	14.8	1.3	20	1	AAZ03074	Human chromosome 2

C 180	14.8	1.3	21	1	ACF62466	Cancer based on CY
C 181	14.8	1.3	21	1	ADB21135	MRP1 based cancer
C 182	14.8	1.3	21	1	ADB21135	MRP1 based cancer
C 183	14.8	1.3	21	1	ADB21135	MRP1 based cancer
C 184	14.8	1.3	21	1	ADB21137	MRP1 based cancer
C 185	14.8	1.3	21	1	ADB88225	Human UGT1A1 varia
C 186	14.8	1.3	21	1	ADB88227	Human UGT1A1 varia
C 187	14.8	1.3	21	1	ADB88224	Human UGT1A1 varia
C 188	14.8	1.3	21	1	ADB88226	Human UGT1A1 varia
C 189	14.8	1.3	21	1	ADB88227	Human UGT1A1 varia
C 190	14.8	1.3	21	1	ADB97207	Human MRP1 variant
C 191	14.8	1.3	21	1	ADB97210	Human MRP1 variant
C 192	14.8	1.3	21	1	ADB97209	Human MRP1 variant
C 193	14.8	1.3	21	1	ADB92401	Human MRP1 variant
C 194	14.8	1.3	21	1	ADB92399	Human MRP1 variant
C 195	14.8	1.3	21	1	ADB92398	Human MRP1 variant
C 196	14.8	1.3	21	1	ADB92400	Human MRP1 variant
C 197	14.8	1.3	21	1	ADP87704	Single nucleotide
C 198	14.8	1.3	21	1	ADP46739	Human c-Cbl siRNA
C 199	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 200	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 201	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 202	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 203	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 204	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 205	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 206	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 207	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 208	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 212	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 215	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 217	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 218	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 219	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 220	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 221	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 222	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 223	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 224	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 226	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 230	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 231	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 232	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 233	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 240	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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C 246	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 247	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 248	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
C 249	14.8	1.3	21	1	ADP46857	Human c-Cbl siRNA
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253 14.2 1.3 19 1 ADR70528 Reverse RTQ primer
 c 254 14.2 1.3 19 1 ADR75949 Human apolipoprote
 c 255 14.2 1.3 19 1 ADR78567 Human apolipoprote
 c 256 14.2 1.3 19 1 ADR78627 Human apolipoprote
 c 257 14.2 1.3 19 1 ADR78845 Human apolipoprote
 258 14.2 1.3 20 1 AAQ35765 M segment 5' fragm
 c 259 14.2 1.3 20 1 AAQ53275 CTV primer 5' Sy
 c 260 14.2 1.3 20 1 AAQ97957 PNA oligomer targe
 c 261 14.2 1.3 20 1 AAQ84260 PKC-epsilon coding
 262 14.2 1.3 20 1 AAQV01278 Guanylate cyclase
 c 263 14.2 1.3 20 1 AAX22647 Human protein kina
 c 264 14.2 1.3 20 1 AAX76903 H2-1 Pagl gene dir
 c 265 14.2 1.3 20 1 AAX78609 Human PKC-epsilon
 c 266 14.2 1.3 20 1 AAX83735 Human protein kina
 c 267 14.2 1.3 20 1 AAX92824 PCR primer used to
 268 14.2 1.3 20 1 AAX94795 PCR primer used to
 c 269 14.2 1.3 20 1 AAX95833 PCR primer used to
 270 14.2 1.3 20 1 AAX97255 Primer used to amp
 c 271 14.2 1.3 20 1 AAX95840 PCR primer used to
 c 272 14.2 1.3 20 1 AAX19212 Human PKC-epsilon
 c 273 14.2 1.3 20 1 AAX227351 Human protein kina
 c 274 14.2 1.3 20 1 AAX275053 Human biallelic ma
 c 275 14.2 1.3 20 1 AAX64912 Antisense oligonuc
 c 276 14.2 1.3 20 1 AAF62444 A thaliana VBN1 ge
 c 277 14.2 1.3 20 1 AAF23509 Primer cadp-R1C.
 c 278 14.2 1.3 20 1 AAC92586 Human nucleolin ph
 c 279 14.2 1.3 20 1 AAI65644 Primer for microsa
 c 280 14.2 1.3 20 1 ABA82285 Zmax1 gene region
 c 281 14.2 1.3 20 1 AAL46974 Cell cycle regulat
 c 282 14.2 1.3 20 1 ABL90939 Human protein kina
 c 283 14.2 1.3 20 1 AAL45924 Murine cystrophin-
 c 284 14.2 1.3 20 1 ABL45469 Human chromosome 2
 c 285 14.2 1.3 20 1 ABL44467 NES-1 gene methyla
 c 286 14.2 1.3 20 1 ABT06471 Mouse syntaxin 4 i
 c 287 14.2 1.3 20 1 ABO62452 Human Zmax1 cDNA r
 c 288 14.2 1.3 20 1 ABE23082 Human RecQ protein
 c 289 14.2 1.3 20 1 ABE68905 Human interleukin-
 c 290 14.2 1.3 20 1 AAD41640 Solid surface aese
 c 291 14.2 1.3 20 1 ADE31838 Multiplex group PC
 c 292 14.2 1.3 20 1 AFT21432 Reverse PCR primer
 c 293 14.2 1.3 20 1 ABE10661 Human HBM STS mark
 c 294 14.2 1.3 20 1 ACC45665 Human protein PPI3
 c 295 14.2 1.3 20 1 ABE280435 Human protein kina
 c 296 14.2 1.3 20 1 ACH11218 RIZ(A)8 tract prim
 c 297 14.2 1.3 20 1 ACA62693 Chimeric antisense
 c 298 14.2 1.3 20 1 AFT44202 Sequence tagged si
 c 299 14.2 1.3 20 1 ADB98363 Oreochromis niloti
 c 300 14.2 1.3 20 1 ADD20426 S. pneumoniae vncs
 c 301 14.2 1.3 20 1 ADH90778 Mammalian inverted
 c 302 14.2 1.3 20 1 ACH00690 Human oligonucleot
 c 303 14.2 1.3 20 1 ABZ91305 Human PDE4C oligon
 c 304 14.2 1.3 20 1 ABZ99318 Human oligonucleot
 c 305 14.2 1.3 20 1 ABE288740 Human oligonucleot
 c 306 14.2 1.3 20 1 ABQ84375 DP10 PCR primer #
 c 307 14.2 1.3 20 1 ABE77118 Human stearyl-CoA
 c 308 14.2 1.3 20 1 ABV99953 Coriolus versicolo
 c 309 14.2 1.3 20 1 ADM83692 Serine protease-li
 c 310 14.2 1.3 20 1 ADM83766 Serine protease-li
 c 311 14.2 1.3 20 1 ABE27535 AA486238-derived o
 c 312 14.2 1.3 20 1 ABE24970 A1138216-derived o
 c 313 14.2 1.3 20 1 ABE32349 Human PDE4C-deri
 c 314 14.2 1.3 20 1 ADH47993 Protein kinase C e
 c 315 14.2 1.3 20 1 ADH58845 Human CDC-like kin
 c 316 14.2 1.3 20 1 ADH58791 Human CDC-like kin
 c 317 14.2 1.3 20 1 ADH65127 Human glucocortic
 c 318 14.2 1.3 20 1 ADH65989 Human glucocortic
 c 319 14.2 1.3 20 1 ADH65276 Human glucocortic
 c 320 14.2 1.3 20 1 ADH64643 Human glucocortic
 c 321 14.2 1.3 20 1 ADH65757 Human glucocortic
 c 322 14.2 1.3 20 1 ADH65015 Human glucocortic
 c 323 14.2 1.3 20 1 ADI79588 Human HMG-CoA redu
 c 324 14.2 1.3 20 1 ADI79785 Human HMG-CoA redu
 325 14.2 1.3 20 1 ADI44833 Human cystic fibro

c 326 14.2 1.3 20 1 ADJ61611 Oligonucleotide as
 c 327 14.2 1.3 20 1 ADJ61203 Oligonucleotide as
 c 328 14.2 1.3 20 1 ADJ19254 Antisense 2-NOE ga
 c 329 14.2 1.3 20 1 ADJ18790 Antisense DNA olig
 c 330 14.2 1.3 20 1 ADJ18263 Antisense DNA olig
 c 331 14.2 1.3 20 1 ADJ18084 Antisense DNA olig
 c 332 14.2 1.3 20 1 ADJ17966 Antisense DNA olig
 c 333 14.2 1.3 20 1 ADJ24119 Human endothelial
 c 334 14.2 1.3 20 1 ADJ24136 Human endothelial
 c 335 14.2 1.3 20 1 ADJ24120 Human endothelial
 c 336 14.2 1.3 20 1 ADK80500 Chimeric phosphoro
 c 337 14.2 1.3 20 1 ADK80983 Chimeric phosphoro
 c 338 14.2 1.3 20 1 ADL97965 Mx2 probe, SEQ ID
 c 339 14.2 1.3 20 1 ADO46593 Human oligonucleot
 c 340 14.2 1.3 20 1 ADO47001 Human oligonucleot
 c 341 14.2 1.3 20 1 ADP12146 Tagman probe set 2
 c 342 14.2 1.3 20 1 ADP68640 Human PPAR-alpha a
 c 343 14.2 1.3 20 1 ADR27036 Human single nucle
 c 344 14.2 1.3 20 1 ADR17228 Human chromosome 1
 c 345 14.2 1.3 20 1 ADR67431 PCR primer used to
 c 346 14.2 1.3 20 1 ADR47879 Human chromosome 1
 c 347 14.2 1.3 20 1 ADS31697 Gene expression in
 c 348 14.2 1.3 20 1 ADS31698 Gene expression in
 c 349 14.2 1.3 20 1 ADR27673 Leptin receptor re
 c 350 14.2 1.3 20 1 AAT54666 Mouse IL-5 hammezh
 c 351 14.2 1.3 20 1 AAZ63871 Substrate for hamh
 c 352 14.2 1.3 20 1 ABX00924 Hepatitis C virus
 c 353 14.2 1.3 20 1 ABT39781 Tumour suppression
 c 354 14.2 1.3 20 1 AAZ71197 Human biallelic ma
 c 355 14.2 1.3 20 1 AAZ69829 Human biallelic ma
 c 356 14.2 1.3 20 1 AAZ71268 Human biallelic ma
 c 357 14.2 1.3 20 1 AAZ34452 Human TREK2 cDNA s
 c 358 14.2 1.3 20 1 ABLN79739 Human Fas target o
 c 359 14.2 1.3 20 1 AAL42518 Alpha-V integrin-s
 c 360 14.2 1.3 20 1 ACH00628 Mammalian inverted
 c 361 14.2 1.3 20 1 ADH77414 Human PTPN12 antis
 c 362 14.2 1.3 20 1 ADL27795 Human Fas cDNA, an
 c 363 14.2 1.3 20 1 ADM53567 Human Fas antisens
 c 364 13.8 1.2 17 1 AAQ40912 C-erb-B2 sense oli
 c 365 13.8 1.2 17 1 AAQ40911 C-erb-B2 antisense
 c 366 13.8 1.2 17 1 AAT05984 COX II forward pri
 c 367 13.8 1.2 17 1 AAAL8772 Human TIE-2 suber
 c 368 13.8 1.2 17 1 AAF04220 Hammerhead ribozym
 c 369 13.8 1.2 17 1 AAF04668 Human NOGO Amberzy
 c 370 13.8 1.2 17 1 ABK02567 COXII PCR primer #
 c 371 13.8 1.2 17 1 AAF69066 COXII PCR primer #
 c 372 13.8 1.2 17 1 AAF69029 COXII PCR primer #
 c 373 13.8 1.2 17 1 AAF69063 COXII PCR primer #
 c 374 13.8 1.2 17 1 AAF69064 COXII PCR primer #
 c 375 13.8 1.2 17 1 AAF69018 Human GRD zinzyme
 c 376 13.8 1.2 17 1 ABL46970 Primer for studyn
 c 377 13.8 1.2 17 1 AAI65652 Human GDMPLP-1 17-m
 c 378 13.8 1.2 17 1 ABLN06757 Human GDMPLP-1 17-m
 c 379 13.8 1.2 17 1 ABLN02571 Human GDMPLP-1 17-m
 c 380 13.8 1.2 17 1 ABLN02572 Human HTPL scannin
 c 381 13.8 1.2 17 1 ABV82997 Human ERG Amberzym
 c 382 13.8 1.2 17 1 ABL31405 Human HLA genotypi
 c 383 13.8 1.2 17 1 ABL31405 Human mitochondria
 c 384 13.8 1.2 17 1 ADA49961 Human mitochondria
 c 385 13.8 1.2 17 1 ADA50007 Human mitochondria
 c 386 13.8 1.2 17 1 ADA49972 Human mitochondria
 c 387 13.8 1.2 17 1 ADA50009 Human mitochondria
 c 388 13.8 1.2 17 1 ADA50006 Human PCR primer 9
 c 389 13.8 1.2 17 1 ADA50271 Human NOGO recepto
 c 390 13.8 1.2 17 1 ADL46684 Human NOGO recepto
 c 391 13.8 1.2 17 1 ADM09493 Human ER+ breast c
 c 392 13.8 1.2 17 1 ADM54293 Human GDMPLP-1 prob
 c 393 13.8 1.2 17 1 ADL82299 Human GDMPLP-1 prob
 c 394 13.8 1.2 17 1 ACN69847 Human GDMPLP-1 prob
 c 395 13.8 1.2 17 1 ACN65662 Human GDMPLP-1 prob
 c 396 13.8 1.2 17 1 ACN65661 Human uncoupling p
 c 397 13.8 1.2 18 1 AAV44608 HEV US-1 amplifin
 c 398 13.8 1.2 18 1 AAZ00111

C 399	13.8	1.2	18	1	AAZ76902	H2-1 Pagl gene dir	472	13.4	1.2	18	1	AAZ90709	Forward primer for
C 400	13.8	1.2	18	1	AAZ71685	Human biallelic ma	473	13.4	1.2	18	1	AAZ71388	Human biallelic ma
C 401	13.8	1.2	18	1	AAZ76996	Human biallelic ma	C 474	13.4	1.2	18	1	AAZ71139	Human biallelic ma
C 402	13.8	1.2	18	1	AAZ70376	Human biallelic ma	C 475	13.4	1.2	18	1	AAZ98939	Dog genomic marker
C 403	13.8	1.2	18	1	ABU54891	PCR primer BV-b5,	C 476	13.4	1.2	18	1	AAAG6260	Human KVLQIT exon
C 404	13.8	1.2	18	1	ACF63028	Human progesterone	C 477	13.4	1.2	18	1	AAAC9949	Neurofibromatosis
C 405	13.8	1.2	18	1	ACF63026	Human progesterone	C 478	13.4	1.2	18	1	AAAS0539	PCR primer used to
C 406	13.8	1.2	18	1	ADM06379	Human PCR primer S	C 479	13.4	1.2	18	1	AAV72174	PCR primer used to
C 407	13.8	1.2	18	1	ADJ65208	Human connexin gen	480	13.4	1.2	18	1	ABV76827	Human cyclin-depen
C 408	13.8	1.2	18	1	ADN35818	Human NSCLC gene a	481	13.4	1.2	18	1	ADK13869	PCR primer 2 used
C 409	13.8	1.2	18	1	AAA83453	Oligonucleotide of	C 482	13.4	1.2	18	1	ADN35810	Human NSCLC gene a
C 410	13.8	1.2	19	1	AAA83453	cd8 ribozyme bind	C 483	13.4	1.2	18	1	ADOS6517	PCR primer 2 used
C 411	13.8	1.2	19	1	AAH56706	Streptococcus pyog	C 484	13.4	1.2	18	1	ADR05071	Oligonucleotide of
C 412	13.8	1.2	19	1	AAH58225	Cell-cycle depende	485	13.4	1.2	18	1	ADR05071	Mouse beta defens
C 413	13.8	1.2	19	1	AAH58615	Cell-cycle depende	486	13.4	1.2	18	1	ADR05071	PCR primer for PGI
C 414	13.8	1.2	19	1	AAH58615	P. furiosus thermo	487	13.4	1.2	18	1	AAV23538	Cdc 25 ha ribozyme
C 415	13.8	1.2	19	1	AAH74684	Human IGF-1R trans	C 488	13.4	1.2	19	1	AAZ01215	Human biallelic ma
C 416	13.8	1.2	19	1	ADF31834	Human IGF-1R trans	489	13.4	1.2	19	1	AAZ76970	Human biallelic ma
C 417	13.8	1.2	19	1	ADF31557	Single nucleotide	C 490	13.4	1.2	19	1	AAZ76970	Thermus thermophil
C 418	13.8	1.2	19	1	ADF84849	Oryza minuta P19 1	C 491	13.4	1.2	19	1	AAH61247	Cdc25 hs ribozyme
C 419	13.8	1.2	19	1	ADJ82304	TCPTP associated s	C 492	13.4	1.2	19	1	AAH61247	Human chromosome 1
C 420	13.8	1.2	19	1	ADN75775	TCPTP associated s	C 493	13.4	1.2	19	1	ABL43540	Human ERG2-targete
C 421	13.8	1.2	19	1	ADQ27278	RNA interference t	C 494	13.4	1.2	19	1	ADF85077	Human ERG2-targete
C 422	13.8	1.2	19	1	ADP48850	Mouse Myoic target	C 495	13.4	1.2	19	1	ADF85253	TCPTP2 siRNA #1.
C 423	13.8	1.2	19	1	ADP48849	Mouse Myoic target	C 496	13.4	1.2	19	1	ADN75949	TCPTP2 siRNA #2.
C 424	13.8	1.2	19	1	ADP48849	Human beta actin P	C 497	13.4	1.2	19	1	ADN75949	Analytical probe c
C 425	13.4	1.2	15	1	ADJ82300	KLMSY-encoding nuc	498	13.4	1.2	19	1	ADN75949	Analytical probe c
C 426	13.4	1.2	15	1	ADJ82300	KLMSY-encoding nuc	499	13.4	1.2	19	1	ADO18480	Human apolipoprote
C 427	13.4	1.2	15	1	ADJ82304	KLMSY-encoding nuc	500	13.4	1.2	19	1	ADO18480	Human apolipoprote
C 428	13.4	1.2	15	1	ADG33597	Human HER1-4 hamme	501	13.4	1.2	19	1	ADR77809	HHV-6 associated M
C 429	13.4	1.2	15	1	ADG33597	PCR primer used to	502	13.4	1.2	18	1	AAQ91053	Collagen gene prom
C 430	13.4	1.2	16	1	ADO49843	H. pylori strain J	C 503	13.2	1.2	18	1	AAAT60161	Transforming growt
C 431	13.4	1.2	16	1	ADO50267	H. pylori strain J	C 504	13.2	1.2	18	1	AAAT60161	Human WISP-2 PCR p
C 432	13.4	1.2	16	1	AAAF04357	Hammerhead ribozym	C 505	13.2	1.2	18	1	AAV48417	Human c-TAP-1 mRNA
C 433	13.4	1.2	17	1	AAAF04357	Hammerhead ribozym	506	13.2	1.2	18	1	AAZ76549	Murine tRNA gene f
C 434	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 507	13.2	1.2	18	1	AAZ22179	Mouse tRNA-Ala(g)
C 435	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	508	13.2	1.2	18	1	AAZ22179	Murine Ala tRNA 3'
C 436	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	509	13.2	1.2	18	1	AAZ22179	Murine genomic SNP
C 437	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	510	13.2	1.2	18	1	AAZ22179	Collagen promoter
C 438	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	511	13.2	1.2	18	1	AAZ22179	CMV GlyB detection
C 439	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 512	13.2	1.2	18	1	AAZ22179	Murine tRNA oligon
C 440	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	513	13.2	1.2	18	1	AAZ22179	Murine tRNA oligon
C 441	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	514	13.2	1.2	18	1	AAZ22179	Human biallelic ma
C 442	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	515	13.2	1.2	18	1	AAZ22179	Human biallelic ma
C 443	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	516	13.2	1.2	18	1	AAZ22179	Human biallelic ma
C 444	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	517	13.2	1.2	18	1	AAZ22179	TM7XN1 cDNA antise
C 445	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 518	13.2	1.2	18	1	AAZ22179	PCR primer used to
C 446	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 519	13.2	1.2	18	1	AAZ22179	Reverse primer #96
C 447	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 520	13.2	1.2	18	1	AAZ22179	Human mGluR1beta G
C 448	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 521	13.2	1.2	18	1	AAZ22179	Human HCN1 DNA amp
C 449	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 522	13.2	1.2	18	1	AAZ22179	Human glial cell d
C 450	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 523	13.2	1.2	18	1	AAZ22179	Haematopoietic cel
C 451	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 524	13.2	1.2	18	1	AAZ22179	Haematopoietic cel
C 452	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 525	13.2	1.2	18	1	AAZ22179	DNA fragment B amp
C 453	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 526	13.2	1.2	18	1	AAZ22179	PGC-1 mutational a
C 454	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 527	13.2	1.2	18	1	AAZ22179	TCV RdRP mutagenic
C 455	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 528	13.2	1.2	18	1	AAZ22179	Xenopus axis dupli
C 456	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	529	13.2	1.2	18	1	AAZ22179	Mammalian inverted
C 457	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 530	13.2	1.2	18	1	AAZ22179	Human PCR primer S
C 458	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 531	13.2	1.2	18	1	AAZ22179	Human cTAP-1 DNA a
C 459	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 532	13.2	1.2	18	1	AAZ22179	Human MD-1 RP105-a
C 460	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 533	13.2	1.2	18	1	AAZ22179	CENPC1 extend prim
C 461	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 534	13.2	1.2	18	1	AAZ22179	Nitrile hydratase
C 462	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 535	13.2	1.2	18	1	AAZ22179	MGB-probe to deter
C 463	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 536	13.2	1.2	18	1	AAZ22179	Murine oligonucleo
C 464	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym	C 537	13.2	1.2	17	1	AAZ22179	
C 465	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							
C 466	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							
C 467	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							
C 468	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							
C 469	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							
C 470	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							
C 471	13.4	1.2	17	1	AAAF04219	Hammerhead ribozym							

ALIGNMENTS

RESULT 1
ACA56897

ID	ACA56897 standard; cDNA; 60 BP.	ID	AAH90177 standard; cDNA; 51 BP.
XX	ACA56897;	XX	AAH90177;
AC		AC	
DT	10-JUN-2003 (first entry)	DT	08-OCT-2001 (first entry)
XX		XX	
DE	Human cDNA encoding an adipocyte bait protein, OBRGRP_v2.	DE	Human clone cg43922807 SNP site, SEQ ID NO:57.
XX		XX	
XX	Human; ss; gene; bait; adipocyte; SID; selected interacting domain;	XX	Human; single nucleotide polymorphism; SNP; chromosome 1; detection;
KW	anorectic; antidiabetic; protein-protein interaction; diabetes;	KW	identification; gene therapy; genetic disorder; ss.
KW	yeast 2-hybrid assay; metabolic disorder; obesity.	XX	
XX		OS	Homo sapiens.
OS	Homo sapiens.	XX	
XX		FH	Key
XX		FT	Location/Qualifiers
PN	WO200286122-A2.	FT	replace(26,T)
PD		FT	/*tag= a
XX	31-OCT-2002.	FT	/standard_name= "single nucleotide polymorphism"
XX		XX	
XX	14-MAR-2002; 2002WO-EF003768.	PN	WO200147942-A2.
PF		XX	
XX	14-MAR-2001; 2001US-0275734P.	PD	05-JUL-2001.
XX		XX	
XX	(HYBR-) HYBRIGENICS.	XX	27-DEC-2000; 2000WO-US035387.
PA		PF	
XX		XX	27-DEC-1999; 99US-00472865.
PI	Legrain P, Daviet L;	PR	
XX		XX	(CURA-) CURAGEN CORP.
XX		PA	
DR	WPI; 2003-103412/09.	PI	Shinkets RA, Leach M;
DR	P-PSDB; ABU70363.	XX	
XX		XX	WPI; 2001-425617/45.
XX		XX	
PT	New complex between two interacting proteins in adipocyte cells, useful	XX	
PT	for identifying selected interacting domains that modulate protein	PT	New polynucleotides containing single nucleotide polymorphisms, for
PT	interactions, or for preventing or treating metabolic disorders such as	PT	detecting the presence of polymorphism, detecting a polymorphic site, and
PT	obesity or diabetes.	PT	treating a patient suffering from a pathology ascribed to the
XX		PT	polymorphism.
PS	Claim 1; Page 41; 382pp; English.	XX	
XX		XX	Claim 1; Page 69; 295pp; English.
CC	The invention relates to a complex between two interacting proteins in	PS	
CC	adipocyte cells, given in the specification. The proteins are identified	XX	
CC	by selecting a bait protein from a known adipocyte marker and then	XX	Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC	performing a yeast 2-hybrid selection to isolate prey proteins encoded by	CC	contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568
CC	members of an adipocyte cDNA library. The proteins are designated SID	CC	(AAH90121-AAH90688) are consecutive pairs of nucleotides which contain
CC	(RTM) (selected interacting domains) proteins. Also included are a	CC	silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive
CC	polynucleotide encoding a polypeptide in the adipocyte cells, a	CC	pairs of nucleotides containing SNPs which result in changes in the
CC	recombinant host cell expressing at least one of the interacting	CC	corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in
CC	polypeptides of the complex, selecting a modulating compound in adipocyte	CC	sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino acid
CC	cells, a SID (RTM) polypeptide comprising any of the 738 amino acid	CC	changes, while those in sequences 575 to 578 (AAH90695-AAH90698) result
CC	sequences given in the specification (including its fragment or variant),	CC	in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699-
CC	a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences	CC	AAH90700) generates a frameshift mutation. The invention also relates to
CC	given in the specification (including its fragment or variant), a vector	CC	a method of detecting a polymorphic site in a nucleic acid and a method
CC	comprising the vector, a protein chip comprising the polypeptides and a	CC	of determining the relatedness of two nucleic acids. It also encompasses
CC	record comprising all or part of the data, listed in the specification.	CC	peptides containing polymorphic sites, antibodies raised against such
CC	The complex, polypeptides, polynucleotides and compounds are useful for	CC	peptides, and a method of detecting polymorphic proteins/peptides using
CC	preventing or treating metabolic disorders such as obesity or diabetes.	CC	the antibodies. The nucleic acids are useful for gene therapy of an
CC	The polynucleotides are useful as probes or primers. The complex is	CC	individual having, suspected of having, or at risk of developing a
CC	particularly useful for identifying selected interacting domains (SID	CC	pathological condition due to the presence of a sequence polymorphism.
CC	(RTM)) for screening drugs that modulate the protein interaction, thus	CC	Such treatment would comprise administration of the wild-type nucleic
CC	exhibiting the therapeutic effect. The present sequence encodes a bait	CC	acid sequence. Antibodies raised against polymorphic peptides can also be
CC	protein used to generate the complexes of the invention	CC	used in the treatment of such individuals
XX		XX	
XX		XX	Sequence 51 BP; 13 A; 17 C; 13 G; 8 T; 0 U; 0 Other;
SQ	Sequence 60 BP; 18 A; 15 C; 15 G; 12 T; 0 U; 0 Other;	SQ	Sequence 51 BP; 13 A; 17 C; 13 G; 8 T; 0 U; 0 Other;
Query Match 5.4%; Score 60; DB 1; Length 60;		Query Match 4.6%; Score 51; DB 1; Length 51;	
Best Local Similarity 100.0%; Pred. No. 1.5e-06;		Best Local Similarity 100.0%; Pred. No. 6.1e-05;	
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	221 ATTGCCAAAGAGTCACTATGACTCAGATGCAACAGTAGTGCCTGTGGGAATGGCA 280	QY	820 AGGCCCTCTCATGACCCAGAGAGCGCGGTGGATCCCTCTTTGTGTGTAG 870
DB	1 ATTGCCAAAGAGTCACTATGACTCAGATGCAACAGTAGTGCCTGTGGGAATGGCA 60	DB	.51 AGGCCCTCTCATGACCCAGAGAGCGCGGTGGATCCCTCTTTGTGTGTAG 1
RESULT 2		RESULT 3	
AAH90177/c		AAH90178/c	

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ID	AAH90178	standard; cdna; 51 BP.	ID	ADR27689	standard; DNA; 22 BP.
XX	AAH90178;		XX	ADR27689;	
XX	08-OCT-2001	(first entry)	XX	04-NOV-2004	(first entry)
XX	Human clone cg43922807	SNP site, SEQ ID NO:58.	XX	OB-RGRP	antisense oligonucleotide, AS 11.
XX	Human; single nucleotide polymorphism; SNP; chromosome 1; detection;		XX	Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;	
XX	Identification; gene therapy; genetic disorder; ss.		XX	Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;	
XX	Homo sapiens.		XX	Leptin receptor related protein; OB-RGRP; leptin receptor;	
XX	Key	Location/Qualifiers	XX	leptin-related disorders; osteoporosis; calcification; obesity; diabetes;	
XX	variation	/tag= a	XX	anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;	
XX		/standard_name= "single nucleotide polymorphism"	XX	thrombus formation; immunity; inflammation; fetal development; cancer;	
XX	WO200147942-A2.		XX	antisense; ss.	
XX	05-JUL-2001.		XX	Synthetic.	
XX	27-DEC-2000; 2000WO-US035387.		XX	Key	Location/Qualifiers
XX	27-DEC-1999; 99US-00472865.		XX	modified_base	1. .20
XX	(CURA-) CURAGEN CORP.		XX		/tag= b
XX	Shimkets RA, Leach M;		XX		/mod_base= OTHER
XX	WPI; 2001-425617/45.		XX		/note= "Optional thioester"
XX	New polynucleotides containing single nucleotide polymorphisms, for		XX	modified_base	1. .5
XX	detecting the presence of polymorphism, detecting a polymorphic site, and		XX		/tag= a
XX	treating a patient suffering from a pathology ascribed to the		XX		/mod_base= OTHER
XX	polymorphism.		XX		/note= "2' O-methylation"
XX	Claim 1; Page 69; 295pp; English.		XX	modified_base	18. .22
XX	Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which		XX		/tag= c
XX	contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568		XX		/mod_base= OTHER
XX	(AAH90121-AAH90688) are consecutive pairs of nucleotides which contain		XX		/note= "2' O-methylation"
XX	silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive		XX		/tag= d
XX	pairs of nucleotides containing SNPs which result in changes in the		XX		/mod_base= OTHER
XX	corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in		XX		/note= "3' triethyleneglycol spacer"
XX	changes, while those in sequences 575 to 578 (AAH90695-AAH90698) result		XX		
XX	in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699-		XX		
XX	AAH90700) generates a frameshift mutation. The invention also relates to		XX		
XX	a method of detecting a polymorphic site in a nucleic acid and a method		XX		
XX	of determining the relatedness of two nucleic acids. It also encompasses		XX		
XX	peptides containing polymorphic sites, antibodies raised against such		XX		
XX	peptides, and a method of detecting polymorphic proteins/ peptides using		XX		
XX	the antibodies. The nucleic acids are useful for gene therapy of an		XX		
XX	individual having, suspected of having, or at risk of developing a		XX		
XX	pathological condition due to the presence of a sequence polymorphism.		XX		
XX	Such treatment would comprise administration of the wild-type nucleic		XX		
XX	acid sequence. Antibodies raised against polymorphic peptides can also be		XX		
XX	used in the treatment of such individuals		XX		
XX	Sequence 51 BP; 13 A; 16 C; 13 G; 9 T; 0 U; 0 Other;		XX		
XX	Query Match	4.4%; Score 49.4; DB 1; Length 51;	XX		
XX	Best Local Similarity	98.0%; Pred. No. 0.00012;	XX		
XX	Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		XX		
QY	820	AGGCTCTCATGACCCAGGAGCCGGGTGGATCCCTTTGTGTGTGAG 870	XX		
Db	51	AGGCTCTCATGACCCAGGAGCCGGGTGGATCCCTTTGTGTGTGAG 1	XX		
RESULT 4			XX		
ADR27689/c			XX		

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Db 1 TTCATCTGAGTTTCCAGCCGTCT 25

RESULT 7
AAV17684/C
ID AAV17684 standard; DNA; 20 BP.
XX
AC AAV17684;
XX
DT 10-JUL-1998 (first entry)
XX
DE PCR primer P1 used to amplify a leptin receptor gene-related protein.
XX
DE Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703;
KW treatment; cancer; connective tissue disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX WO9805792-A2.
XX
PD 12-FEB-1998.
XX
PF 25-JUL-1997; 97WO-US014191.
XX
PR 01-AUG-1996; 96US-00691071.
PR 15-APR-1997; 97US-00843370.
XX (INCY-) INCYTE PHARM INC.
XX
XX Akerblom IE;
XX
XX WPI; 1998-145624/13.
XX
XX DNA encoding human leptin receptor gene-related protein - useful for,
PT e.g. screening for drugs used in treatment of metabolic, reproductive,
PT developmental and connective tissue disorders or cancer.
XX
XX Disclosure; Page 36; 60pp; English.
XX
XX PCR primers AAV17684-87 are used in a reverse transcriptase PCR (RT-PCR)
CC reaction to amplify DNA encoding human leptin receptor gene-related
CC protein (LRGRP). The cDNA sequence was first isolated in Incyte clone
CC 492703 from the hNT2 cell line cDNA library through a computer generated
CC search for amino acid sequence alignments. The LRGRP protein has some
CC homology to the membrane associated proteins of Caenorhabditis elegans
CC ORF C30B.2 and Saccharomyces cerevisiae ORF YJR044c. The agonists of LRGRP
CC can be used to treat metabolic, reproductive and developmental disorders,
CC whilst antagonists of LRGRP can be used for treatment of cancer or
CC connective tissue disorders e.g. rheumatoid arthritis and Sjogren's
CC syndrome. Polynucleotides which hybridise to the LRGRP nucleotide
CC sequence can be used for detection
XX
XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 354 AATGGGGAGCTGCGGCTT 373
Db 20 AATGGGGAGCTGCGGCTT 1
XX
RESULT 8
AAV17685
ID AAV17685 standard; DNA; 20 BP.
XX
AC AAV17685;
XX
XX 10-JUL-1998 (first entry)
DT
XX PCR primer P2 used to amplify a leptin receptor gene-related protein.
DE

XX
KW Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703;
KW treatment; cancer; connective tissue disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX WO9805792-A2.
XX
PD 12-FEB-1998.
XX
PF 25-JUL-1997; 97WO-US014191.
XX
PR 01-AUG-1996; 96US-00691071.
PR 15-APR-1997; 97US-00843370.
XX (INCY-) INCYTE PHARM INC.
XX
XX Akerblom IE;
XX
XX WPI; 1998-145624/13.
XX
XX DNA encoding human leptin receptor gene-related protein - useful for,
PT e.g. screening for drugs used in treatment of metabolic, reproductive,
PT developmental and connective tissue disorders or cancer.
XX
XX Disclosure; Page 36; 60pp; English.
XX
XX PCR primers AAV17684-87 are used in a reverse transcriptase PCR (RT-PCR)
CC reaction to amplify DNA encoding human leptin receptor gene-related
CC protein (LRGRP). The cDNA sequence was first isolated in Incyte clone
CC 492703 from the hNT2 cell line cDNA library through a computer generated
CC search for amino acid sequence alignments. The LRGRP protein has some
CC homology to the membrane associated proteins of Caenorhabditis elegans
CC ORF C30B.2 and Saccharomyces cerevisiae ORF YJR044c. The agonists of LRGRP
CC can be used to treat metabolic, reproductive and developmental disorders,
CC whilst antagonists of LRGRP can be used for treatment of cancer or
CC connective tissue disorders e.g. rheumatoid arthritis and Sjogren's
CC syndrome. Polynucleotides which hybridise to the LRGRP nucleotide
CC sequence can be used for detection
XX
XX Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 44 AGCAGCGCGCGGCCAGTTC 63
Db 1 AGCAGCGCGCGGCCAGTTC 20
XX
RESULT 9
AAK95054/C
ID AAK95054 standard; DNA; 20 BP.
XX
AC AAK95054;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone-specific primer, SEQ ID NO: 4299.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX 05-SEP-2001.
PD
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
PR

PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 DR 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PT
 XX
 PS Example 18; Page 129; 1380pp + Sequence Listing; English.
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a primer used to amplify a human cDNA
 CC clone provided in the invention
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 1.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1029 GAGAAGTAAACATCACACC 1048
 Db 20 GAGAAGTAAACATCACACC 1
 RESULT 10
 ADL32266/c
 ID ADL32266 standard; DNA; 20 BP.
 XX
 AC ADL32266;
 XX
 DT 20-MAY-2004 (first entry)
 DE Clone specific PCR primer to amplify human full length cDNA SeqID 4299.
 XX human; medicine; signal transduction; glycoprotein; transcription;
 KW oligo-capping method; ss; PCR; primer.
 XX Homo sapiens.
 XX
 XX EP1396543-A2.
 XX
 PD 10-MAR-2004.
 XX
 XX 07-JUL-2000; 2003EP-00025638.
 XX
 XX 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2004-204755/20.
 DR New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 PT
 XX

PS Example 18; SEQ ID NO 4299; 1340pp; English.
 XX This invention relates to a novel primers useful for synthesising full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This oligonucleotide sequence is a
 CC human clone specific PCR primer used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 1.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1029 GAGAAGTAAACATCACACC 1048
 Db 20 GAGAAGTAAACATCACACC 1
 RESULT 11
 ADR27690/c
 ID ADR27690 standard; DNA; 20 BP.
 XX
 AC ADR27690;
 XX
 DT 04-NOV-2004 (first entry)
 DE OB-RGRP antisense oligonucleotide, AS 12.
 XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
 KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW Leptin receptor related protein; OB-RGRP; leptin receptor;
 KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW antisense; ss.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 modified_base 1..20 /tag= b
 /mod_base= OTHER
 /note= "Optional thioester"
 modified_base 1..5 /tag= a
 /mod_base= OTHER
 /note= "2, O-methylation"
 modified_base 16..20 /tag= c
 /mod_base= OTHER
 /note= "2, O-methylation"
 modified_base 20 /tag= d
 /mod_base= OTHER
 /note= "3, triethyleneglycol spacer"
 FR2850971-A1.
 XX
 PD 13-AUG-2004.
 XX
 PF 10-FEB-2003; 2003FR-00001543.
 XX
 PR 10-FEB-2003; 2003FR-00001543.
 XX (AVET) AVENTIS PHARMA SA.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX

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PI Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis; obesity; diabetes; anorexia; disorders of sexual maturity,
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 269 CGGGAACCTGGCATATTTCTT 288
XX |||||
XX DB 20 CGGGAACCTGGCATATTTCTT 1
XX
XX RESULT 12
XX ADR27680/c
XX ID ADR27680 standard; DNA; 20 BP.
XX
XX AC ADR27680;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX DE OB-RGRP antisense oligonucleotide, AS 02.
XX
XX KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
XX Leptin receptor related protein; OB-RGRP; leptin receptor;
XX Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
XX anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
XX thrombus formation; immunity; inflammation; fetal development; cancer;
XX antisense; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Optional thioester"
XX
XX FT modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2' O-methylation"
XX
XX FT modified_base 16..20

```

```

FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
XX FR2850571-A1.
XX
XX 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis; obesity; diabetes; anorexia; disorders of sexual maturity,
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 56 CCACGTTCCGGACACATGGC 75
XX |||||
XX DB 20 CCACGTTCCGGACACATGGC 1
XX
XX RESULT 13
XX ADR27685/c
XX ID ADR27685 standard; DNA; 20 BP.
XX
XX AC ADR27685;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX XX OB-RGRP antisense oligonucleotide, AS 07.
XX DE Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
XX XX
XX KW

```

KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW Leptin receptor related protein; OB-RGRP; leptin receptor;
 KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW antisense; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Optional thioester"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2' O-methylation"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2' O-methylation"
 FT modified_base 20
 FT /tag= d
 FT /mod_base= OTHER
 FT /note= "3' triethyleneglycol spacer"
 FT XX
 PN FR2850971-A1.
 XX
 PD 13-AUG-2004.
 XX
 PF 10-FEB-2003; 2003FR-00001543.
 XX
 PR 10-FEB-2003; 2003FR-00001543.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Jockers R, Couturier C, Uhlmann E;
 XX
 DR WPI; 2004-595751/58.
 XX
 PT New oligonucleotides that inhibit expression of the leptin receptor
 PT related protein, useful for treatment and prevention of e.g.
 PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
 PT angiogenesis.
 XX
 PS Example 6; Fig 1; 104pp; French.
 XX
 CC The present invention relates to a leptin receptor related protein (OB-
 CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
 CC specifically with and inhibits the expression of ADR27652. The ON
 CC promotes expression of leptin receptors on the cell surface and may
 CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
 CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
 CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
 CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
 CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
 CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
 CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
 CC protein (YFP) for detecting compounds that modify the interaction between
 CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
 CC treat leptin-related disorders. ON, also related interfering RNA, are
 CC used for prevention and/or treatment of leptin-related disorders, e.g.
 CC osteoporosis (or other conditions involving reduced bone density);
 CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
 CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
 CC and inflammation, fetal development and cancer. The present OB-RGRP
 CC antisense oligonucleotide was used to illustrate the invention.
 XX
 SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 143 TGTGCTTTAGAGGATTATGG 162
 |||||
 DB 20 TGTGCTTTAGAGGATTATGG 1
 |||||
 RESULT 14
 ADR27653/c
 ID ADR27653 standard; DNA; 20 BP.
 XX
 AC ADR27653;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE OB-RGRP antisense oligonucleotide, SEQ ID 2.
 XX
 KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
 KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW Leptin receptor related protein; OB-RGRP; calcification; obesity;
 KW Leptin-related disorders; osteoporosis; calcification; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN FR2850971-A1.
 XX
 PD 13-AUG-2004.
 XX
 PF 10-FEB-2003; 2003FR-00001543.
 XX
 PR 10-FEB-2003; 2003FR-00001543.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Jockers R, Couturier C, Uhlmann E;
 XX
 DR WPI; 2004-595751/58.
 XX
 PT New oligonucleotides that inhibit expression of the leptin receptor
 PT related protein, useful for treatment and prevention of e.g.
 PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
 PT angiogenesis.
 XX
 PS Claim 4; SEQ ID NO 2; 104pp; French.
 XX
 CC The present invention relates to a leptin receptor related protein (OB-
 CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
 CC specifically with and inhibits the expression of ADR27652. The ON
 CC promotes expression of leptin receptors on the cell surface and may
 CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
 CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
 CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
 CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
 CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
 CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
 CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
 CC protein (YFP) for detecting compounds that modify the interaction between
 CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
 CC treat leptin-related disorders. ON, also related interfering RNA, are
 CC used for prevention and/or treatment of leptin-related disorders, e.g.
 CC osteoporosis (or other conditions involving reduced bone density);
 CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
 CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
 CC and inflammation, fetal development and cancer.
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;

```

Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 ACATGTGCACATGCGGCATT 540
   |||||
Db 20 ACATGTGCACATGCGGCATT 1

RESULT 15
ADR27682/c
ID ADR27682 standard; DNA; 20 BP.
XX
AC ADR27682;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 04.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
DR WPI; 2004-595751/58.
XX
PT New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, haematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a

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```

triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
(RNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
protein (YFP) for detecting compounds that modify the interaction between
the leptin receptor and OB-RGRP proteins, which can be used to prevent or
treat leptin-related disorders. ON, also related interfering RNA, are
used for prevention and/or treatment of leptin-related disorders, e.g.
osteoporosis (or other conditions involving reduced bone density);
calcification; obesity; diabetes; anorexia; thrombus formation; disorders of immunity
haematopoiesis, angiogenesis, fetal development and cancer. The present OB-RGRP
and inflammation, fetal development and cancer. The present OB-RGRP
antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 ATGGCGGCGGTAAAGCTCT 90
Db 20 ATGGCGGCGGTAAAGCTCT 1

RESULT 16
ADR27688/c
ID ADR27688 standard; DNA; 20 BP.
XX
AC ADR27688;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 10.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX

```

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PA (AVET ) AVENTIS PHARMA SA.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
DR
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 58% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TGCCTGTCGGGAACCTGGCAT 281
DB 20 TGCCTGTCGGGAACCTGGCAT 1
|||||
|||||

RESULT 17
ADR27681/c
ID ADR27681 standard; DNA; 20 BP.
XX
AC ADR27681;
XX
XX 04-NOV-2004 (first entry)
XX
XX OB-RGRP antisense oligonucleotide, AS 03.
DE
XX
XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a

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FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /*mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /*mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
XX FR2850971-A1.
XX
XX 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 58% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 CGGAGACATGCGGGCGGTT 82
DB 20 CGGAGACATGCGGGCGGTT 1
|||||
|||||

RESULT 18
ADR27687/c
ID ADR27687 standard; DNA; 20 BP.
XX
AC ADR27687;
XX
XX 04-NOV-2004 (first entry)
XX
XX

```

Fri Aug 19 11:00:00 2005

DE OB-RGRP antisense oligonucleotide, AS 09.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

KW Leptin receptor related protein; OB-RGRP; leptin receptor;

KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;

KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;

KW thrombus formation; immunity; inflammation; fetal development; cancer;

XX antisense; ss.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Optional thioester"

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 20

FT /*tag= d

FT /mod_base= OTHER

FT /note= "3' triethyleneglycol spacer"

XX FR2850971-AL.

XX

XX 13-AUG-2004.

XX

XX 10-FEB-2003; 2003FR-00001543.

XX

XX 10-FEB-2003; 2003FR-00001543.

XX

XX (AVET) AVENTIS PHARMA SA.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

XX Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

XX

XX New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis.

XX

XX Example 6; Fig 1; 104pp; French.

XX

XX The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their coding sequences comprising OB-RGRP or MYO47 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also, related interfering RNA, are used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes; anorexia; disorders of sexual maturity, haematopoiesis, angiogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present OB-RGRP antisense oligonucleotide was used to illustrate the invention.

XX

SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GGCCTTTTACTGGCCCTTATT 180

|||||

DB 20 GGCCTTTTACTGGCCCTTATT 1

RESULT 19

ADR27679/c

ID ADR27679 standard; DNA; 20 BP.

XX

XX ADR27679;

XX

XX 04-NOV-2004 (first entry)

XX

XX OB-RGRP antisense oligonucleotide, AS 01.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

KW Leptin receptor related protein; OB-RGRP; leptin receptor;

KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;

KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;

KW thrombus formation; immunity; inflammation; fetal development; cancer;

XX antisense; ss.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Optional thioester"

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 20

FT /*tag= d

FT /mod_base= OTHER

FT /note= "3' triethyleneglycol spacer"

XX FR2850971-AL.

XX

XX 13-AUG-2004.

XX

XX 10-FEB-2003; 2003FR-00001543.

XX

XX 10-FEB-2003; 2003FR-00001543.

XX

XX (AVET) AVENTIS PHARMA SA.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

XX Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

XX

XX New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis.

XX

XX Example 6; Fig 1; 104pp; French.

XX

XX The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their coding sequences comprising OB-RGRP or MYO47 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also, related interfering RNA, are used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes; anorexia; disorders of sexual maturity, haematopoiesis, angiogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present OB-RGRP antisense oligonucleotide was used to illustrate the invention.

XX

PS 10-FEB-2003; 2003FR-00001543.

XX

XX 10-FEB-2003; 2003FR-00001543.

XX

XX (AVET) AVENTIS PHARMA SA.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

XX Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

XX

XX New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis.

XX

XX Example 6; Fig 1; 104pp; French.

XX

XX The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CC specifically with and inhibits the expression of ADR27652. The ON
 CC promotes expression of leptin receptors on the cell surface and may
 CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
 CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
 CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
 CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
 CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
 CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
 CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
 CC protein (YFP) for detecting compounds that modify the interaction between
 CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
 CC treat leptin-related disorders. ON, also related interfering RNA, are
 CC used for prevention and/or treatment of leptin-related disorders, e.g.
 CC osteoporosis (or other conditions involving reduced bone density);
 CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
 CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
 CC and inflammation, fetal development and cancer. The present OB-RGRP
 CC antisense oligonucleotide was used to illustrate the invention.

XX Sequence 20 BP; 1 A; 9 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CCCGGCGGTGCAGGAAGC 39
 DB 20 CCCGGCGGTGCAGGAAGC 1

RESULT 20

ADR27692/c

ID ADR27692 standard; DNA; 20 BP.

XX ADR27692;

DT 04-NOV-2004 (first entry)

DE OB-RGRP antisense oligonucleotide, AS 14.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
 KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW leptin receptor related protein; OB-RGRP; leptin receptor;
 KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW antisense; ss.

XX Synthetic.

Key Location/Qualifiers
 modified_base 1..20
 /tag= b
 /mod_base= OTHER
 /note= "Optional thioester"
 modified_base 1..5
 /tag= a
 /mod_base= OTHER
 /note= "2' O-methylation"
 modified_base 16..20
 /tag= c
 /mod_base= OTHER
 /note= "2' O-methylation"
 modified_base 20
 /tag= d
 /mod_base= OTHER
 /note= "3' triethyleneglycol spacer"

XX FR2850971-A1.

XX 13-AUG-2004.

XX 10-FEB-2003; 2003FR-00001543.

XX 10-FEB-2003; 2003FR-00001543.

XX (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

XX New oligonucleotides that inhibit expression of the leptin receptor
 PT related protein, useful for treatment and prevention of e.g.
 PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
 PT angiogenesis.

XX Example 6; Fig 1; 104pp; French.

CC The present invention relates to a leptin receptor related protein (OB-
 RGRP) antisense oligonucleotide (ON; ADR27653), that hybridizes
 CC specifically with and inhibits the expression of ADR27652. The ON
 CC promotes expression of leptin receptors on the cell surface and may
 CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
 CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
 CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
 CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
 CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
 CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
 CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
 CC protein (YFP) for detecting compounds that modify the interaction between
 CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
 CC treat leptin-related disorders. ON, also related interfering RNA, are
 CC used for prevention and/or treatment of leptin-related disorders, e.g.
 CC osteoporosis (or other conditions involving reduced bone density);
 CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
 CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
 CC and inflammation, fetal development and cancer. The present OB-RGRP
 CC antisense oligonucleotide was used to illustrate the invention.

XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 ACATGTGCACATGCGGCATT 540

DB 20 ACATGTGCACATGCGGCATT 1

RESULT 21

ADR27683/c

ID ADR27683 standard; DNA; 20 BP.

XX ADR27683;

DT 04-NOV-2004 (first entry)

DE OB-RGRP antisense oligonucleotide, AS 05.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
 KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW leptin receptor related protein; OB-RGRP; leptin receptor;
 KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW antisense; ss.

XX Synthetic.

Key Location/Qualifiers
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 /tag= b
 /mod_base= OTHER

Fri Aug 19 11:00:00 2005

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FT /note= "2' O-methylation"
FT 16..20
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FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT 20
FT modified_base /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
XX FR2850971-A1.
XX
XX 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and their
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 84 AGCTCTCTGGCATTATCC 103
XX |||||
XX Db 20 AAGCTCTCTGGCATTATCC 1
XX
XX RESULT 22
XX ADR27686/c
XX ID ADR27686 standard; DNA; 20 BP.
XX
XX AC ADR27686;
```

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XX 04-NOV-2004 (first entry)
XX
XX OB-RGRP antisense oligonucleotide, AS 08.
XX
XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
XX Leptin receptor; related protein; OB-RGRP; leptin receptor;
XX Leptin-related disorders; osteoporosis; calcification; diabetes;
XX anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
XX thrombus formation; immunity; inflammation; fetal development; cancer;
XX antisense; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
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XX /*tag= b
XX /mod_base= OTHER
XX /note= "Optional thioester"
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2' O-methylation"
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2' O-methylation"
XX modified_base 20
XX /*tag= d
XX /mod_base= OTHER
XX /note= "3' triethyleneglycol spacer"
XX
XX FR2850971-A1.
XX
XX 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and their
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
```

```

CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 GAGGATTATGGCGTTTACTG 171
Db 20 GAGGATTATGGCGTTTACTG 1

RESULT 23
ADR27684/c
ID ADR27684 standard; DNA; 20 BP.
XX
AC ADR27684;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 06.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-Al.
XX
XX 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann B;
XX
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX

```

```

XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity;
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 CTTATGCTGGGATGCGCTT 150
Db 20 CTTATGCTGGGATGCGCTT 1

RESULT 24
ADR27691/c
ID ADR27691 standard; DNA; 20 BP.
XX
AC ADR27691;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 13.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
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FT /note= "2' O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-Al.
XX

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Fri Aug 19 11:00:00 2005

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PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX PT angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
XX expression of OB-RGRP. Also claimed are fusion proteins (Fps) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 370 CCTGTGTTGGCAGCAATG 389
XX 20 CCTGTGTTGGCAGCAATG 1
XX
XX RESULT 25
XX ADR711351
XX ID ADR711351 standard; DNA; 20 BP.
XX
XX AC ADR711351;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Forward primer for amplifying OB-RGRP, seq id 14.
XX
XX KW Antidiabetic; anorectic; weight loss; weight gain; diabetes; LEPROTL1;
XX KW leptin receptor overlapping transcript-like 1; OB-RGRP;
XX KW leptin receptor gene related protein; intracellular transport; obesity;
XX KW PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX PN FR2852397-A1.
XX
XX PD 17-SEP-2004.
XX
10-MAR-2003; 2003FR-00002931.
XX
10-MAR-2003; 2003FR-00002931.
XX
(CNRS ) CNRS CENT NAT RECH SCI.
XX
Baillleul B, Rouille Y, Seron K, Belouzard S;
XX
WPI; 2004-671009/66.
XX
Identifying compounds useful for treating loss or gain of weight or
diabetes, from their ability to modulate expression or transport of
proteins related to the leptin receptor.
XX
Example 3; SEQ ID NO 14; 38pp; French.
XX
The invention relates to a method for identifying compounds (I) that are
active against loss or gain of weight or diabetes in humans or animals.
The method comprises measuring the effect of a test compound on the
expression of at least one of the genes LEPROTL1 (leptin receptor
overlapping transcript-like 1) or OB-RGRP (leptin receptor gene related
protein). Alternatively the method comprises measuring the effect of the
compound on intracellular transport as far as the cell membrane (CM), the
presence at CM, and internalisation from the membrane of proteins (X)
encoded by the specified genes, or parts of them. Compounds of the
invention are used to treat or prevent obesity, weight loss and diabetes.
The current sequence represents a primer for the amplification of OB-
RGRP.
XX
Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 44 AGCAGCCGCGGCCCGAGTTC 63
XX 1 AGCAGCCGCGGCCCGAGTTC 20
XX
XX RESULT 26
XX ABK39905/c
XX ID ABK39905 standard; DNA; 25 BP.
XX
XX AC ABK39905;
XX
XX DT 21-MAY-2002 (first entry)
XX
XX DE Human Parathyroid hormone 3' RT-PCR primer.
XX
XX KW Human; ss; PCR; embryonic stem cell; differentiation; primer;
XX KW transplantation; heart muscle damage; kidney tissue degeneration;
XX KW skin damage; liver degeneration; brain degeneration; spinal cord injury;
XX KW anaemia; immunodeficiency; adrenal degeneration;
XX KW biomedical engineering human development.
XX
XX OS Homo sapiens.
XX
XX FN WO200210347-A2.
XX
XX PD 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-IB001719.
XX
XX 01-AUG-2000; 2000US-0222160P.
XX
XX 09-FEB-2001; 2001US-0267559P.
XX
XX (YISS ) YISSUM RES & DEV CO.
XX
XX Benvenisty N;
XX
XX WPI; 2002-180078/23.
XX

```

PT Mapping a pathway of or directing differentiation of human embryonic
PT cells, comprises exposing cells to an exogenous factor and measuring gene
PT expression products characteristic of the particular cell type or
PT lineage.

XX Example 1; Fig 5; 52pp; English.

CC The invention relates to mapping a pathway of differentiation of a
CC population of embryonic cells, comprising (a) selecting: (i) a set of
CC gene expression products, where each gene expression product in the set
CC is characteristic of a cell type that has undergone differentiation, so
CC that several differentiated cell types are represented in the set and
CC (ii) an exogenous factor from a library of exogenous factors, (b)
CC applying the exogenous factor to the population of embryonic cells, (c)
CC characterising the effect of the exogenous factor on the differentiation
CC pathway of the population of cells by determining gene expression
CC products in the set and (d) mapping the pathway of differentiation of the
CC cells. The method is useful for directing differentiation of embryonic
CC stem cells. The method is particularly useful for manipulating
CC differentiation of human embryonic stem cells to provide a uniform
CC population of precursors and differentiated cells of a desired lineage.
CC The differentiated cells may be used for treating a medical condition in
CC a human, e.g. as a source of cells for transplantation in numerous human
CC pathologies, (e.g. heart muscle damage, kidney tissue degeneration, skin
CC damage, liver degeneration, brain degeneration, spinal cord injury,
CC anaemia, immunodeficiency, and adrenal degeneration) or as a component in
CC biomedical engineering as well as providing clues on early stages of
CC human development. The present sequence is an RT-PCR (reverse
CC transcriptase PCR) primer used to amplify the one member of the set of
CC expression products from embryonic stem cells in the method of the
CC invention

XX Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 794 CTTGGAGGCGAGATAACGCTGA 816
Db 23 CTTGGAGGCGAGACAACTGA 1

RESULT 27

AAT64982
ID AAT64982 standard; DNA; 19 BP.

XX AAT64982;

XX 23-FEB-1998 (first entry)

DE Human OB receptor 5' untranslated region PCR primer HOBR 1F-2.

KW Ob receptor; obesity; leptin; rat; rodent; animal model; ligand; fatty;
KW fa mutation; therapy; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9731015-A1.

XX 28-AUG-1997.

XX 18-FEB-1997; 97WO-US002397.

XX 22-FEB-1996; 96US-009040SP.

XX 22-MAR-1996; 96US-0013969P.

XX 25-APR-1996; 96GS-00008473.

XX (MERI) MERCK & CO INC.

XX Hess JW, Caskey CT, Liu Q, Phillips MS;

XX

DR WPI; 1997-435085/40.

XX Rat wild-type and mutant ob receptor protein - useful in identification
PT of new ligands for prevention and treatment of obesity.

XX Example 6; Page 13; 35pp; English.

CC This oligonucleotide comprises forward PCR primer HOBR 1F-2, which is
CC based on the 5' untranslated region (5'UTR) of the human ob receptor (OB-
CC R) sequence. Primers HOBR 1F (AAT64981) and HOBR 1F-2 were paired with
CC rat OB-R specific reverse primers ROBR 11 (AAT64983) or ROBR 12
CC (AAT64984) to amplify the 5' end of rat OB-R cDNA. The largest product,
CC obtained with HOBR 1F-2 and ROBR11, was a 500 bp fragment that covered
CC the 5' region and included a Met codon. Full-length sequences for lean
CC rat OB-R cDNA (AAT64961) and fatty (fa) mutant rat OB-R cDNA (AAT64062),
CC which differ by only 1 bp, were subsequently obtained

SQ Sequence 19 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 TCGTGGCATTATCCTTCAG 108
Db 1 TCGTGGCATTATCCTTCAG 19

RESULT 28

ACK10811

ID ACK10811 standard; DNA; 25 BP.

XX ACK10811;

XX 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 110792.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW Genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (APFY-) APFYMATRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 110792; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more

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gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 179 TTGCTCTGATTTTCCACGCCATCT 203
DB 1 TTGCTCTGATTTTCCACGCCGCT 25

RESULT 29
ACI63081/C
ID ACI63081 standard; DNA; 25 BP.
AC ACI63081;
DT 13-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 63072.
DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

OS Homo sapiens.
XX US2003104410-A1.
XX 05-JUN-2003.
XX 15-MAR-2002; 2002US-00098263.
XX 16-MAR-2001; 2001US-02767599.
XX (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 63072; 9pp; English.
XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring

gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 8 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 271 GGAAGTGGCATATTTCTTCACTA 293
DB 24 GGAAGTGGCATATTTCTTCACTA 2

RESULT 30
AAT64981
ID AAT64981 standard; DNA; 18 BP.

AC AAT64981;

DT 23-FEB-1998 (first entry)

XX Human OB receptor 5' untranslated region PCR primer HOBR 1F.

DE Ob receptor; obesity; leptin; rat; rodent; animal model; ligand; fatty;
KW fa mutation; therapy; PCR; primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9731015-A1.

XX 28-AUG-1997.

XX 18-FEB-1997; 97WO-US002397.

XX 22-FEB-1996; 96US-0090405P.

XX 22-MAR-1996; 96US-0013969P.

XX 25-APR-1996; 96GB-00008473.

XX (MERI) MERCK & CO INC.

XX Hess JW, Caskey CT, Liu Q, Phillips MS;

XX WPI; 1997-435085/40.

XX Rat wild-type and mutant ob receptor protein - useful in identification of new ligands for prevention and treatment of obesity.

XX Example 6; Page 13; 35pp; English.

XX This oligonucleotide comprises forward PCR primer HOBR 1F, which is based on the 5' untranslated region (5'UTR) of the human ob receptor (OB-R) sequence. Primers HOBR 1F and HOBR 1F-2 (AAT64982) were paired with rat OB-R specific reverse primers ROBR 11 (AAT64983) or ROBR 12 (AAT64984) to amplify the 5' end of rat OB-R cDNA. Full-length sequences for lean rat OB-R cDNA (AAT64961) and fatty (fa) mutant rat OB-R cDNA (AAT64062), which differ by only 1 bp, were subsequently obtained

Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 CTTATGCTGGGATGCCC 148
 Db 1 CTTATGCTGGGATGCCC 18

RESULT 31
 AAT85600/c
 ID AAT85600 standard; DNA; 18 BP.
 XX AC AAT85600;
 XX DT 17-MAR-1998 (first entry)
 XX DE Sense oligonucleotide -47 for human WSX receptor cDNA.
 XX Human; WSX receptor; identification; purification; ligand; activator;
 KW antibody; agonist; proliferation; obesity; differentiation; anaemia;
 KW treatment; neoplasia; arteriosclerosis; Type II diabetes;
 KW polycystic ovarian disease; cardiovascular disease; osteoarthritis;
 KW dermatological disorder; hypertension; insulin resistance;
 KW hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis;
 KW sense; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9725425-A1.
 XX PD 17-JUL-1997.
 XX PF 07-JAN-1997; 97WO-US0000325.
 XX PR 08-JAN-1996; 96US-00585005.
 XX PR 20-JUN-1996; 96US-00667197.
 XX PA (GETH) GENENTECH INC.
 XX PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 XX WPI; 1997-372864/34.
 XX WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving haematopoiesis or
 PT for treating tumours.
 XX Example 8; Fig 7; 219pp; English.

The present sequence is the sense oligonucleotide -47 for the human WSX receptor cDNA. The receptor can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and cholelithiasis

Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGCTCTTAGA 153
 Db 18 GCTGGGATGCTCTTAGA 1

RESULT 32
 AAT85601
 ID AAT85601 standard; DNA; 18 BP.
 XX AC AAT85601;
 XX DT 17-MAR-1998 (first entry)
 XX DE Antisense oligonucleotide -47 for human WSX receptor cDNA.
 XX Human; WSX receptor; identification; purification; ligand; activator;
 KW antibody; agonist; proliferation; obesity; differentiation; anaemia;
 KW treatment; neoplasia; arteriosclerosis; Type II diabetes;
 KW polycystic ovarian disease; cardiovascular disease; osteoarthritis;
 KW dermatological disorder; hypertension; insulin resistance;
 KW hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis;
 KW antisense; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9725425-A1.
 XX PD 17-JUL-1997.
 XX PF 07-JAN-1997; 97WO-US0000325.
 XX PR 08-JAN-1996; 96US-00585005.
 XX PR 20-JUN-1996; 96US-00667197.
 XX PA (GETH) GENENTECH INC.
 XX PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 XX WPI; 1997-372864/34.
 XX WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving haematopoiesis or
 PT for treating tumours.
 XX Example 8; Fig 7; 219pp; English.

The present sequence is the antisense oligonucleotide +85 for the human WSX receptor cDNA. The receptor can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and cholelithiasis

Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Aug 19 11:00:00 2005

CC for WSX receptor. A composition comprising the WSX polypeptide is useful
 CC as an antagonist for reducing activation of endogenous WSX receptor, and
 CC to treat metabolic disorders (e.g. anorexia or steroid-induced
 CC truncalobesity), stem cell tumours and other tumours which express WSX
 CC receptor. The present sequence represents a human WSX receptor probe used
 CC in an antisense inhibition assay
 XX
 SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 136 GCTGGGATGTCCTTAGA 153
 DB 18 GCTGGGATGTCCTTAGA 1
 RESULT 34
 ACA75491
 ID ACA75491 standard; DNA; 18 BP.
 AC ACA75491;
 XX
 DT 07-JUL-2003 (first entry)
 XX
 DE Human WSX receptor -47nt sense oligonucleotide.
 XX
 OS Homo sapiens.
 XX
 XX US2003004109-A1.
 XX
 XX 02-JAN-2003.
 XX
 XX 06-AUG-2002; 2002US-00214802.
 XX
 XX 08-JAN-1996; 96US-0064855P.
 XX
 XX 08-JAN-1997; 97US-00780562.
 XX
 XX (BENN/) BENNETT B.
 XX (MATT/) MATTHEWS W.
 XX
 XX Bennett B, Matthews W;
 XX
 XX WPI; 2003-416605/39.
 XX
 XX Novel isolated cytokine receptor, termed WSX receptor, useful for
 XX treating diseases characterized by a decrease in hematopoietic cells e.g.
 XX anemia, or for treating myeloproliferative thrombocytotic diseases.
 XX
 XX Example 8; Fig 7; 77pp; English.
 XX
 XX The invention relates to an isolated cytokine receptor which plays a role
 XX in enhancing proliferation and/or differentiation of hematopoietic
 XX cells, termed WSX receptor comprising the amino acid sequence of mature
 XX human WSX receptor variant 13.2 or its extracellular domain. The WSX
 XX receptor is useful for identifying a molecule which binds to and/or
 XX activates the WSX receptor, as a diagnostic tool for measuring serum
 XX levels of endogenous WSX ligand, for treating diseases characterized by a
 XX decrease in hematopoietic cells (such as anaemia, thrombocytopaenia,
 XX hypoplasia, disseminated intravascular coagulation, myelodysplasia,
 XX immune (autoimmune) thrombocytopenic purpura (ITP) and HIV induced ITP),
 XX myeloproliferative thrombocytotic diseases, thrombocytosis from
 XX inflammatory conditions and in iron deficiency, obesity or diabetes, for
 XX enhancing repopulation of mature blood cell lineages in cells having
 XX undergone chemo- or radiation therapy or bone marrow transplantation
 XX therapy, or for promoting kidney, liver and lung growth and/or repair.
 XX The WSX receptor is useful for producing anti-WSX receptor antibodies,
 XX for affinity purification of WSX ligand, for competitive screening of
 XX potential agonists or antagonists for binding to the WSX receptor, as
 XX molecular weight markers, as reagents for mechanism studies of the WSX
 XX receptor or its ligands, to study the role of the WSX receptor and WSX
 XX ligand in normal growth and development, as well as abnormal growth and
 XX development, e.g., in malignancies, or as standards or controls in assays

QY 136 GCTGGGATGTCCTTAGA 153
 DB 1 GCTGGGATGTCCTTAGA 18
 RESULT 33
 ID ACA75490/c
 AC ACA75490 standard; DNA; 18 BP.
 AC ACA75490;
 XX
 DT 07-JUL-2003 (first entry)
 XX
 DE Human WSX receptor -47nt antisense oligonucleotide.
 XX
 OS Homo sapiens.
 XX
 XX US2003004109-A1.
 XX
 XX 02-JAN-2003.
 XX
 XX 06-AUG-2002; 2002US-00214802.
 XX
 XX 08-JAN-1996; 96US-0064855P.
 XX
 XX 08-JAN-1997; 97US-00780562.
 XX
 XX (BENN/) BENNETT B.
 XX (MATT/) MATTHEWS W.
 XX
 XX Bennett B, Matthews W;
 XX
 XX WPI; 2003-416605/39.
 XX
 XX Novel isolated cytokine receptor, termed WSX receptor, useful for
 XX treating diseases characterized by a decrease in hematopoietic cells e.g.
 XX anemia, or for treating myeloproliferative thrombocytotic diseases.
 XX
 XX Example 8; Fig 7; 77pp; English.
 XX
 XX The invention relates to an isolated cytokine receptor which plays a role
 XX in enhancing proliferation and/or differentiation of hematopoietic
 XX cells, termed WSX receptor comprising the amino acid sequence of mature
 XX human WSX receptor variant 13.2 or its extracellular domain. The WSX
 XX receptor is useful for identifying a molecule which binds to and/or
 XX activates the WSX receptor, as a diagnostic tool for measuring serum
 XX levels of endogenous WSX ligand, for treating diseases characterized by a
 XX decrease in hematopoietic cells (such as anaemia, thrombocytopaenia,
 XX hypoplasia, disseminated intravascular coagulation, myelodysplasia,
 XX immune (autoimmune) thrombocytopenic purpura (ITP) and HIV induced ITP),
 XX myeloproliferative thrombocytotic diseases, thrombocytosis from
 XX inflammatory conditions and in iron deficiency, obesity or diabetes, for
 XX enhancing repopulation of mature blood cell lineages in cells having
 XX undergone chemo- or radiation therapy or bone marrow transplantation
 XX therapy, or for promoting kidney, liver and lung growth and/or repair.
 XX The WSX receptor is useful for producing anti-WSX receptor antibodies,
 XX for affinity purification of WSX ligand, for competitive screening of
 XX potential agonists or antagonists for binding to the WSX receptor, as
 XX molecular weight markers, as reagents for mechanism studies of the WSX
 XX receptor or its ligands, to study the role of the WSX receptor and WSX
 XX ligand in normal growth and development, as well as abnormal growth and
 XX development, e.g., in malignancies, or as standards or controls in assays

CC immune (autoimmune) thrombocytopenic purpura (ITP) and HIV induced ITP),
 CC myeloproliferative thrombocytotic diseases, thrombocytosis from
 CC inflammatory conditions and in iron deficiency, obesity or diabetes, for
 CC enhancing repopulation of mature blood cell lineages in cells having
 CC undergone chemo- or radiation therapy or bone marrow transplantation
 CC therapy, or for promoting kidney, liver and lung growth and/or repair.
 CC The WSX receptor is useful for producing anti-WSX receptor antibodies,
 CC for affinity purification of WSX ligand, for competitive screening of
 CC potential agonists or antagonists for binding to the WSX receptor, as
 CC molecular weight markers, as reagents for mechanism studies of the WSX
 CC receptor or its ligands, to study the role of the WSX receptor and WSX
 CC ligand in normal growth and development, as well as abnormal growth and
 CC development, e.g., in malignancies, or as standards or controls in assays
 CC for WSX receptor. A composition comprising the WSX polypeptide is useful
 CC as an antagonist for reducing activation of endogenous WSX receptor, and
 CC to treat metabolic disorders (e.g. anorexia or steroid-induced
 CC truncalobesity), stem cell tumours and other tumours which express WSX
 CC receptor. The present sequence represents a human WSX receptor probe used
 CC in an antisense inhibition assay

XX
 SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153
 |||||
 Db 1 GCTGGGATGTCCTTAGA 18

RESULT 35
 ACH66797
 ID ACH66797 standard; DNA; 18 BP.
 XX ACH66797;
 AC ACH66797;
 XX
 DT 06-NOV-2003 (first entry)
 XX Human WSX receptor antisense oligonucleotide for position -47.
 XX
 DE Leptin receptor; WSX receptor; metabolic disorder; ITP; ss; antisense;
 KW anorexia; steroid-induced truncalobesity; stem cell tumour; tumour; DIC;
 KW anaemia; thrombocytopenia; hypoplasia; myelodysplasia; HIV-induced ITP;
 KW disseminated intravascular coagulation; immune thrombocytopenic purpura;
 KW myeloproliferative thrombocytotic disease; thrombocytosis;
 KW inflammatory condition; iron deficiency; diabetes; renal failure;
 KW haematopoietic cell proliferation; bone marrow transplantation.
 XX
 OS Homo sapiens.
 XX
 PN US6541604-B1.
 XX
 PD 01-APR-2003.
 XX
 PF 08-JAN-1997; 97US-00780562.
 XX
 PR 08-JAN-1996; 96US-0064855P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Bennett B, Matthews W;
 XX
 DR WPI; 2003-539731/51.
 XX
 XX New WSX receptor, useful for preparing a composition for treating
 PT diseases mediated by WSX receptor e.g., diabetes or obesity.
 PT
 XX
 XX Example 8; Fig 7; 142pp; English.
 XX
 CC The invention relates to an isolated leptin/WSX receptor comprising a
 CC sequence of mature human WSX receptor variant 12.1. Also disclosed are
 CC the 13.2 and 6.4 WSX receptor variants (and DNA molecules encoding all 3
 CC proteins), a partial mouse WSX receptor and its encoding DNA sequence.
 XX The WSX receptor is useful for preparing a composition for treating
 CC diseases mediated by WSX receptor, especially diseases characterised by a
 CC decrease in haematopoietic cells, e.g., anaemia, thrombocytopenia,
 CC hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia,

CC proteins), a partial mouse WSX receptor and its encoding DNA sequence.
 CC The WSX receptor is useful for preparing a composition for treating
 CC diseases mediated by WSX receptor, especially diseases characterised by a
 CC decrease in haematopoietic cells, e.g., anaemia, thrombocytopenia,
 CC hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia,
 CC immune (autoimmune) thrombocytopenic purpura (ITP), and HIV induced ITP.
 CC The WSX receptor is also useful for treating metabolic disorders such as
 CC anorexia, obesity (e.g. steroid-induced truncalobesity) tumours such as
 CC stem cell tumours, inflammatory conditions, iron deficiency, diabetes,
 CC renal failure, conditions related to haematopoietic cell proliferation
 CC (such as in bone marrow transplantation and for promoting kidney, lung
 CC and liver growth and/or repair. An experiment was performed to show
 CC antisense inhibition of human and mouse WSX receptors. The present
 CC sequence is an antisense oligonucleotide used in the experiment

XX
 SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153
 |||||
 Db 1 GCTGGGATGTCCTTAGA 18

RESULT 36
 ACH66796/c
 ID ACH66796 standard; DNA; 18 BP.
 XX ACH66796;
 AC ACH66796;
 XX
 DT 06-NOV-2003 (first entry)
 XX Human WSX receptor sense oligonucleotide for position -47.
 XX
 DE Leptin receptor; WSX receptor; metabolic disorder; ITP; ss; anorexia;
 KW steroid-induced truncalobesity; stem cell tumour; tumour; DIC; anaemia;
 KW thrombocytopenia; hypoplasia; myelodysplasia; HIV-induced ITP;
 KW disseminated intravascular coagulation; immune thrombocytopenic purpura;
 KW myeloproliferative thrombocytotic disease; thrombocytosis;
 KW inflammatory condition; iron deficiency; diabetes; renal failure;
 KW haematopoietic cell proliferation; bone marrow transplantation.
 XX
 OS Homo sapiens.
 XX
 PN US6541604-B1.
 XX
 PD 01-APR-2003.
 XX
 PF 08-JAN-1997; 97US-00780562.
 XX
 PR 08-JAN-1996; 96US-0064855P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Bennett B, Matthews W;
 XX
 DR WPI; 2003-539731/51.
 XX
 XX New WSX receptor, useful for preparing a composition for treating
 PT diseases mediated by WSX receptor e.g., diabetes or obesity.
 PT
 XX
 XX Example 8; Fig 7; 142pp; English.
 XX
 CC The invention relates to an isolated leptin/WSX receptor comprising a
 CC sequence of mature human WSX receptor variant 12.1. Also disclosed are
 CC the 13.2 and 6.4 WSX receptor variants (and DNA molecules encoding all 3
 CC proteins), a partial mouse WSX receptor and its encoding DNA sequence.
 CC The WSX receptor is useful for preparing a composition for treating
 CC diseases mediated by WSX receptor, especially diseases characterised by a
 CC decrease in haematopoietic cells, e.g., anaemia, thrombocytopenia,
 CC hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia,

CC immune (autoimmune) thrombocytopenic purpura (ITP), and HIV induced ITP.
CC The WSX receptor is also useful for treating metabolic disorders such as
CC anorexia, obesity (e.g. steroid-induced truncal obesity) tumours such as
CC stem cell tumours, inflammatory conditions, iron deficiency, diabetes,
CC renal failure, conditions related to haematopoietic cell proliferation
CC (such as in bone marrow transplantation and for promoting kidney, lung
CC and liver growth and/or repair. An experiment was performed to show
CC antisense inhibition of human and mouse WSX receptors. The present
CC sequence is a sense (control) oligonucleotide used in the experiment
XX
XX Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153
DB 18 GCTGGGATGTCCTTAGA 1

RESULT 37
ADC08932
ID ADC08932 standard; DNA; 18 BP.

XX ADC08932;
XX
XX 18-DEC-2003 (first entry)
XX Human WSX receptor DNA antisense oligonucleotide #8.

XX Human; WSX receptor; ss; weight reduction; obesity; bulimia;
KW metabolic disorder; diabetes; insulin level reduction; food consumption;
KW type II adult onset diabetes; infertility; hypercholesterolaemia;
KW hyperlipidaemia; cardiovascular disease; arteriosclerosis;
KW polycystic ovarian disease; osteoarthritis; dermatological disorder;
KW insulin resistance; hypertriglyceridaemia; cancer; cholelithiasis;
KW hypertension; kidney ailment; lung dysfunction; emphysema; haemorrhage;
KW anaemia; thrombocytopenia; hypoplasia; cachexia; anorexia; appetite loss;
KW tumour; antisense.

XX Homo sapiens.
XX US2002193571-A1.
XX 19-DEC-2002.
XX 07-JAN-1997; 97US-00779457.
XX 08-JAN-1996; 96US-00585005.
XX 20-JUN-1996; 96US-00667197.
XX (CART/) CARTER P J.
XX (CHIA/) CHIANG N Y.
XX (KIMK/) KIM K J.
XX (MATT/) MATTHEWS W.
XX (RODR/) RODRIGUES M L.

XX Carter PJ, Chiang NY, Kim KJ, Matthews W, Rodrigues ML;
XX WPI; 2003-657237/62.

XX Novel agonist antibody useful for activating WSX receptor and for
XX enhancing proliferation or differentiation of a cell comprising WSX
XX receptor, which specifically binds to the WSX receptor.

XX Example 8; SEQ ID NO 31; 140pp; English.

XX The invention relates to agonist antibodies which specifically bind to
XX the human WSX receptor. The agonist antibodies are useful for activating
XX the WSX receptor and for enhancing proliferation or differentiation of a
XX cell comprising the WSX receptor, by exposing the cell to an antibody.
XX The antibodies are also useful for reducing weight, specifically in the

CC treatment of obesity, bulimia and other disorders associated with
CC abnormal expression or functions of WSX receptor genes, for treating
CC metabolic disorders such as diabetes, for reducing excessive levels of
CC insulin in human patients and for treating patients suffering from food
CC consumption and related pathological conditions such as type II adult
CC onset diabetes, infertility, hypercholesterolaemia, hyperlipidaemia,
CC cardiovascular diseases, arteriosclerosis, polycystic ovarian disease,
CC osteoarthritis, dermatological disorders, insulin resistance,
CC hypertriglyceridaemia, cancer, cholelithiasis and hypertension. The
CC antibodies are also useful for treating kidney ailments, lung
CC dysfunctions such as emphysema, haemorrhages, diseases characterised by
CC decrease in blood cells such as anaemia, thrombocytopenia, hypoplasia,
CC metabolic disorders such as cachexia, anorexia and loss of appetite, and
CC other tumour related disorders. This sequence represents a human WSX
CC receptor DNA antisense oligonucleotide.

XX Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153
DB 1 GCTGGGATGTCCTTAGA 18

RESULT 38
ADC08931/c
ID ADC08931 standard; DNA; 18 BP.

XX ADC08931;
XX
XX 18-DEC-2003 (first entry)
XX Human WSX receptor DNA antisense oligonucleotide #7.

XX Human; WSX receptor; ss; weight reduction; obesity; bulimia;
KW metabolic disorder; diabetes; insulin level reduction; food consumption;
KW type II adult onset diabetes; infertility; hypercholesterolaemia;
KW hyperlipidaemia; cardiovascular disease; arteriosclerosis;
KW polycystic ovarian disease; osteoarthritis; dermatological disorder;
KW insulin resistance; hypertriglyceridaemia; cancer; cholelithiasis;
KW hypertension; kidney ailment; lung dysfunction; emphysema; haemorrhage;
KW anaemia; thrombocytopenia; hypoplasia; cachexia; anorexia; appetite loss;
KW tumour; antisense.

XX Homo sapiens.
XX US2002193571-A1.
XX 19-DEC-2002.
XX 07-JAN-1997; 97US-00779457.
XX 08-JAN-1996; 96US-00585005.
XX 20-JUN-1996; 96US-00667197.

XX (CART/) CARTER P J.
XX (CHIA/) CHIANG N Y.
XX (KIMK/) KIM K J.
XX (MATT/) MATTHEWS W.
XX (RODR/) RODRIGUES M L.
XX Carter PJ, Chiang NY, Kim KJ, Matthews W, Rodrigues ML;
XX WPI; 2003-657237/62.

XX Novel agonist antibody useful for activating WSX receptor and for
XX enhancing proliferation or differentiation of a cell comprising WSX
XX receptor, which specifically binds to the WSX receptor.

XX Example 8; SEQ ID NO 30; 140pp; English.

XX The invention relates to agonist antibodies which specifically bind to
 CC the human WSX receptor. The agonist antibodies are useful for activating
 CC the WSX receptor and for enhancing proliferation or differentiation of a
 CC cell comprising the WSX receptor, by exposing the cell to an antibody.
 CC The antibodies are also useful for reducing weight, specifically in the
 CC treatment of obesity, bulimia and other disorders associated with
 CC abnormal expression or functions of WSX receptor genes, for treating
 CC metabolic disorders such as diabetes, for reducing excessive levels of
 CC insulin in human patients and for treating patients suffering from food
 CC consumption and related pathological conditions such as type II adult
 CC onset diabetes, infertility, hypercholesterolaemia, hyperlipidaemia,
 CC cardiovascular diseases, arteriosclerosis, polycystic ovarian disease,
 CC osteoarthritis, dermatological disorders, insulin resistance,
 CC hypertriglyceridaemia, cancer, cholelithiasis and hypertension. The
 CC antibodies are also useful for treating kidney ailments, lung
 CC dysfunctions such as emphysema, haemorrhages, diseases characterised by
 CC decrease in blood cells such as anaemia, thrombocytopenia, hypoplasia,
 CC metabolic disorders such as cachexia, anorexia and loss of appetite, and
 CC other tumour related disorders. This sequence represents a human WSX
 CC receptor DNA antisense oligonucleotide.
 XX
 SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 136 GCTGGGATGTCCTTAGA 153
 DB 18 GCTGGGATGTCCTTAGA 1

RESULT 39
 AAD38375/c
 ID AAD38375 standard; DNA; 24 BP.
 XX
 AC AAD38375;
 DT 10-SEP-2002 (first entry)
 XX
 DE Human BAT-25 locus amplifying PCR primer #3.
 XX
 KW Human; microsatellite loci; tumour; familial tumour predisposition;
 KW microsatellite instability; MSI; cancer; gastrointestinal system;
 KW endometrium; BAT-25 locus; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002058265-A1.
 XX
 PD 16-MAY-2002.
 XX
 PP 24-APR-2001; 2001US-00841366.
 XX
 PR 15-SEP-2000; 2000US-00663020.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Bacher JW, Flanagan L, Nassif N;
 XX
 DR WPI; 2002-443805/47.
 XX
 XX Analyzing microsatellite loci for detecting microsatellite instability
 PT that can be used for prognostic tumor diagnosis, comprises coamplifying a
 PT mononucleotide repeat locus and two tetranucleotide repeat loci.
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX

XX The present invention relates to a method for analysing microsatellite
 CC loci. The method involves coamplifying a set of 3 microsatellite loci,
 CC comprising a specific mononucleotide repeat locus selected from the group
 CC consisting of BAT-25, BAT-26, BAT-40, MONO-11 and MONO-15 and two

CC tetranucleotide repeat loci selected from FGA, D18S18, D17S1299 etc from
 CC a sample of genomic DNA and determining the size of the amplified
 CC fragments. The method is useful for analysing microsatellite loci and for
 CC detecting microsatellite instability (MSI) in genomic DNA. The
 CC instability in the set of microsatellite loci are used in prognostic
 CC tumour diagnosis for the diagnosis of familial tumour predisposition. It
 CC is also used to detect cancerous tumours in the gastrointestinal system
 CC and of the endometrium. The cancerous tumours are preferably from a
 CC colorectal cancer. The present DNA sequence is a PCR primer which is used
 CC for amplifying human BAT-25 locus. This primer is used in the
 CC exemplification of the invention
 XX
 SQ Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 921 AGAGCCTTATTAGAAATGCAAT 944
 DB 24 AGAGCCATAGTAAATGCAAT 1

RESULT 40
 ABT03742
 ID ABT03742 standard; DNA; 24 BP.
 XX
 AC ABT03742;
 DT 13-SEP-2002 (first entry)
 XX
 DE Human Phox2b gene PCR primer SEQ ID NO: 263.
 XX
 KW Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
 KW transcription factor; PCR; primer; ss.

XX Homo sapiens.
 XX
 PN WO200240716-A2.
 XX
 PD 23-MAY-2002.
 XX

PF 13-NOV-2001; 2001WO-US043461.
 XX
 PR 16-NOV-2000; 2000US-0249508P.
 XX
 PA (CEMI-) CEMINES LLC.

XX Palm K;
 XX
 DR WPI; 2002-537346/57.
 XX

PT Determining the presence of neoplastic molecular markers, by identifying
 PT the presence of markers in host test sample using array of neoplastic
 PT molecular marker specific reagents and analyzing the array of the
 PT reagents.

XX Example 1; Page 18; 41pp; English.

XX The present invention relates to a method for determining the presence of
 CC neoplastic molecular markers in a host, involving the use of neoplastic
 CC molecular marker specific reagents to detect such markers and analyzing
 CC the array of reagents, allowing the identification of the neoplastic
 CC disease present. This can be used to determine the best treatment for
 CC cancers, in particular neural cell, lung and prostate tumours. The
 CC present sequence is a PCR primer useful for detecting the coding
 CC sequences of markers of the invention

XX Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Fri Aug 19 11:00:00 2005

```
QY      834 CCAGGAAGCCGGGTGGATCCCT 857
DB      1 CCAGTATGCCGGGTGGATACCT 24

RESULT 41
AAD36414/c
ID      AAD36414 standard; DNA; 24 BP.
XX
AC      AAD36414;
XX
DT      09-AUG-2002 (first entry)
XX
DE      Human BAT-25 loci amplifying primer #3.
XX
KW      Human; microsatellite locus; microsatellite instability; MSI; tumour;
KW      cancer; primer; ss.
XX
OS      Homo sapiens.
XX
PN      W0200222879-A2.
XX
PD      21-MAR-2002.
XX
PF      14-SEP-2001; 2001WO-US028647.
XX
PR      15-SEP-2000; 2000US-00663020.
XX
PA      (PROM-) PROMEGA CORP.
XX
PI      Bacher JW, Flanagan L, Nassif N;
XX
DR      WPI; 2002-393975/42.
XX
PT      Analyzing micro-satellite loci for detecting or diagnosing cancer, by co-
PT      amplifying set of three microsatellite loci from DNA sample in multiplex
PT      reaction using primers, and determining size of amplified fragments.
XX
PS      Claim 6; Page 73; 73pp; English.
XX
CC      The present invention relates to a method of analysing microsatellite
CC      loci. The method involves co-amplifying a set of three microsatellite
CC      loci comprising at least one mononucleotide repeat locus and at least two
CC      tetra-nucleotide repeat loci from a sample of genomic DNA in a multiplex
CC      amplification reaction using primers and determining the size of the
CC      amplified DNA fragments obtained. The method is useful for analysing
CC      microsatellite loci and for detecting microsatellite instability (MSI) in
CC      genomic DNA microsatellite loci of the second genomic DNA, where the MSI
CC      results are useful in prognostic tumour diagnosis, in diagnosis of the
CC      familial tumour predisposition, to detect cancerous tumours of the
CC      gastrointestinal system and of the endometrium, where the cancerous
CC      tumours are tumours from a colorectal cancer. The method is useful for
CC      detecting or diagnosing diseases associated with MSI such as certain
CC      types of cancer and predisposition for cancer and in diagnostic assays to
CC      be used to determine treatment and prognosis of disease. The present DNA
CC      sequence is a primer which is used for amplifying human BAT-25 locus.
CC      This primer is used in the method of the invention.
XX
SQ      Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
      Query Match 1.6%; Score 17.6; DB 1; Length 24;
      Best Local Similarity 83.3%; Pred. No. 51;
      Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921 AGAGCCTTATTAGAAATGCAGAAAT 944
DB      24 AGAGCCATAGTTAAATGCAGAAAT 1

RESULT 42
AAD31191/c
ID      ADD31191 standard; DNA; 24 BP.
XX
AC      ADD31191;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human microsatellite locus PCR primer #60.
XX
KW      ss; PCR; primer; human; microsatellite locus;
KW      prognostic tumour diagnosis; familial tumour predisposition;
KW      cancerous tumour; gastrointestinal cancer; endometrial cancer;
KW      colorectal cancer.
XX
OS      Homo sapiens.
XX
PN      US2003180758-A1.
XX
PD      25-SEP-2003.
XX
PF      09-DEC-2002; 2002US-00314810.
XX
PR      15-SEP-2000; 2000US-00663020.
XX
PA      (PROM-) PROMEGA CORP.
XX
PI      Bacher JW, Flanagan L, Nassif N;
XX
DR      WPI; 2003-830985/77.
XX
PT      Analyzing microsatellite instability by amplification of multiple loci
PT      including mono-nucleotide and tetra-nucleotide repeats useful to detect
PT      cancerous gastrointestinal or endometrium tumors particularly colorectal
PT      cancer.
XX
PS      Claim 4; SEQ ID NO 60; 48pp; English.
XX
CC      The invention relates to a method of analysing microsatellite loci. The
CC      invention is used to detect microsatellite instability in prognostic
CC      tumour diagnosis, particularly a familial tumour predisposition,
CC      especially to detect cancerous tumours of the gastrointestinal system or
CC      endometrium, most particularly colorectal cancer. The present sequence
CC      represents a human microsatellite locus PCR primer.
XX
SQ      Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
      Query Match 1.6%; Score 17.6; DB 1; Length 24;
      Best Local Similarity 83.3%; Pred. No. 51;
      Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921 AGAGCCTTATTAGAAATGCAGAAAT 944
DB      24 AGAGCCATAGTTAAATGCAGAAAT 1

RESULT 43
AC187101/c
ID      AC187101 standard; DNA; 25 BP.
XX
AC      AC187101;
XX
DT      14-OCT-2003 (first entry)
XX
DE      Human microarray DNA oligonucleotide SEQ ID NO 87092.
XX
KW      EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW      genetic variation; biallelic marker; polymorphism; human;
KW      cross-species comparison.
XX
OS      Homo sapiens.
XX
PN      US2003104410-A1.
XX
PD      05-JUN-2003.
```

XX 15-MAR-2002; 2002US-00098263.
 PF XX
 PR XX
 PA (AFFY-) APFYMATRIX INC.
 XX PI Mitmann MP;
 XX WPI; 2003-567953/53.
 DR XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX PS Claim 1; SEQ ID NO 87092; 9pp; English.
 XX CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library.
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX SQ Sequence 25 BP; 7 A; 2 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 1.6%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 652 CAATTTAGATTATGTTACTCAAA 675
 DB 24 CAATTTAAACTATGTCACGAA 1
 RESULT 44
 ADI51286
 ID ADI51286 standard; DNA; 17 BP.
 XX AC ADI51286;
 XX DT 15-APR-2004 (first entry)
 XX DE Human tumour suppression/reversion-related DNA sequence SeqID3789.
 XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX OS Homo sapiens.
 XX PN WO2003025177-A2.
 XX PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004523.
 XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijinder M;
 XX WPI; 2003-313354/30.
 DR XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX PS Disclosure; SEQ ID NO 3789; 30pp; French.
 XX CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX SQ Sequence 17 BP; 6 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 1.5%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 981 GATCCAAAGGAGTTGTA 997
 DB 1 GATCCAAAGGAGTTGTA 17
 RESULT 45
 ADJ25095
 ID ADJ25095 standard; DNA; 20 BP.
 XX AC ADJ25095;
 XX DT 20-MAY-2004 (first entry)
 XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3493.
 XX KW Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
 KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
 KW cardiovascular disorder; metabolic syndrome X; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "This oligonucleotide has a phosphorothioate
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
 FT and 3' ends, which are 4 nucleotides in length. Also all
 FT cytidine residues are 5-methylcytidines"
 XX PN WO2004009541-A2.
 XX PD 29-JAN-2004.

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XX 18-JUL-2003; 2003WO-US022410.
XX PF
XX 19-JUL-2002; 2002US-0397106P.
XX PR
XX (PHAA ) PHARMACIA CORP.
XX PA
XX Bhat BG;
XX PI
XX WPI; 2004-132912/13.
XX DR
XX New antisense oligonucleotide for modulating endothelial lipase
XX PT expression, for diagnosing, preventing or treating e.g. dyslipidaemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX PT
XX Claim 3; SEQ ID NO 3493; 1007pp; English.
XX PS
XX The present invention relates to antisense oligonucleotides (ADJ21603-
XX CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX CC
XX SQ Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 CCCGGCGCGTGGCAGGAAGC 39
DB 1 CCCGGCGCGTGGCAGGAAGC 20

RESULT 46
ADJ25250
ID ADJ25250 standard; DNA; 20 BP.
XX AC ADJ25250;
XX DT 20-MAY-2004 (first entry)
XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3648.
XX KW Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX KW Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
XX KW cardiovascular disorder; metabolic syndrome X; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT modified_base 1..20 a
XX FT /mod_base= OTHER
XX FT /note= "This oligonucleotide has a phosphorothioate
XX FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
XX FT and 3' ends, which are 4 nucleotides in length. Also all
XX FT cytidine residues are 5-methylcytidines"
XX
XX WO2004009541-A2.
XX PN
XX 29-JAN-2004.
XX PD
XX 18-JUL-2003; 2003WO-US022410.
XX PF
XX 19-JUL-2002; 2002US-0397106P.
XX PR
XX (PHAA ) PHARMACIA CORP.
XX PA

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XX Bhat BG;
XX PI
XX WPI; 2004-132912/13.
XX DR
XX New antisense oligonucleotide for modulating endothelial lipase
XX PT expression, for diagnosing, preventing or treating e.g. dyslipidaemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX PT
XX Claim 3; SEQ ID NO 3648; 1007pp; English.
XX PS
XX The present invention relates to antisense oligonucleotides (ADJ21603-
XX CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX CC
XX SQ Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GCCCGGCGCGTGGCAGGAAG 38
DB 1 GCCCGGCGCGTGGCAGGAAG 20

RESULT 47
AAA50752/c
ID AAA50752 standard; DNA; 21 BP.
XX AC AAA50752;
XX DT 01-SEP-2000 (first entry)
XX DE PCR primer 1F used in FIS2 gene identification.
XX KW Seed; development; FIS; endospore; autonomous embryogenesis;
XX KW transgenic plant; seedless fruit; parthenocarpic; citrus fruit;
XX KW stone fruit; PCR primer; ss.
XX OS Arabidopsis thaliana.
XX OS WO200016609-A1.
XX PN
XX 30-MAR-2000.
XX PD
XX 21-SEP-1999; 99WO-AU000805.
XX PF
XX 21-SEP-1998; 98US-0101184P.
XX PR
XX 22-SEP-1998; 98AU-00006061.
XX PR
XX 22-SEP-1998; 98AU-00006062.
XX PR
XX 22-SEP-1998; 98AU-00006063.
XX PR
XX 01-JUL-1999; 99AU-00001345.
XX PR
XX 01-JUL-1999; 99AU-00001346.
XX PS
(CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PA
XX Bilodeau P, Chaudhury AM, Dennis ES, Koltunow AMG, Luo M;
XX PI Peacock WJ;
XX PT WPI; 2000-283392/24.
XX DR
XX Induction of seed development in plants in the absence of fertilization
XX PT by inhibiting or preventing the expression of a negative regulator of
XX PT seed formation for production of seedless or soft-seeded fruit.
XX PS
Example 13; Page 107; 207pp; English.

```

XX The present invention relates to a method of inducing the development of
 CC seeds in a plant, comprising inhibiting, interrupting or reducing the
 CC expression of a negative regulator of seed formation in one or more
 CC female reproductive cells, tissues, or organs of the plant or a
 CC progenitor cell, tissue or organ. The negative regulator is a
 CC polypeptide. The FIS family of genes are known to be capable of
 CC regulating autonomous endosperm development and/or autonomous
 CC embryogenesis. In the invention the reduced expression of the negative
 CC regulator is achieved by the introduction of a transgene which comprises
 CC a FIS genetic sequence, which may inhibit FIS activity. The present
 CC sequence represents a PCR primer used to identify the FIS2 gene. Plants
 CC produced using the method of the invention produce parthenocarpic fruit
 CC or soft-seeded fruit, where the fruit are made parthenocarpic or have
 CC soft seed by a process comprising expressing the introduced nucleic acid
 CC molecule in a tissue or organ of the fruit. The plant produces seed
 CC independent of fertilization. The isolated FIS nucleic acid molecules are
 CC used in the production of an antisense molecule, a ribozyme, a co-
 CC suppression molecule, a gene-targeting molecule, a gene-silencing
 CC molecule and a dominant-negative sense molecule where the member is used
 CC for the production of a transformed plant. The transformed plant is
 CC apomictic or produces soft-seeded or parthenocarpic fruit. Production of
 CC soft-seeded fruit has large economic value, since it makes the fruit more
 CC desirable to customers. Examples include stone fruits such as apricots
 CC and peaches, citrus fruits such as oranges, lemons, grapefruit and
 CC mandarins and other fruits such as grapes, apples, melons, pears and
 CC berries. The plants which undergo autonomous seed formation do not
 CC require fertilization to reproduce, and may express desirable
 CC characteristics stably between generations. Antibodies produced to the
 CC FIS polypeptides can be used to detect the peptides of the invention and
 CC can be used in an enzyme linked immunosorbent assay (ELISA),
 CC radioimmunoassay or histochemical tests
 XX
 SQ Sequence 21 BP; 4 A; 5 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 66;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 606 ACTTCATAGGAGAGATGCA 625
 |||||
 DB 20 ACTTCATAGGAGAGATGCA 1

RESULT 48
 AAT89716
 ID AAT89716 standard; DNA; 24 BP.

XX
 AC AAT89716;

XX 05-FEB-1998 (first entry)

DE PCR primer used for hepatitis C virus genotyping.

XX Hepatitis C virus; HCV; genotype determination; 1a; 1b; 2a; 2b; 3a; 3b;
 KW 4; 5a; 6a; 6b; diagnosis; amplification; PCR; primer; ss.

XX Synthetic.

OS Hepatitis C virus.

XX JP09234072-A.

PD 09-SEP-1997.

XX 01-FEB-1996; 96JP-00038875.

XX 01-FEB-1995; 95JP-00035997.

PR 30-DEC-1995; 95JP-000352511.

XX (SRLS-) SRL KK.

XX WPI; 1997-497313/46.

XX

PT Primers used for determining hepatitis C virus genotype - provide a rapid
 PT and accurate method of hepatitis C virus genotyping.
 XX
 PS Claim 28; Page 15; 33pp; Japanese.
 XX
 CC AAT89689-T89744 are individually claimed oligonucleotides used as PCR
 CC (polymerase chain reaction) primers for the discrimination of the
 CC genotype of hepatitis C virus (HCV). Classification of the genotype of
 CC HCV can be achieved precisely and simply according to the International
 CC Standardisation of Classification. The primers can be used to distinguish
 CC between HCV genotypes 1a, 1b, 2a, 2b, 3a, 3b, 4, 5a, 6a and 6b
 XX
 SQ Sequence 24 BP; 3 A; 8 C; 8 G; 4 T; 0 U; 1 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 81.8%; Pred. No. 70;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 9 TCGGAGGCTGCCGGGCGGTG 30
 |||||
 DB 1 TCGACAGCGKGGCGGGCGTGTG 22

RESULT 49

ABA99037

ID ABA99037 standard; DNA; 24 BP.

XX
 AC ABA99037;

XX 22-JUL-2002 (first entry)

DE PCR primer corresponding to the plasmid backbone of pUK148.

KW PCR; primer; site-specific gene replacement; irreversible recombination;
 KW irreversible recombination site; IRS; ss.

OS Unidentified.

XX WO200208409-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023049.

XX 21-JUL-2000; 2000US-0220062P.

XX (USDA) US DEPT OF AGRICULTURE.

XX Ow DW;

XX WPI; 2002-195874/25.

PT Obtaining site-specific gene replacement, useful for obtaining specific
 PT and stable integration of nucleic acids into chromosomes of eukaryotes,
 PT by employing irreversible recombination sites (IRS) and irreversible
 PT recombinationases.

XX Example 1; Page 32; 84pp; English.

XX The sequence represents a PCR primer used in the invention to prepare the
 CC attB-ura4-attB linear DNA, as a PCR product using pLT50 as a template.
 CC The invention relates to a novel method for obtaining site-specific gene
 CC replacement in a eukaryotic cell comprising employing irreversible
 CC recombination sites (IRS) and irreversible recombinationases. The method is
 CC useful for obtaining specific and stable integration of nucleic acids
 CC into chromosomes of eukaryotes or for obtaining site-specific replacement
 CC of nucleic acids in a target construct. The method may also be used to
 CC stably integrate a polynucleotide into any eukaryotic cell that can be
 CC transformed by a polynucleotide

SQ Sequence 24 BP; 3 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred. No. 70; Mismatches 2; Indels 0; Gaps 0; Matches 18; Conservative 0;

QY 294 CTGGAATGCTTCTGTCGCC 313
||| ||||| ||||| |||||
Db 5 CTGGAATGCTTCTGTCGCC 24

RESULT 50
AAS03279/C
ID AAS03279 standard; DNA; 23 BP.
XX AC AAS03279;
XX DT 07-SEP-2001 (first entry)
XX DE Rat PDGF-associated protein, PRO, PCR primer Ag197#1.
XX KW Rat; platelet-derived growth factor; PDGF; PRO; tumour; cancer;
KW PDGF-associated disorder; myofibroblast development; wound healing;
KW angiogenesis; cancer; tumour; muscle wasting disease; PCR primer; ss.
XX Rattus sp.
OS
XX WO200131010-A1.
XX PN
XX PD 03-MAY-2001.
XX PF 25-OCT-2000; 2000WO-US029391.
XX PR 25-OCT-1999; 99US-0161315P.
XX PR 24-OCT-2000; 2000US-00695366.
XX PA (CURA-) CURAGEN CORP.
XX PI Burgess C, Rastelli L;
XX WPI; 2001-308644/32.
XX Polypeptides related to platelet-derived growth factor-associated
PT proteins, useful for increasing muscle mass and to treat wasting
PT diseases.
XX Example 1; Page 75; 95pp; English.
XX The sequence represents a PCR primer used to isolate nucleic acid
CC molecules encoding a platelet-derived growth factor (PDGF) associated
CC protein, PRO. Polypeptides, nucleic acids and antibodies of the invention
CC are used to treat or prevent a pathological state in a mammal,
CC particularly a PDGF-associated disorder in a human. Specifically, these
CC molecules can be used to control myofibroblast development, wound healing
CC or angiogenesis, for example in the treatment of cancer and tumours, or
CC muscle wasting diseases
XX
XX Sequence 23 BP; 9 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 75; Mismatches 4; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 386 AATGCAGTCATTTTCTTACAAAT 408
||| ||||| ||||| |||||
Db 23 ACTGCATTCGTTTCTGACAAAT 1

RESULT 51
ABZ30445/C
ID ABZ30445 standard; DNA; 23 BP.
XX AC ABZ30445;
XX DT 30-JAN-2003 (first entry)
XX

Candida albicans GRACE strain PCR primer SEQ ID NO 4596.
XX Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
XX Candida albicans.
XX WO200253728-A2.
XX 11-JUL-2002.
XX 26-DEC-2001; 2001WO-US049486.
XX 29-DEC-2000; 2000US-0259128P.
XX 20-FEB-2001; 2001US-00792024.
XX 22-AUG-2001; 2001US-0314050P.
XX (ELIT-) ELITRA PHARM INC.
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlseen KL;
XX WPI; 2002-566694/60.
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX Claim 36; SEQ ID NO 4596; 167pp + Sequence Listing; English.
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC agent, an antifungal agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
XX Sequence 23 BP; 10 A; 6 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 75; Mismatches 4; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 477 TGATTACAGTCGATTCGAATTTCT 499
||| ||||| ||||| |||||
Db 23 TGATTGCGATTCGATTCGAATTTCT 1

RESULT 52
ADK67738/C
ID ADK67738 standard; DNA; 23 BP.
XX AC ADK67738;
XX DT 06-MAY-2004 (first entry)
XX

XX DE Murine fancg/xrcc9 gene primer G34.
 XX KW Transgenic; knockout; gene therapy; bacterial artificial chromosome;
 KW mouse; fancg/xrcc9 gene; PCR; primer; ss.
 XX OS Mus sp.
 XX PN WO2004013299-A2.
 XX PD 12-FEB-2004.
 XX PF 01-AUG-2003; 2003WO-US024322.
 XX PR 02-AUG-2002; 2002US-0400900P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI Seed B, Yang Y;
 XX WI WIPI; 2004-157118/15.
 XX PT Producing a genetically modified mammalian cell, useful in producing
 PT modified non-human mammal for screening compounds to treat or prevent
 PT cancer, by inserting into mammalian cells an artificial chromosome
 PT comprising a cassette.
 XX PS Disclosure; SEQ ID NO 9; 80pp; English.
 XX CC The present invention relates to methods for generating cell lines and
 CC mammals with site-specific genetic modification. The methods use
 CC homologous recombination between an artificial chromosome having the
 CC modification and an endogenous chromosome of a cell. The resulting
 CC modified cells can be used to generate genetically modified mammals
 CC useful in screening methods to identify compounds of therapeutic
 CC interest. Cells can also be modified to eliminate a mutation associated
 CC with a disease, e.g. cancer, and then transplanted into patients for
 CC treatment of the disease. In an example of the method, bacterial
 CC artificial chromosomes (BACs) containing mutations in fancg/xrcc9 were
 CC used to modify mouse embryonic stem (ES) cells for the generation of
 CC fancg/xrcc9 knockout mice. The present primer, designated G34, was used
 CC in a nested PCR to screen modified BAC clones for correct targeting
 CC events.
 XX SQ Sequence 23 BP; 3 A; 9 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. NO. 75;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 20 CCCGGCCCGTGGCAGGAAGCCGG 42
 DB 23 CCCGTCCTCGTGGCTGGAGACGG 1
 RESULT 53
 AAQ82600
 ID AAQ82600 standard; DNA; 21 BP.
 XX AC AAQ82600;
 XX DT 25-MAR-2003 (revised)
 XX DT 14-SEP-1995 (first entry)
 XX DE Chromosome 11 (locus D11S870) STS primer 350.
 XX KW sequence sampled mapping; genomic analysis; complex genome mapping;
 KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
 XX OS Synthetic.
 XX PN WO9429486-A1.
 XX PD

PD 22-DEC-1994.
 XX PF 15-JUN-1994; 94WO-US006810.
 XX PR 15-JUN-1993; 93US-00078471.
 PR 07-SEP-1993; 93US-00117952.
 XX PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX PI Evans GA, Smith MW;
 XX WI WIPI; 1995-036508/05.
 XX PT Sequencing complex genomes, present as fragments in a cosmid library - by
 PT sequencing end-specific nucleotides of each clone then correlating with
 PT spatial relationship of cosmid, esp. for mammalian chromosomes.
 XX PS Example 4; Page 89; 128pp; English.
 XX CC Sequences were determined from the ends of chromosome 11-specific cosmids
 CC by automated sequencing without intermediate subcloning. A sample of 371
 CC DNA sequence fragments were determined and of these, 277 were suitable
 CC for STS primer prediction by computer analysis (using the "Primer"
 CC program available from E.Lander, MIT). The STSs and cosmids were mapped
 CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
 CC this method, 370 STSs specific for human chromosome 11 were generated and
 CC most of them were regionally mapped. This procedure illustrates a novel
 CC method for sequencing complex genomes, designated "sequence sampled
 CC mapping". The sequence sampled mapping method is useful for the
 CC completion of high density sequence-based maps, and ultimately, for the
 CC complete sequencing of genomic DNA directly from cosmid clones. See
 CC AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers. (Updated on 25-MAR-
 XX CC 2003 to correct PN field.)
 SQ Sequence 21 BP; 5 A; 3 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. NO. 84;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 513 ATCTGTATACATGTCACATG 533
 DB 1 ATCTGTATATATGTCACCTG 21
 RESULT 54
 AAT65977
 ID AAT65977 standard; DNA; 21 BP.
 XX AC AAT65977;
 XX DT 25-MAR-2003 (revised)
 XX DT 18-JUN-1997 (first entry)
 XX DE Primer #2 to amplify repeat sequence marker Mfd90.
 XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.
 XX OS Synthetic.
 XX PN US5582979-A.
 XX PD 10-DEC-1996.
 XX PF 04-APR-1994; 94US-00222177.
 XX PR 21-APR-1989; 89US-00341562.
 PR 05-SEP-1991; 91US-00754351.
 XX PA (MARS-) MARSHFIELD CLINIC.

XX PI Weber JL;

XX DR WPI; 1997-042299/04.

XX PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -

XX PT using novel nucleic acid mols. as primers.

XX PS Disclosure; Col 11-12; 186pp; English.

XX CC The invention relates to the isolation of polymorphic repeat sequences

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC repeats, especially for use in e.g. paternity or maternity testing, human

CC genetic analysis such as linkage analysis of genetic disease, commercial

CC animal or plant breeding or pedigree analysis. Clones containing the

CC repeat sequences were isolated by hybridisation of chromosome-specific

CC phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100

CC repeat blocks were isolated. The primers AAT65798-766047 were used to PCR

CC amplify the inserts from the isolated clones containing the repeat

CC sequences. The primers AAT65976-7 were used to amplify the repeat

CC sequence marker clone Mfd90. (Updated on 25-MAR-2003 to correct PF

CC field.)

XX SQ Sequence 21 BP; 5 A; 3 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 84;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 513 ATCTGTATACATGTGCACATG 533

Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 55

ABS98440

ID ABS98440 standard; DNA; 21 BP.

XX AC ABS98440;

XX DT 23-DEC-2002 (first entry)

XX DE Human multidrug resistance associated protein 3 polymorphic sequence #62.

XX KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase; NNMT;

KW NNMT; kallikrein 2; KIK2; nicotinamide-N-methyl transferase; STM;

KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase 2B7;

KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

KW multidrug resistance associated protein 3; cancer; prostate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological; SNP;

XX KW single nucleotide polymorphism.

XX OS Homo sapiens.

XX PN WO200257410-A2.

XX PD 25-JUL-2002.

XX PF 28-NOV-2001; 2001WO-US044838.

XX PR 28-NOV-2000; 2000US-00724389.

XX PR

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes

e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers

for locating, identifying and characterizing the genes responsible for

disorder-related traits.

Example 24; Page 153; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid

molecule comprising at least one base variation from that of a known

human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),

cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),

aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator

(ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding

inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating

protein (FLAP), glutathione-S-transferase 12 (GSTI2), histamine-N-methyl

transferase (NNMT), (kallikrein 2) KIK2, nicotinamide -N-methyl

transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),

sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4

(UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1

(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3

(MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic

receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.

The polymorphisms in the human genes cited in the invention are useful as

genetic linkage markers for locating and characterising the genes that

are responsible for specific traits within the genome and eventually

identifying the genes responsible for a variety of disorder-related

traits as a result of their e.g., overexpression, constitutive

expression, mutation or underexpression. The nucleic acid molecules comprising the

and/or treating the disorders. The nucleic acid molecules comprising the

polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,

ARNT, EPHX2, GSTI2, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,

MDR1 and/or MDR3 are useful for screening individuals for altered drug

metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,

AHR, MDR1 and/or MDR3 may also be used to screen individuals for

susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are

used to screen for altered cardiovascular function, in COX2 for altered

susceptibility to colorectal tumours, in DBI or CHMR1 for altered central

nervous system function, in FLAP and NNMT for altered pulmonary,

immunological or haematological function, in KIK2 for altered serine

protease activity in the prostate, in LTF for altered immunological or

haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and

peripheral nervous system function. The present sequence represents a

polymorphic DNA sequence of the invention

Sequence 21 BP; 4 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 84;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 616 TAGGAGTGTGATTTTATCTC 636

Db 1 TAGTAGCTGAGTTTGATCTC 21

RESULT 56

ABK86295/c

ID ABK86295 standard; DNA; 23 BP.

XX AC ABK86295;

XX DT 27-AUG-2002 (first entry)

XX DE Human TGR342 RT-PCR primer #2.

XX PR Human; TGR342; primer; ss; G-protein coupled receptor; GPCR; TGR; RT-PCR;

KW TGR-associated disorder; signal transduction; renal failure; nephritis;
 KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
 KW diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
 KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;
 KW circadian rhythm; reverse transcriptase.

XX Homo sapiens.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-US043404.

XX 22-NOV-2000; 2000US-0252841P.

XX 22-DEC-2000; 2000US-0257636P.

XX 12-JAN-2001; 2001US-0261377P.

XX 28-MAR-2001; 2001US-0279554P.

XX 29-MAR-2001; 2001US-0280696P.

XX (TULA-) TULARIK INC.

XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;

XX WPI; 2002-463633/49.

XX New isolated G-protein couple receptor polypeptide, termed TGR, for
 PT diagnosis and treatment of diseases such as renal failure, nephritis,
 PT hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.

XX Example 2; Page 65; 98pp; English.

XX The invention relates to a G-protein coupled receptor polypeptide (GPCR),
 CC termed TGR, and its associated nucleic acid. The sequences of the
 CC invention are useful for identifying a compound that modulates signal
 CC transduction and for identifying a mammal having a TGR-associated
 CC disorder. The proteins and nucleic acids are useful in diagnosis and
 CC treatment of diseases or conditions such as renal failure, nephritis,
 CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
 CC diabetes insipidus, hyperprolactinaemia and disturbances of thirst,
 CC sleep, temperature regulation, appetite, blood pressure or any other
 CC syndrome or disease associated with the hypothalamus. The sequences can
 CC be used in regulation of circadian rhythms, for use as genetic markers
 CC for the identification of mutations associated with diseases resulting
 CC from GPCR inactivation in particular cell types and for identification of
 CC modulators of GPCR signal transduction. This sequence represents a
 CC reverse transcriptase PCR (RT-PCR) primer for human TGR342 DNA

XX Sequence 23 BP; 11 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 88;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 117 TTGACTGACCTTTCTTATGC 137

DB 22 TTGGAATGCTTTCTTATTC 2

RESULT 57

ADB16943

ID ADB16943 standard; DNA; 23 BP.

XX ADB16943;

XX 20-NOV-2003 (first entry)

XX EKN1-1R human-specific intronic PCR primer for DYX1C1.

XX EKN1-1R; ss; human; DYX1C1; dyslexia; neurological disorder;
 KW reading disability; phonological processing; rapid naming;
 KW verbal short-term memory; primer; PCR.

XX

OS Homo sapiens.

XX WO2003068814-A1.

XX 21-AUG-2003.

XX 12-FEB-2003; 2003WO-FI000110.

XX 12-FEB-2002; 2002US-0355782P.

XX (LICN) LICENTIA LTD.

XX Kere J, Taipale M, Nopola-Hemmi J, Kaminen N;

XX WPI; 2003-646482/61.

XX New isolated, purified DYX1C1 nucleic acid for studying brain processes,
 PT e.g. reading, phonological processing, rapid naming or verbal short-term
 PT memory, or for diagnosing dyslexia or assessing the predisposition to
 PT dyslexia.

XX Disclosure; Page 23; 135pp; English.

XX This invention relates to a novel isolated human gene DYX1C1 that is
 CC functionally related to dyslexia, more particularly it describes single
 CC nucleotide polymorphisms thought to predispose an individual in to
 CC developing dyslexia. This is a neurological disorder with a genetic basis
 CC (DYX1C1 has been isolated to chromosome 15q21), which manifests itself as
 CC a specific reading disability. Specifically, DYX1C1 can be useful in
 CC study of brain processes such as reading, phonological processing, rapid
 CC naming and verbal short-term memory. Accordingly, the present invention
 CC describes methods and materials for analysing allelic variations in the
 CC DYX1C1 gene, and also provides DYX1C1 as an antigen for the production of
 CC antibodies used in the diagnosis of dyslexia. This oligonucleotide is the
 CC EKN1-1R PCR primer that is specific for human intronic DYX1C1, and is used
 CC to amplify exon 1 in an exemplification of the invention.

XX Sequence 23 BP; 9 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 88;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1000 CACATGAAAGTTTGAGAACCA 1020

DB 1 CACACCAAGTTTGAGAACCA 21

RESULT 58

ADR27674/c

ID ADR27674 standard; DNA; 16 BP.

XX ADR27674;

XX 04-NOV-2004 (first entry)

XX Leptin receptor related protein, OB-RGRP, RT-PCR primer #2.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
 KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
 KW Leptin receptor related protein; OB-RGRP; leptin receptor;
 KW leptin-related disorders; osteoporosis; calcification; diabetes;
 KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
 KW thrombus formation; immunity; inflammation; fetal development; cancer;
 KW human; RT-PCR; primer; ss.

XX Homo sapiens.

XX FR2850971-A1.

XX 13-AUG-2004.

XX 10-FEB-2003; 2003FR-00001543.

Fri Aug 19 11:00:00 2005

XX 10-FEB-2003; 2003FR-00001543.
 XX (AVET) AVENTIS PHARMA SA.
 XX (INRM) INSERM INST SANTÉ & RECH MEDICALE.
 XX Jockers R, Couturier C, Uhlmann E;
 XX WPI; 2004-595751/58.
 XX New oligonucleotides that inhibit expression of the leptin receptor
 PT related protein, useful for treatment and prevention of e.g.
 PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
 PT angiogenesis.
 XX Disclosure; Page 23; 104pp; French.
 XX The present invention relates to a leptin receptor related protein (OB-
 CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
 CC specifically with and inhibits the expression of ADR27652. The ON
 CC promotes expression of leptin receptors on the cell surface and may
 CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
 CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
 CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
 CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
 CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
 CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
 CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
 CC protein (YFP) for detecting compounds that modify the interaction between
 CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
 CC treat leptin-related disorders. ON, also related interfering RNA, are
 CC used for prevention and/or treatment of leptin-related disorders, e.g.
 CC osteoporosis (or other conditions involving reduced bone density);
 CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
 CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
 CC and inflammation, fetal development and cancer. The present sequence is a
 CC RT-PCR primer used to illustrate the invention.
 XX Sequence 16 BP; 6 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 1.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 332 CTTGCTCGTGGCTG 347
 DB 16 CTTGCTCGTGGCTG 1
 RESULT 59
 ADI52070
 ID ADI52070 standard; DNA; 17 BP.
 XX ADI52070;
 XX 15-APR-2004 (first entry)
 DT Human tumour suppression/reversion-related DNA sequence SeqID4573.
 XX
 DE
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosolic; virucide; neuroprotective; nontropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX Homo sapiens.
 OS WO2003025177-A2.
 XX
 PN 27-MAR-2003.
 XX
 PD 17-SEP-2002; 2002WO-IB004523.
 XX
 PF 17-SEP-2001; 2001FR-00011980.
 XX

XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; SEQ ID NO 4573; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nontropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.4%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 981 GATCCAAAGGAGTTGT 996
 DB 1 GATCCAAAGGAGTTGT 16
 RESULT 60
 AAS97676/C
 ID AAS97676 standard; DNA; 20 BP.
 XX AAS97676;
 XX 12-MAR-2002 (first entry)
 DT Human SAC1 gene-specific oligonucleotide PCR primer #37.
 XX
 DE Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
 KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
 KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
 KW protein replacement therapy.
 XX Homo sapiens.
 OS WO200183749-A2.
 XX
 PN 08-NOV-2001.
 XX
 PD 25-APR-2001; 2001WO-US013387.
 XX
 PF 28-APR-2000; 2000US-0200794P.
 XX 28-JUL-2000; 2000US-0221419P.
 XX 10-NOV-2000; 2000US-0247443P.
 XX (WARN) WARNER LAMBERT CO.
 XX (MONE-) MONELL CHEM SENSES CENT.
 XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
 XX Ohnen JD, Reed DR, Ross D, Tordoff MG;
 XX

XX WPI; 2002-075162/10.

XX Novel isolated polypeptide comprising variant form of mouse or human SAC1

PT polypeptide, and is associated with altered preference for carbohydrates

PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

PS Claim 14; Page 84; 239pp; English.

XX The invention relates to an isolated polypeptide, comprising a variant

CC form of mouse or human SAC1 polypeptide. The variant form is associated

CC with altered preference for carbohydrates, other sweeteners or ethanol.

CC The polypeptide and its associated DNA sequence can be produced by

CC recombinant techniques and is useful for preventing obesity, diabetes or

CC alcoholism associated with SAC1 expression. The sequences are useful in

CC screening for drugs and sweeteners. Recombinant cell lines and transgenic

CC embryos may be used in screening for and identifying agents that induce

CC or repress function of SAC1. Predisposition to diabetes, obesity or

CC alcoholism can be ascertained by testing any fluid or tissue of a human

CC (such as blood, pancreas or tongue) for sequence variations of the SAC1

CC gene. A sequence variation of the SAC1 locus may indicate a

CC predisposition to diabetes, obesity and/or alcoholism and may provide a

CC diagnostic mark. The polynucleotide can be detected in a biological

CC sample by contacting the DNA with a probe to form a hybridisation complex

CC which is then detected. The sequences represent cDNA encoding human and

CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes

XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

SQ

Query Match 1.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACTGCTCAT 1107

DB 16 GGTGTTACTGCTCAT 1

RESULT 61

AAS97674/c

ID AAS97674 standard; DNA; 20 BP.

XX AAS97674;

AC AAS97674;

XX 12-MAR-2002 (first entry)

DT Human SAC1 gene-specific oligonucleotide PCR primer #35.

DE Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;

KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;

KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;

KW protein replacement therapy.

XX Homo sapiens.

OS

XX WO200183749-A2.

PN

XX 08-NOV-2001.

PD

XX 25-APR-2001; 2001WO-US013387.

PF

XX 28-APR-2000; 2000US-0200794P.

XX 28-JUL-2000; 2000US-0221419P.

PR

XX 10-NOV-2000; 2000US-0247443P.

PR

XX (WARN) WARNER LAMBERT CO.

PA (MONE-) MONELL CHEM SENSES CENT.

PA

XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;

PI Ohmen JD, Reed DR, Ross D, Tordoff MG;

PI WPI; 2002-075162/10.

XX

PT Novel isolated polypeptide comprising variant form of mouse or human SAC1

PT polypeptide, and is associated with altered preference for carbohydrates

XX or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

PS Claim 14; Page 84; 239pp; English.

XX The invention relates to an isolated polypeptide, comprising a variant

CC form of mouse or human SAC1 polypeptide. The variant form is associated

CC with altered preference for carbohydrates, other sweeteners or ethanol.

CC The polypeptide and its associated DNA sequence can be produced by

CC recombinant techniques and is useful for preventing obesity, diabetes or

CC alcoholism associated with SAC1 expression. The sequences are useful in

CC screening for drugs and sweeteners. Recombinant cell lines and transgenic

CC embryos may be used in screening for and identifying agents that induce

CC or repress function of SAC1. Predisposition to diabetes, obesity or

CC alcoholism can be ascertained by testing any fluid or tissue of a human

CC (such as blood, pancreas or tongue) for sequence variations of the SAC1

CC gene. A sequence variation of the SAC1 locus may indicate a

CC predisposition to diabetes, obesity and/or alcoholism and may provide a

CC diagnostic mark. The polynucleotide can be detected in a biological

CC sample by contacting the DNA with a probe to form a hybridisation complex

CC which is then detected. The sequences represent cDNA encoding human and

CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes

XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

SQ

Query Match 1.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACTGCTCAT 1107

DB 16 GGTGTTACTGCTCAT 1

RESULT 62

ADJ93118

ID ADJ93118 standard; DNA; 20 BP.

XX ADJ93118;

AC ADJ93118;

XX 06-MAY-2004 (first entry)

DT Human G-coupled receptor protein HGPBMY30 gene primer GPCR99-28.

DE

XX immunosuppressive; cardiac; antinflammatory; cytostatic; anti-HIV;

KW antirheumatic; antiarthritic; antibacterial; antiseborrheic;

KW dermatological; antipsoriatic; neuroprotective; nootropic;

KW antiparkinsonian; antidiabetic; ophthalmological; antiaschmatic;

KW antidepressant; neuroleptic; hypotensive; tranquilizer; hypertensive;

KW anorectic; metabolic; virucide; osteopathic; antianginal; vulnery;

KW gene therapy; G-protein coupled receptor protein; HGPBMY30;

KW immune disorder; cardiovascular disorder; inflammatory disorder;

KW metabolic disorder; reproductive disorder; testicular cancer;

KW neural disorder; endocrine disorder; gastrointestinal disorder;

KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism; asthma;

KW schizophrenia; obesity; anorexia; osteoporosis; angina pectoris;

KW myocardial infarction; primer; ss.

XX Homo sapiens.

OS

XX WO200296946-A1.

PN

XX 05-DEC-2002.

PD

XX 30-MAY-2002; 2002WO-US017085.

PF

XX 30-MAY-2001; 2001US-0294411P.

PR

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA

XX Feder JN, Mintier GA, Ramanathan C;

PI

XX

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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR (RIBO-) RIBOZYME PHARM INC.
PR Mcswiggen J, Beigelman L;
XX WPI; 2003-712622/67.
XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of cancer or autoimmune disease, downregulates expression of
XX the BCL2 gene.
XX Example 3; SEQ ID NO 805; 148pp; English.
XX The invention relates to a novel short interfering nucleic acid (siNA)
XX that downregulates expression of the BCL2 gene by RNA interference. A
XX siNA of the invention has cytostatic, immunosuppressive, virucide, and
XX anti-HIV activity. The siNA are useful for modulation (inhibition) of
XX expression or activity of BCL2 by RNA interference. siNA are used to
XX modulate expression of BCL2 genes, in cells, tissue explants or
XX organisms, e.g. for treating cancer, autoimmune diseases and viral
XX infections (including by HIV) but also for drug screening, diagnosis,
XX target identification and validation, genetic engineering,
XX pharmacogenomics, studying gene function and gene mapping (e.g. of single
XX -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
XX represent siNA of the invention.
XX Sequence 19 BP; 8 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. NO. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ACAGTGCATTGAAATTCCTT 500
DB 19 ACAGTGGATTCATTCTT 1

RESULT 67
ADF49663
ID ADF49663 standard; RNA; 19 BP.
AC ADF49663;
XX
XX 12-FEB-2004 (first entry)
DE Human BCL2 siNA upper sequence SEQ ID NO:391.
XX
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
XX
XX WO2003070969-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-US004908.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR (RIBO-) RIBOZYME PHARM INC.
PR Mcswiggen J, Beigelman L;
XX WPI; 2003-712622/67.
XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of cancer or autoimmune disease, downregulates expression of
XX the BCL2 gene.
XX Example 3; SEQ ID NO 391; 148pp; English.
XX The invention relates to a novel short interfering nucleic acid (siNA)
XX that downregulates expression of the BCL2 gene by RNA interference. A
XX siNA of the invention has cytostatic, immunosuppressive, virucide, and
XX anti-HIV activity. The siNA are useful for modulation (inhibition) of
XX expression or activity of BCL2 by RNA interference. siNA are used to
XX modulate expression of BCL2 genes, in cells, tissue explants or
XX organisms, e.g. for treating cancer, autoimmune diseases and viral
XX infections (including by HIV) but also for drug screening, diagnosis,
XX target identification and validation, genetic engineering,
XX pharmacogenomics, studying gene function and gene mapping (e.g. of single
XX -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
XX represent siNA of the invention.
XX Sequence 19 BP; 4 A; 3 C; 4 G; 0 T; 8 U; 0 Other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. NO. 95;
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 482 ACAGTGCATTGAAATTCCTT 500
DB 1 ACAGUGGAUUGCAUUCUU 19

RESULT 68
AAT36558
ID AAT36558 standard; DNA; 20 BP.
XX
XX AAT36558;
XX
XX 10-FEB-1997 (first entry)
DE Campylobacter fetus specific probe.
XX
XX c-gtp; guanosine 5'-triphosphate; GTPase; enzyme; probe;
KW GTP-binding protein; primer; detection; differentiation; microorganism;
KW biological sample; thermophilic; veterinary; Campylobacter; jejuni; coli;
KW lari; upsaliensis; human; pathogen; diarrhoea; infection; fetus;
KW hyointestinalis; mucosalis; ss.
XX
XX Synthetic.
XX
XX WO9613608-A2.
XX
XX 09-MAY-1996.
XX
XX 30-OCT-1995; 95WO-EP004264.
XX
XX 28-OCT-1994; 94EP-00870171.
XX
XX (INNO-) INNOGENETICS NV.
XX (DELTA-) DELTA DIAGNOSTIC LAB BV.
XX
XX Giesendorf B, Quint W, Van Doorn L;
XX
XX WPI; 1996-239513/24.
XX
XX GTPase gene family sequences derived from Campylobacter species - for use

```


PT in the detection and differentiation of thermophilic and veterinary
 species of Campylobacter.

XX
 XX
 XX
 XX
 CC Claim 21; Page 62; 104pp; English.

CC The present sequence is a Campylobacter fetus c-gtp gene specific probe.
 CC The c-gtp gene encodes a guanosine 5'-triphosphatase (GTPase) enzyme, or
 CC GTP-binding protein. The gene can be used in the prepn. of probes and
 CC primers, i.e. the present sequence, for the detection and differentiation
 CC of microorganisms in biological samples. Thermophilic and veterinary
 CC Campylobacter sp. can be detected with probes or primers derived from the
 CC c-gtp-1 and c-gtp-2 gene families, respectively. Thermophilic
 CC Campylobacter sp. include C. jejuni, C. coli, C. lari and C. upsaliensis,
 CC which are human pathogens involved in diarrhoea causing infections.
 CC Veterinary Campylobacter sp., encompass sp. which are important in
 CC veterinary infections, e.g. C. fetus, C. hyointestinalis and C. mucosalis
 XX
 XX
 SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 97;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 931 TAGAATGCAGAACTCGAA 949
 ||| ||||| ||||| |||
 DB 2 TAGCAATGCAGAACTCGCA 20

RESULT 69
 ADG37263
 ID ADG37263 standard; DNA; 20 BP.
 XX
 AC ADG37263;
 DT 26-FEB-2004 (first entry)
 DE Fox specific PCR primer #2.
 DE fur textile; animal fur; ss; PCR; primer; fox.
 KW Canidae.
 OS
 XX
 XX JP2003204798-A.
 PN
 PD 22-JUL-2003.
 XX
 XX 31-OCT-2002; 2002JP-00317866.
 PF
 XX 31-OCT-2001; 2001JP-00334739.
 PR
 XX (NIBO-) ZH NIPPON BOSEKI KENSA KYOKAI.
 XX
 XX WPI; 2003-819736/77.
 XX
 XX
 PT Identifying fur textiles involves amplifying DNA fragment specific for
 PT each animal fur, and analyzing amplified DNA.
 XX
 PS Claim 1; SEQ ID NO 2; 9pp; Japanese.
 XX
 CC The invention relates to a method of identifying textiles of fur,
 CC comprising amplifying DNA fragment specific for each animal fur, and
 CC analysing amplified DNA. The method is useful for identifying fur
 CC textiles. The method effectively distinguishes the origin of animal fur.
 CC The present sequence represents a fox specific PCR primer.
 XX
 XX
 SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 97;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 791 GTGCTTGAGAGCGAGATA 809
 ||| ||||| ||||| |||

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Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGATGCTTTGGAGA 801
||| ||||| ||||| |||||
Db 1 TTGTAGATGCTTTGGAGA 19

RESULT 71
ADG86960/c
ID ADG86960 standard; cDNA; 20 BP.
XX
AC ADG86960;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PPAR antisense oligonucleotide target sequence #22.
XX
KW Human; ss; PPAR delta; peroxisome proliferative activated receptor delta;
KW antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer;
KW osteoporosis; diabetes; endocrine disorder.
XX
OS Homo sapiens.
XX
FN US2003224514-A1.
XX
PD 04-DEC-2003.
XX
PF 31-MAY-2002; 2002US-00160807.
XX
PR 31-MAY-2002; 2002US-00160807.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde W, Freier SM, Watt AT;
XX
DR WPI; 2004-022078/02.
XX
XX New antisense oligonucleotides of 8-80 nucleobases, useful for treating
cancer, diabetes, osteoporosis or various endocrine disorders.
XX
PS Example 16; SEQ ID NO 196; 155pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising 8-80
CC nucleobases in length targeted to the coding region of a nucleic acid
CC molecule encoding PPAR-delta (peroxisome proliferative activated receptor
CC delta), where the antisense compound inhibits the expression of the PPAR-
CC delta and has any of the 66 sequences of 20 amino acids fully defined in
CC the specification. Also included are a compound of 8-80 nucleobases in
CC length that specifically hybridizes with at least an 8-nucleobase portion
CC of a preferred target region on a nucleic acid molecule encoding PPAR-
CC delta and a composition comprising the antisense oligonucleotide and a
CC carrier. The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage (preferably a phosphorothioate linkage), at least
CC one sugar moiety (preferably 2'-O-methoxyethyl moiety) and at least one
CC modified nucleobase (which is a 5-methyl cytosine). The antisense
CC compounds are useful for treating cancer, osteoporosis, diabetes or
CC various endocrine disorders. The Human PPAR delta gene is located on
CC chromosome 6p21. The present sequence is a human PPAR delta cDNA target
CC sequence for the antisense oligonucleotides of the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGATGCTTTGGAGA 801
||| ||||| ||||| |||||
Db 20 TTGTAGATGCTTTGGAGA 2

RESULT 72
ADJ61530/c
ID ADJ61530 standard; DNA; 20 BP.
XX
AC ADJ61530;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to IL5R-X61176 #222.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
OS Homo sapiens.
XX
FN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPTG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandraagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codons and introns of respiratory disease-relevant genes e.g.,
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
XX disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 2386; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 624 GAGTTTATTCTCAGCAA 642
||| ||||| ||||| |||||
Db 20 GACTTTATTCTCAGCAA 2

RESULT 73
ADJ24889
ID ADJ24889 standard; DNA; 20 BP.
XX
AC ADJ24889;

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XX 20-MAY-2004 (first entry)
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 3287.
XX Antilipaeic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX WO2004009541-A2.
XX 29-JAN-2004.
XX 18-JUL-2003; 2003WO-US022410.
XX 19-JUL-2002; 2002US-0397106P.
XX (PHAA ) PHARMACIA CORP.
XX Bhat BG;
XX WPI; 2004-132912/13.
XX New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX Claim 3; SEQ ID NO 3287; 1007pp; English.
XX The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX Sequence 20 BP; 3 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 19 GCCCGGGCGTGCAGGAA 37
DB 2 GCCCGGGCGTGCAGGGA 20
RESULT 74
ADJ23864
ID ADJ23864 standard; DNA; 20 BP.
XX ADJ23864;
XX Antilipaeic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX 20-MAY-2004 (first entry)
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 2262.
XX Antilipaeic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX WO2004009541-A2.
XX 29-JAN-2004.
XX 18-JUL-2003; 2003WO-US022410.
XX 19-JUL-2002; 2002US-0397106P.
XX (PHAA ) PHARMACIA CORP.
XX Bhat BG;
XX WPI; 2004-132912/13.
XX New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX Claim 3; SEQ ID NO 2262; 1007pp; English.
XX The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX Sequence 20 BP; 3 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 CCGGCGCGTGCAGGAGC 39
DB 1 CCGGCGCGTGCAGGAGC 19
RESULT 75
ADL34750
ID ADL34750 standard; DNA; 20 BP.
XX ADL34750;
XX 17-JUN-2004 (first entry)
XX Antisense oligonucleotide ISIS 136891.
XX Antisense; PPAR-delta; human; hybridisation; inhibitor;
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
KW hyperproliferative disorder; cancer; cytostatic; gene therapy; ss;
KW primer.
XX Synthetic.
XX

```

```

PN US2004063129-A1.
XX
XX 01-APR-2004.
XX
XX 05-SEP-2003; 2003US-00655847.
XX
XX 31-MAY-2002; 2002US-00160807.
XX
XX (GAAR/) GAARDE W.
XX (FREL/) FREIER S M.
XX (WATT/) WATT A T.
XX
XX Gaarde W, Freier SM, Watt AT;
XX
XX WPI; 2004-282460/26.
XX
XX New antisense oligonucleotide, having a sequence targeted to a nucleic
XX acid encoding PPAR-delta, useful for preparing a composition for treating
XX hyperproliferative disorder, e.g., cancer.
XX
XX Example 15; SEQ ID NO 48; Opp; English.
XX
XX This invention describes novel antisense oligonucleotides targeted to a
XX nucleic acid encoding PPAR-delta, which specifically hybridise to and
XX inhibit expression of PPAR-delta. The oligonucleotide specifically
XX hybridises with at least an 8-nucleobase portion of an active site on the
XX nucleic acid molecule encoding the PPAR-delta and comprises at least one
XX modified internucleoside linkage, which is a 2'-O-methoxyethyl sugar
XX moiety or at least one modified nucleobase, which is a 5-methylcytosine.
XX The antisense oligonucleotides are useful for preparing a composition for
XX treating hyperproliferative disorders, e.g., cancer. The oligonucleotides
XX of the invention have cytostatic activity and can be used for gene
XX therapy.
XX
XX Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 20;
XX Best Local Similarity 89.5%; Pred. No. 97;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 783 TTGGGGATGCTGTGGAGA 801
XX ||| |||||||||
XX Db 1 TTGTAGATGCTGTGGAGA 19
XX
XX RESULT 76
XX ID ADL34898/c
XX ADL34898 standard; DNA; 20 BP.
XX
XX AC ADL34898;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human PPAR-delta target site ID 50011.
XX
XX antisense; PPAR-delta; human; hybridisation; inhibitor;
XX phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
XX hyperproliferative disorder; cancer; cytostatic; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX US2004063129-A1.
XX
XX 01-APR-2004.
XX
XX 05-SEP-2003; 2003US-00655847.
XX
XX 31-MAY-2002; 2002US-00160807.
XX
XX (GAAR/) GAARDE W.
XX (FREL/) FREIER S M.
XX (WATT/) WATT A T.
XX
XX Gaarde W, Freier SM, Watt AT;
XX
XX WPI; 2004-282460/26.
XX
XX New antisense oligonucleotide, having a sequence targeted to a nucleic
XX acid encoding PPAR-delta, useful for preparing a composition for treating
XX hyperproliferative disorder, e.g., cancer.
XX
XX Example 16; SEQ ID NO 196; Opp; English.
XX
XX This invention describes novel antisense oligonucleotides targeted to a
XX nucleic acid encoding PPAR-delta, which specifically hybridise to and
XX inhibit expression of PPAR-delta. The oligonucleotide specifically
XX hybridises with at least an 8-nucleobase portion of an active site on the
XX nucleic acid molecule encoding the PPAR-delta and comprises at least one
XX modified internucleoside linkage, which is a phosphorothioate linkage, at
XX least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar
XX moiety or at least one modified nucleobase, which is a 5-methylcytosine.
XX The antisense oligonucleotides are useful for preparing a composition for
XX treating hyperproliferative disorders, e.g., cancer. The oligonucleotides
XX of the invention have cytostatic activity and can be used for gene
XX therapy.
XX
XX Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 20;
XX Best Local Similarity 89.5%; Pred. No. 97;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 783 TTGGGGATGCTGTGGAGA 801
XX ||| |||||||||
XX Db 20 TTGTAGATGCTGTGGAGA 2
XX
XX RESULT 77
XX ADO46920/c
XX ID ADO46920 standard; DNA; 20 BP.
XX
XX AC ADO46920;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human oligonucleotide #2286.
XX
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
XX CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
XX asthma; lung allergy; inflammation; inflammatory disease;
XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;
XX acute respiratory distress syndrome; pulmonary hypertension;
XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
XX Homo sapiens.
XX
XX US2004049022-A1.
XX
XX 11-MAR-2004.
XX
XX 25-JUL-2003; 2003US-00627930.
XX
XX 23-APR-2002; 2002WO-US013135.
XX 23-APR-2002; 2002WO-US013143.
XX
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUILAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LUHH/) LU H.

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PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-293804/27.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCRI,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
XX Claim 2; SEQ ID NO 2386; 174pp; English.
XX
XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCRI, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase B, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCRI, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase B, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX
XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 624 GAGTTTATCTTCACGAAA 642
Db 20 GACTTTTATCTTCACGAAA 2

RESULT 78
ABV76832/c
ID ABV76832 standard; DNA; 21 BP.
XX
XX ABV76832;
AC
XX
XX 12-FEB-2003 (first entry)
DT
XX
XX Control PCR primer used to amplify a beta-actin cDNA fragment.
DE
XX
XX Arthritic condition; CD21L; lymphotoxin-beta; chemoattractant; arthritis;
KW beta-actin; PCR; primer; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200280010-A1.
PN
XX
XX 10-OCT-2002.
PD
XX
XX 22-MAR-2002; 2002WO-US008856.
PF
XX
XX 23-MAR-2001; 2001US-00816814.
XX

(MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Goronzy JJ, Weyand CM;
XX
XX WPI; 2003-058450/05.
XX
XX Determining the severity of arthritic conditions, e.g. rheumatoid
PT arthritis, in a mammal or human by detecting whether a sample contains
PT elevated levels of marker(s), e.g. CD21L polypeptides or lymphotoxin-beta
PT polypeptides.
XX
XX Example 2; Page 12; 27pp; English.
XX
XX The specification describes a method for determining the severity of an
CC arthritic condition in a mammal. The method comprises determining whether
CC or not a sample from the mammal contains at least 1 marker (e.g. an
CC elevated level of a CD21L polypeptide, an elevated level of a lymphotoxin
CC -beta polypeptide, or an elevated level of a chemoattractant
CC polypeptide). The presence of the marker indicates that the arthritis
CC condition is severe. The method is useful for diagnosing the severity of
CC an arthritic condition (e.g. rheumatoid arthritis) in a mammal,
CC particularly a human. Control PCR primers ABV76832-33 were used to
CC amplify a beta-actin cDNA fragment from a synovial tissue sample. The
CC primers were used in the method of the invention
XX
XX Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 99;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 38 GCCGAGCAGCAGCGCGCC 56
Db 21 GCTGAGCAGCAGCGTGCC 3

RESULT 79
ADA73990/c
ID ADA73990 standard; DNA; 21 BP.
XX
XX ADA73990;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX PCR primer #1 for DNA encoding human beta-actin.
DE
XX
XX Rheumatoid arthritis condition; RA; cytokine; interleukin-1 beta;
KW IL-1beta; interleukin-4; IL-4; interleukin-10; IL-10; interferon-gamma;
KW IFN-gamma; tumour necrosis factor-alpha; TNF-alpha;
KW transforming growth factor-beta; TGF-beta; diffuse; follicular;
KW granulomatous; human; beta-actin; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX US6555320-B1.
PN
XX
XX 29-APR-2003.
PD
XX
XX 01-SEP-1999; 99US-00387467.
PF
XX
XX 01-SEP-1998; 99US-0098718P.
PR
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA
XX
XX Goronzy JJ, Weyand CM;
PI
XX
XX WPI; 2003-687206/65.
XX
XX Evaluating rheumatoid arthritis condition in patient, by comparing
PT cytokine levels in sample from patient to reference levels to obtain
PT information about condition, and classifying condition based on the
PT information.
XX
XX

```

Fri Aug 19 11:00:00 2005

PS Example 1; Col 9; 25pp; English.

XX The present invention relates to a method for evaluating rheumatoid

CC arthritis (RA) condition in a patient. The method involves determining

CC the level of cytokines (e.g. interleukin-1 (IL-1) beta, interleukin-4 (IL

CC -4), interleukin-10 (IL-10), interferon gamma, tumour necrosis factor-

CC alpha (TNF-alpha), and transforming growth factor-beta (TGF-beta)) within

CC the sample from a patient, comparing the level to reference levels to

CC obtain information about the RA condition, and classifying the RA

CC condition as being or not being diffuse, follicular or granulomatous

CC condition based on information. The method is useful for classifying a RA

CC condition as diffuse, follicular, or granulomatous, and for determining

CC if an individual suffering from a RA condition will develop severe

CC disease. The present sequence represents a PCR primer used in the

CC examples of the present invention.

XX

XX Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

XX

Query Match 1.4%; Score 15.8; DB 1; Length 21;

Best Local Similarity 89.5%; Pred. No. 99;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 GCCGAGACGACCGCGGCC 56

Db 21 GCTGGAAGCAGCGGTGGCC 3

RESULT 80

AAS23701/C

ID AAS23701 standard; DNA; 22 BP.

XX

AC AAS23701;

XX

DT 04-DEC-2001 (first entry)

XX

XX Primer A #15 used as probe for identifying C. albicans GRACE strain.

DE

XX Gene identification; essential gene; GRACE; pathogenic fungus;

XX gene replacement and conditional expression; fungal infection; probe; ss.

KW

XX Candida albicans.

OS

XX Synthetic.

XX

XX WO200160975-A2.

FN

XX

XX 23-AUG-2001.

PD

XX

XX 20-FEB-2001; 2001WO-US005551.

PF

XX

XX 18-FEB-2000; 2000US-0183534P.

PR

XX (ELIT-) ELITRA PHARM INC.

PA

XX

XX Roemer T, Jiang B, Boone C, Bussey H;

PI

XX

XX WPI; 2001-489080/53.

DR

XX

XX Identifying genes essential to fungal metabolisms and identifying

XX potential therapeutic agents that target these genes.

PT

XX

XX Disclosure; Page 303; 324pp; English.

PS

XX

XX The present invention relates to novel methods for constructing fungal

CC strains useful for identification and validation of gene products as

CC targets for therapeutic agents, for creating a collection of identified

CC essential genes, and screening assays for the discovery of new drugs. The

CC invention provides the GRACE (gene replacement and conditional

CC expression) method for the construction of mutant organisms referred to

CC as GRACE strains of the organism. The invention can be applied to any

CC organism, particularly a pathogenic fungus e.g. Candida albicans,

CC Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful

CC to identify agents that may be used in the treatment of fungal

CC infections. AAS23687-AAS23747 represent primers A #1-61 used as probes

CC

CC for identifying C. albicans GRACE strains

XX

XX Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

XX

Query Match 1.4%; Score 15.8; DB 1; Length 22;

Best Local Similarity 89.5%; Pred. No. 1e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 337 TCCTGTGGCTGTGATCAAA 355

Db 19 TCCTGTGGCTGTGATCAAA 1

RESULT 81

ABZ29880/C

ID ABZ29880 standard; DNA; 22 BP.

XX

AC ABZ29880;

XX

XX 30-JAN-2003 (first entry)

XX

XX Candida albicans GRACE strain PCR primer SEQ ID NO 4031.

DE

XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;

KW signal transduction; DNA replication; cell division; growth;

KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.

XX

XX Candida albicans.

OS

XX WO200253728-A2.

FN

XX

XX 11-JUL-2002.

PD

XX

XX 26-DEC-2001; 2001WO-US049486.

PF

XX

XX 29-DEC-2000; 2000US-0259128P.

PR

XX 20-FEB-2001; 2001US-00792024.

PR

XX 22-AUG-2001; 2001US-0314050P.

XX

XX (ELIT-) ELITRA PHARM INC.

PA

XX

XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

PI

XX

XX WPI; 2002-566694/60.

DR

XX

XX Constructing strains for identifying gene products as effective targets

PT for therapeutic intervention, by inactivating in the strain one allele of

PT a gene and placing other allele of the gene under conditional expression.

XX

XX Claim 36; SEQ ID NO 4031; 167pp + Sequence Listing; English.

PS

XX

XX The invention relates to constructing (M1) a strain of diploid fungal

CC cells in which both alleles of a gene are modified, comprising modifying

CC one allele by insertion or replacement by a cassette having an

CC expressible selectable marker and modifying other allele by

CC recombination, of a promoter replacement fragment with a heterologous

CC promoter, so that expression of the second allele is regulated by the

CC promoter. (M1) is useful for constructing a strain of diploid fungal

CC cells in which both alleles of a gene are modified. The diploid fungal

CC cells having both alleles modified are useful for identifying a gene that

CC is essential to the virulence or growth of a fungus, a gene that

CC contributes to the virulence and/or pathogenicity of a fungus, a gene

CC that contributes to the resistance of a diploid fungus to an antifungal

CC agent, an antifungal agent that inhibits the growth of a diploid fungus

CC and for identifying a therapeutic agent for treatment of a mammalian

CC disease. (M1) is useful for identifying a compound which modulates the

CC activity of a gene product, preferably enzymatic activity, carbon

CC compound catabolism, biosynthetic, transporter, transcriptional,

CC translational, signal transduction, DNA replication and cell division

CC activity. The method is useful for identifying a compound having the

CC ability to inhibit growth or proliferation of C. albicans cells and for

CC treating infection by C. albicans. The present sequence is that of a PCR

CC primer used in the method of the invention. Note: The sequence data for

CC this patent is not represented in the printed specification but is based
 CC on sequence information supplied to Derwent by the European Patent Office
 XX Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 337 TCGTGTGGCTGTGATCAAA 355
 Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 82

AAV73536
 ID AAV73536 standard; DNA; 20 BP.

XX AAV73536;

XX 22-MAR-2000 (first entry)

XX H. pylori vacA probe P4S1 DNA.

XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP005614.

XX 16-OCT-1996; 96EP-00870131.

XX 09-SEP-1997; 97EP-00870133.

XX (INNO-) INNOGENETICS NV.
 PA (DDLJ-) DDL BV.

XX Quint W, Van Doorn L;

XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and cagA gene.

XX Claim 3; Page 46; 122pp; English.

CC This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements involved
 CC in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785

XX Sequence 20 BP; 2 A; 1 C; 7 G; 8 T; 0 U; 2 Other;

Query Match 1.4%; Score 15.6; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 103 CTTTCAGTGGGCTATTGG 120
 Db 2 CTTTCAGTGGGCTATTGG 19

RESULT 83

ADH42586

ID ADH42586 standard; DNA; 22 BP.

XX ADH42586;

XX 25-MAR-2004 (first entry)

XX Novel human nucleic acid NOVX gene probe Ag650 forward primer.

XX cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
 KW antiparkinsonian; antiasthmatic; antifertility; cardiomyopathy;
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine; primer; ss.

OS Homo sapiens.

XX WO2003102159-A2.

XX 11-DEC-2003.

XX 04-JUN-2003; 2003WO-US017573.

XX 04-JUN-2002; 2002US-0385490P.

XX 04-JUN-2002; 2002US-0385615P.

XX 04-JUN-2002; 2002US-0385755P.

XX 05-JUN-2002; 2002US-0386041P.

XX 06-JUN-2002; 2002US-0386355P.

XX 06-JUN-2002; 2002US-0386357P.

XX 06-JUN-2002; 2002US-0386447P.

XX 06-JUN-2002; 2002US-0386459P.

XX 06-JUN-2002; 2002US-0386465P.

XX 06-JUN-2002; 2002US-0386864P.

XX 07-JUN-2002; 2002US-0386701P.

XX 07-JUN-2002; 2002US-0386796P.

XX 07-JUN-2002; 2002US-0386931P.

XX 07-JUN-2002; 2002US-0387078P.

XX 07-JUN-2002; 2002US-0387081P.

XX 07-JUN-2002; 2002US-0387083P.

XX 10-JUN-2002; 2002US-0387429P.

XX 10-JUN-2002; 2002US-0387540P.

XX 10-JUN-2002; 2002US-0387866P.

XX 11-JUN-2002; 2002US-0387606P.

XX 11-JUN-2002; 2002US-0387610P.

XX 11-JUN-2002; 2002US-0387659P.

XX 11-JUN-2002; 2002US-0387668P.

XX 11-JUN-2002; 2002US-0387696P.

XX 11-JUN-2002; 2002US-0387859P.

XX 12-JUN-2002; 2002US-0387934P.

XX 12-JUN-2002; 2002US-0387960P.

XX 12-JUN-2002; 2002US-0388022P.

XX 12-JUN-2002; 2002US-0388096P.

XX 12-JUN-2002; 2002US-0388432P.

XX 12-JUN-2002; 2002US-0388479P.

XX 13-JUN-2002; 2002US-0389123P.

XX 14-JUN-2002; 2002US-0389120P.

XX 14-JUN-2002; 2002US-0389146P.

XX 17-JUN-2002; 2002US-0389742P.

XX 18-JUN-2002; 2002US-0389604P.

XX 18-JUN-2002; 2002US-0389884P.

XX 19-JUN-2002; 2002US-0390066P.

	19-JUN-2002; 2002US-0390144P.	
PR	19-JUN-2002; 2002US-0390209P.	
PR	25-JUN-2002; 2002US-0391726P.	
PR	06-AUG-2002; 2002US-0401628P.	
PR	09-AUG-2002; 2002US-0402268P.	
PR	12-AUG-2002; 2002US-0402822P.	
PR	13-AUG-2002; 2002US-0403458P.	
PR	15-AUG-2002; 2002US-0403617P.	
PR	15-AUG-2002; 2002US-0403732P.	
PR	16-AUG-2002; 2002US-0406182P.	
PR	12-SEP-2002; 2002US-0410085P.	
PR	13-SEP-2002; 2002US-0410505P.	
PR	23-SEP-2002; 2002US-0412955P.	
PR	30-SEP-2002; 2002US-0415195P.	
PR	23-OCT-2002; 2002US-0420627P.	
PR	23-OCT-2002; 2002US-0420718P.	
PR	24-OCT-2002; 2002US-0420852P.	
PR	31-OCT-2002; 2002US-0422750P.	
PR	01-NOV-2002; 2002US-0423095P.	
PR	05-NOV-2002; 2002US-0423748P.	
XX		
PA	(CURA-) CUPAGEN CORP.	
XX	Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;	
PI	Burgess CE, Casman SJ, Catterton E, Dhanabai M, Edinger SR;	
PI	Billerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;	
PI	Grosz WM, Gunther E, Guo X, Gusev VV, Herrmann JL, Ji W, Kekuda R;	
PI	Khrantsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;	
PI	Machlanson T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CB;	
PI	Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;	
PI	Rieger DK, Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G;	
PI	Sytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CM, Voss EZ;	
PI	Wolenc AR, Zhong M, Zhong H;	
XX		
DR	WFI: 2004-053467/05.	
XX		
XX	New NOVX polypeptides and nucleic acid molecules useful for preventing or	
PT	treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, or in	
PT	atherosclerosis or diabetes, in chromosome mapping, tissue typing or in	
PT	pharmacogenomics.	
XX		
FS	Disclosure; SEQ ID NO 1139; 1503pp; English.	
XX		
CC	The invention relates to 566 new isolated human polypeptides and their	
CC	encoding genes, sequences that are at least 95% identical to these or	
CC	sequences comprising one or more conservative substitutions in these. The	
CC	polypeptide, polynucleotide and antibodies against the polypeptides are	
CC	useful in diagnosing, treating or preventing NOVX-associated disorders,	
CC	e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,	
CC	diabetes, AIDS, multiple sclerosis, graft-versus-host disease,	
CC	Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.	
CC	The nucleic acids are further used as hybridization probes, in chromosome	
CC	mapping, tissue typing, preventive medicine, and pharmacogenomics. The	
CC	polypeptides are also useful as vaccines. This sequence represents an	
CC	example of the forward primer used to amplify a probe to isolate the	
CC	nucleic acid sequences of the invention.	
XX		
SQ	Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;	
	Best Local Similarity 1.4%; Score 15.6; DB 1; Length 22;	
	Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps	
QY	478 GATTACAGTCGATTCGATTTCT 499	
Db		
	1 GTTTTCATTCGATTCGATTTCT 22	
RESULT 84		
ID ADS575784		
ID ADS575784 standard; DNA; 22 BP.		
XX		
AD	ADS575784;	

PN WO2004081225-A2.
 XX 23-SEP-2004.
 XX 08-MAR-2004; 2004WO-US006983.
 XX 07-MAR-2003; 2003US-0453060P.
 XX (RUBI-) RUBICON GENOMICS INC.
 XX Kamberov E, Sun T, Bruening E, Pinter J, Sleptsova I, Kurihara T;
 PI Makarov VL;
 XX WPI; 2004-677550/66.
 XX Preparing and amplifying a genome or a transcriptome comprises subjecting
 PT the molecule/primer mixture to a polymerase.
 XX Example 25; SEQ ID NO 93; 208pp; English.
 XX The present invention relates to a method for preparing and amplifying a
 CC genome, a transcriptome, or both, or a nucleic acid, e.g. DNA or RNA
 CC molecule or a DNA molecule generated from at least one mRNA molecule. The
 CC method comprises subjecting the DNA molecule/primer mixture or the RNA
 CC molecule/primer mixture or the ssDNA molecule/primer mixture to a
 CC polymerase, under conditions where the subjecting steps generate
 CC molecules including all or part of the constant region at each end. The
 CC present sequence was used to illustrate the method of the invention.
 XX Sequence 22 BP; 2 A; 2 C; 6 G; 12 T; 0 U; 0 Other;
 SQ
 Query Match 1.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 297 GAATTTGTTCTTCGCTTTGG 318
 DB 1 GAAATTTGTTCTTCGCTTTGG 22
 RESULT 86
 ID ABK18401
 XX ABK18401 standard; RNA; 17 BP.
 XX
 AC ABK18401;
 XX
 XX 09-APR-2002 (first entry)
 XX Human ERG hammerhead ribozyme target sequence, Seq ID No 1048.
 DE
 XX Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNzyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO200188124-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 16-MAY-2001; 2001WO-US015866.
 XX
 XX 16-MAY-2000; 2000US-00572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082395/11.
 XX Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 XX Claim 4; Page 78; 149pp; English.
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 1.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 958 CTGGACCAGGACATTT 974
 DB 1 CUGGACUCAGGACAUU 17
 RESULT 87
 ID ABT38549/c
 XX ABT38549 standard; DNA; 17 BP.
 XX
 AC ABT38549;
 XX
 DT 12-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 4186.
 DE
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO2003025175-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004208.
 XX
 XX 17-SEP-2001; 2001FR-00011978.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA

Fri Aug 19 11:00:00 2005

```
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX
XX Disclosure; Page 523; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence
XX given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 838 GAAGCGCGGGTGGATC 854
Db 17 GAAGCGCTGGTGGATC 1

RESULT 88
ADB42880/c
ID ADB42880 standard; DNA; 17 BP.
AC ADB42880;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #3203.
DE
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
FN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
```

```
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
PT
XX
XX Disclosure; Page 406; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 838 GAAGCGCGGGTGGATC 854
Db 17 GAAGCGCTGGTGGATC 1

RESULT 89
AAZ77304
ID AAZ77304 standard; DNA; 18 BP.
XX
XX AAZ77304;
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:11660.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9954500-A2.
FN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-IB000822.
PF
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX
```

DR WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 9; Page 2716; 2745pp; English.
XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterization of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 18 BP; 4 A; 2 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 104 TTCAGTGGGGCTATTGG 120
|||||
DB 2 TTCATGGGGCTATTGG 18

RESULT 90
ADD24780/c
ID ADD24780 standard; DNA; 18 BP.
XX
AC ADD24780;
XX
XX 15-JAN-2004 (first entry)
DT
DE Human CYP2D6 C100T mutant probe H154.
XX
XX diagnostic; pharmaceutical tolerance; side effect; drug; human;
KW allelic variability; polymorphism; phase I; phase II;
KW detoxification mechanism; PCR; primer; probe; NAT2; CYP2D6; CYP1A2;
KW CYP3A4; mEH; TPMT; MTHFR; paraoxonase; CYP2C9; CYP2C19; CYP2E1; DPD; ss.
XX
OS Homo sapiens.
XX
XX WO2003018837-A2.
PN
XX
PD 06-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-EP009386.
PF
XX 24-AUG-2001; 2001DE-01040651.
PR
XX 30-APR-2002; 2002DE-01019373.
PR
XX (ADNA-) ADNAGEN AG.
PA
XX
XX Waschuetza S, Schnakenberg E, Lustig M;
PI
XX
XX WPI; 2003-290079/28.
DR
XX Diagnostic kit, useful for assessing a subject's tolerance of drugs,
PT comprises reagents for determining alleles of genes encoding
PT detoxification enzymes.
XX
XX Claim 6; Page 13; 156pp; German.
PS
XX This invention describes a novel diagnostic kit for determining tolerance
CC

of pharmaceuticals in humans by determining allelic variability of at
least two polymorphisms of a human enzyme involved in phase I and/or II
of the detoxification mechanism in a blood, tissue or other human sample,
where tolerance is determined from presence or absence of alleles. The
kit comprises two pairs of oligonucleotide primers, in which each pair
amplifies, by PCR, part of a gene for a human detoxification mechanism-
associated enzyme. The kit may also contain two further pairs of
oligonucleotides, serving as probes for detection of amplified DNA
segments, especially where the probes are complementary to a single
strand of one allele of the target gene. The probes are labelled with
fluorophores (LC-Red640 or LC-Red705 for 5'-labelling or fluorescein for
3'-labelling) which generate a different signal in the hybridized and non
hybridized condition. The enzymes detected include NAT2, CYP2D6, CYP1A2,
CYP3A4, mEH, TPMT, MTHFR, paraoxonase, CYP2C9, CYP2C19, CYP2E1 or DPD.
The kit is used to determine an individual's tolerance of a particular
drug, to establish a suitable dose and/or to predict if a subject will
show side-effects to a drug. The kit provides minimally invasive, safe
and reliable determination of the metabolic capacity of phase I and/or II
enzymes at the molecular level. This sequence represents a probe used in
the kit of the invention.
XX
XX Sequence 18 BP; 1 A; 9 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 19 GCCCGGGCGGTGGCAGG 35
|||||
DB 17 GCCCGGGCGGTGGCAGG 1

RESULT 91
AAQ81302/c
ID AAQ81302 standard; mRNA; 19 BP.
XX
AC AAQ81302;
XX
XX 25-MAR-2003 (revised)
DT
XX 07-SEP-1995 (first entry)
DT
DE Ribozyme target sequence in TGF-beta mRNA (bases 2447-2465).
XX
XX Target site; ribozyme; hammerhead; hairpin; hepatitis delta virus;
KW group 1 intron; RNaseP RNA motif; transforming growth factor-beta;
KW TGF-beta; fibrous; connective; tissue disease; TGF-alpha; inhibin;
KW epidermal growth factor; EGF; activin; amphiregulin; insulin;
KW bone morphogenic protein; fibroblast growth factor; relaxin; ss.
XX
OS Homo sapiens.
XX
XX WO9429452-A2.
PN
XX
PD 22-DEC-1994.
XX
XX 02-JUN-1994; 94WO-US006331.
PF
XX 09-JUN-1993; 93US-00074343.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Draper KG;
PI
XX
XX WPI; 1995-051612/07.
DR
XX Enzymatic RNA molecule with, e.g. a hammerhead or hairpin motif - cleaves
PT mRNA associated with fibrous or connective tissue disease, and is useful
PT for treatment or prophylaxis of such diseases.
XX
XX Claim 3; Page 5; 63pp; English.
PS
XX The sequences (AAQ81238-304) represent the target sites where a ribozyme
CC (hammerhead, hairpin, hepatitis delta virus, group 1 intron or RNaseP RNA

CC motif) cleaves the mRNA of the transforming growth factor-beta (TGF-beta)
CC gene. This sequence corresponds to bases 2447-2465 of the TGF-beta mRNA.
CC The ribozymes can also target the mRNAs of genes associated with the
CC development or maintenance of fibrous or connective tissue disease in
CC order to prevent or treat these diseases. Such genes include TGF-alpha or
CC beta, epidermal growth factor, inhibitors, activins, amphiregulin, bone
CC morphogenic proteins, fibroblast growth factors a and b, insulin growth
CC factor 1 or 2, insulin or relaxin. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 19 BP; 6 A; 3 C; 8 G; 0 T; 2 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1077 CACTTAACCTCTCTGGG 1093
Db 18 CCCTTAACCTCTCTGGG 2

RESULT 92
AAH85723/c
ID AAH85723 standard; DNA; 19 BP.
XX
XX AAH85723;
XX
XX 04-DEC-2000 (first entry)
DT
XX
XX Cyclin B1 ribozyme binding site #52.
DE
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KW
XX
XX Mammalia.
OS
XX
XX WO200032765-A2.
FN
XX
XX 08-JUN-2000.
PD
XX
XX 06-DEC-1999; 99WO-US028772.
PF
XX
XX 04-DEC-1998; 98US-0110954P.
PR
XX
XX (IMMU-) IMMUSOL INC.
PA
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI
XX
XX WPI; 2000-412314/35.
DR
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
PT
XX
XX Disclosure; Page 96; 109pp; English.
PS
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
XX
XX Sequence 19 BP; 5 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 790 TGTGCTTGGAGGCAG 806
Db 18 TGGCCTTGGAGGCAG 2

RESULT 93
AAH60885/c
ID AAH60885 standard; DNA; 19 BP.
XX
XX AAH60885;
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Cyclin B1 ribozyme binding site SEQ ID NO:3309.
DE
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytosatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiskinning; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO200130362-A2.
PN
XX
XX 03-MAY-2001.
PD
XX
XX 26-OCT-2000; 2000WO-US029500.
PF
XX
XX 26-OCT-1999; 99US-0161532P.
PR
XX
XX (IMMU-) IMMUSOL INC.
PA
XX
XX Robbins JM, Tritz R;
PI
XX
XX WPI; 2001-300427/31.
DR
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
PT
XX
XX Example 1; Page 312; 408pp; English.
PS
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (i). (I) can have antipsoriatic,
CC dermatological, vulnary, keratolytic and virucide activities, and
CC ophthalmological, antiseborrheic, antidiabetic, antiskinning, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX
XX Sequence 19 BP; 5 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 790 TGTGCTTGGAGGCAG 806
Db 18 TGGCCTTGGAGGCAG 2

```

Db      18  TGGGCTTGGAGAGCAG 2
|| |||||
RESULT 94
AAT50899/c
ID  AAT50899 standard; DNA; 20 BP.
XX
AC  AAT50899;
XX
DT  26-AUG-1997 (first entry)
XX
DE  Probe #13 for interleukin-6 receptor.
XX
KW  Probe; interleukin-6 receptor; IL-6R; cytokine; cellular proliferation;
KW  transmembrane glycoprotein receptor; signal transducer; gp130; inhibitor;
KW  IL-6; cancer; renal cell carcinoma; autoimmune disease; viral infection;
KW  therapy; ss.
XX
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  misc_feature 1..20
FT  /tag= a
FT  /note= "optionally phosphorothioated"
XX
PN  EP747386-A2.
XX
PD  11-DEC-1996.
XX
PF  07-JUN-1996; 96EP-00304315.
XX
PR  07-JUN-1995; 95US-00484666.
XX  07-JUN-1995; 95US-00486408.
XX
PA  (GENP-) GEN-PROBE INC.
XX
PI  Brown SJ, Dattagupta N, Naidu YM;
XX  WPI; 1997-023093/03.
XX
PT  Oligo:nucleotide(s) complementary to interleukin-6 receptor mRNA - for
PT  treating proliferative diseases, e.g. cancer, auto-immune diseases or
PT  viral infections.
XX
PS  Claim 1; Page 16; 18pp; English.
XX
CC  AAT50897-T50904 represent oligonucleotides of the invention. These
CC  sequences are all probes for interleukin-6 receptor (IL-6R) mRNA. IL-6 is
CC  one of the most well characterised of the cytokines. It functions through
CC  interacting with at least two transmembrane glycoprotein receptor
CC  molecules on the surface of target cells. The receptors are the IL-6R,
CC  and the signal transducer gp130. Signal transduction by IL-6 involves the
CC  concerted action of both IL-6R and gp130. IL-6 overproduction is
CC  implicated in many different disease states, particularly in cellular
CC  proliferation associated with these diseases. These sequences bind to the
CC  IL-6R coding sequence, thereby inhibiting IL-6R production. The sequences
CC  therefore inhibit the functioning of IL-6. These sequences can be used
CC  for inhibiting disease-associated cellular proliferation. The
CC  oligonucleotides are especially useful for treating cancer (e.g. renal
CC  cell carcinoma), autoimmune diseases or viral infections. They can also
CC  be used as probes for detecting IL-6 receptor mRNA, especially for
CC  evaluating the effectiveness of drugs in reducing IL-6 receptor mRNA
CC  levels
XX
SQ  Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
    Query Match 1.4%; Score 15.4; DB 1; Length 20;
    Best Local Similarity 94.1%; Pred. No. 1.1e+02;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      18  CAGGAAGCCGGCAGCAG 2
|| |||||
RESULT 95
AAS97050
ID  AAS97050 standard; DNA; 20 BP.
XX
AC  AAS97050;
XX
DT  26-FEB-2002 (first entry)
XX
DE  TRA-8 heavy and light chain RT-PCR primer H55S2.
XX
KW  Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW  TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW  autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW  rheumatoid arthritis; Sjogren's syndrome; Crohn's disease; anaemia;
KW  Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW  myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW  allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW  glomerular nephritis; cancer; antibody; PCR primer; chromosome 8p21-22;
KW  TRA-8; ss.
XX
OS  Synthetic.
XX
PN  WO200193560-A1.
XX
PD  08-NOV-2001.
XX
PF  02-MAY-2001; 2001WO-US014151.
XX
PR  02-MAY-2000; 2000US-0201344P.
XX
PA  (UABR-) UAB RES FOUND.
XX
PI  Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX  WPI; 2002-049338/06.
XX
PT  Novel antibody specific for tumor necrosis factor-related apoptosis-
PT  inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS  Example 16; Page 72; 229pp; English.
XX
CC  The invention describes a novel antibody which recognizes a tumour
CC  necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC  DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC  activity to a cell expressing DR5 in vivo. It is also useful for
CC  preparing a therapeutic for selective apoptosis of abnormal or
CC  dysregulated cells, and for inhibiting cell proliferation in a cell,
CC  preferably a human breast, ovary, colon, haematopoietic, prostate,
CC  lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC  also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC  antibody is used to treat an autoimmune disease, systemic lupus
CC  erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC  host disease, Sjogren's syndrome, Crohn's disease, pernicious anaemia,
CC  Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC  haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC  Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC  disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC  nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC  and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC  breast tissue. This primer was used to isolate the mouse TRAIL TRA-8, a
CC  ligand of the DR5 receptor and the TRAIL on which the humanised
CC  antibodies of the invention are based
XX
SQ  Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
    Query Match 1.4%; Score 15.4; DB 1; Length 20;
    Best Local Similarity 94.1%; Pred. No. 1.1e+02;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      992  GTTGTATGCACATGAAA 1008
|| |||||

```

```

Db          ||||| 3 GTTGTATGCACATGAGA 19
RESULT 96
AAL60465
ID AAL60465 standard; DNA; 20 BP.
XX
AC AAL60465;
XX
XX 27-AUG-2003 (first entry)
XX
XX Mouse anti-human DR5 antibody (TRA-8) cDNA cloning PCR primer, H5S52.
XX
XX Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
XX inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
XX Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
XX multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
XX Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
XX Crohn's disease; diabetes mellitus; TRA-8 antibody; mouse; PCR; primer;
XX ss.
XX Mus sp.
XX WO2003037913-A2.
XX
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035333.
XX
XX 01-NOV-2001; 2001US-0346402P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX WPI; 2003-441350/41.
XX
XX New purified antibody that specifically binds a TNF-related apoptosis-
XX inducing ligand receptor DR4 or DR5, useful for treating cancer,
XX inflammatory disease or autoimmune disease in a subject, e.g. asthma or
XX rheumatoid arthritis.
XX
XX Example 16; Page 77; 251pp; English.
XX
XX The invention relates to an antibody that specifically binds a tumour
XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
XX DR4 or DR5. Antibodies of the invention are useful for selectively
XX inducing apoptosis in target cells expressing DR4, for inhibiting
XX proliferation of target cells expressing DR4 or for treating cancer,
XX inflammatory disease or autoimmune disease in a subject e.g. systemic
XX lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
XX versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
XX sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
XX glomerular nephritis. The present sequence is a PCR primer used to clone
XX mouse anti-human DR5 antibody (TRA-8) cDNA
XX
XX Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
Db 3 GTTGTATGCACATGAGA 19
||| 3 GTTGTATGCACATGAGA 19
RESULT 97
ADF87587/c
ID ADF87587 standard; DNA; 20 BP.
XX
XX ADF87587;
AC

26-FEB-2004 (first entry)
Single nucleotide polymorphism detection primer, SEQ ID No 1170.
human; single nucleotide polymorphism; microarray; side effect; ss;
primer; PCR.
Synthetic.
Homo sapiens.
JP2003235571-A.
26-AUG-2003.
12-FEB-2002; 2002JP-00034717.
12-FEB-2002; 2002JP-00034717.
(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
WPI; 2003-820454/77.
Novel polynucleotide useful for detecting single nucleotide polymorphisms
in human gene.
Claim 2; SEQ ID NO 1170; 704pp; Japanese.
The invention relates to a novel polynucleotide isolated and purified
from a human gene having any one of 935 fully defined sequences as given
in specification, or a sequence having a base substitution. The invention
further relates to: an oligonucleotide containing single nucleotide
polymorphisms; a PCR primer set chosen from the combination of two DNA
fragments from any one of 1220 fully defined sequences as given in
specification; a labelling probe containing the SNP containing oligo; and
a microarray equipped with the SNP containing the single nucleotide
gene of the invention is useful for detecting the single nucleotide
polymorphisms in human gene. The isolated human gene is also useful for
diagnosis of disease and determination of side effect to a medical agent.
The isolated human gene is also effective in detecting single nucleotide
polymorphisms in a human gene. This polynucleotide sequence represents
one of the PCR primers used in the single nucleotide polymorphism
detection method of the invention.
Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1018 GCATCATCATAGAGAG 1034
Db 17 GCATCATCACAGAGAAG 1
||| 17 GCATCATCACAGAGAAG 1
RESULT 98
ADJ79773
ID ADJ79773 standard; DNA; 20 BP.
XX
XX ADJ79773;
XX
XX 06-MAY-2004 (first entry)
XX
XX TRA-8 antibody PCR primer #4.
XX
XX ss; primer; nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
XX antiallergic; antiinflammatory; antidiabetic; haemostatic;
XX neuroprotective; antiinfertility; immunosuppressive; dermatological;
XX antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
XX proliferation;
XX tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
XX TRAIL; synovial cell; lymphocyte; neutrophil;
XX systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
XX

```

KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
 KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
 KW autoimmune hemolytic anemia; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
 KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
 KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003038043-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 25-OCT-2002; 2002WO-US034420.
 XX
 PR 01-NOV-2001; 2001US-0346402P.
 PR 24-JUN-2002; 2002US-0391478P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;
 PI Lobuglio AF, Buchsbaum DJ;
 XX
 DR WPI; 2003-421518/39.
 XX
 PT Inducing apoptosis and inhibiting proliferation of target cells
 PT expressing DR5, by contacting the target cell with an antibody that binds
 PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
 PT agents.
 XX
 PS Example 16; SEQ ID NO 9; 274pp; English.
 XX
 CC The invention relates to a method of selectively inducing apoptosis in
 CC and inhibiting (M1) proliferation of target cells expressing DR5,
 CC comprising contacting the cell with an antibody that specifically binds
 CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
 CC receptor DR5, where the antibody, in its soluble form, has in vivo and in
 CC vitro apoptosis-inducing activity in the cell expressing DR5, and
 CC contacting the cell with one or more therapeutic agents. M1 is useful for
 CC inducing apoptosis in target cell and inhibiting proliferation of target
 CC cell expressing DR5, where the target cell is an abnormally proliferating
 CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated
 CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
 CC cell. M2 is useful for treating a subject having inflammatory and
 CC autoimmune diseases. The inflammatory or autoimmune disease are selected
 CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
 CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
 CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
 CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
 CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerular nephritis, and hypoplastic anemia. This sequence represents a
 CC primer used in the method of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 992 GTTGTATGCACATGAAA 1008
 Db 3 GTTGTATGCACATGAGA 19
 RESULT 99
 ADJ25296
 ID ADJ25296 standard; DNA; 20 BP.
 XX
 XX ADJ25296;
 XX

DT 20-MAY-2004 (first entry)
 XX Human endothelial lipase antisense oligonucleotide, SEQ ID 3694.
 DE Antilipase; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
 XX Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
 KW cardiovascular disorder; metabolic syndrome X; ss.
 XX
 OS Homo sapiens.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /mod_base= a
 FT /note= "This oligonucleotide has a phosphorothioate
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
 FT and 3' ends, which are 4 nucleotides in length. Also all
 FT cytidine residues are 5-methylcytidines"
 XX
 PN WO2004009541-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 18-JUL-2003; 2003WO-US022410.
 XX
 PR 19-JUL-2002; 2002US-0397106P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Bhat BG;
 XX
 DR WPI; 2004-132912/13.
 XX
 PT New antisense oligonucleotide for modulating endothelial lipase
 PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
 PT high density lipoprotein or cardiovascular disorders.
 XX
 PS Claim 3; SEQ ID NO 3694; 1007pp; English.
 XX
 CC The present invention relates to antisense oligonucleotides (ADJ21603-
 CC ADJ25510) targeted to human endothelial lipase (EL) coding sequence
 CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
 CC with and inhibits the expression of EL. The antisense oligonucleotides
 CC are useful for modulating the expression of endothelial lipase in cells
 CC or tissues to treat diseases associated with EL expression, such as
 CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
 CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
 CC used for diagnostics, prophylaxis, or as research reagents or kits.
 XX
 SQ Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 19 GCCCGGCGCGTGGCAGG 35
 Db 4 GCCCGGCGCGTGGCAGG 20
 RESULT 100
 ADJ24880
 ID ADJ24880 standard; DNA; 20 BP.
 XX
 XX ADJ24880;
 AC
 XX
 DT 20-MAY-2004 (first entry)
 XX Human endothelial lipase antisense oligonucleotide, SEQ ID 3278.
 DE Antilipase; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
 KW Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
 KW

[illegible]

CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 459 AGTGGTAGCACTTTATCTG 478
 |||||
 Db 20 AGCGGTAGCAGTTCTCTG 1

RESULT 107
 AAC67691/c
 ID AAC67691 standard; DNA; 20 BP.
 AC AAC67691;
 DT 16-FEB-2001 (first entry)
 DE Oligonucleotide #2 ISIS #116870.
 KW Antiinflammatory; cytostatic; antibacterial; methionine aminopeptidase 2;
 KW inhibitor; MetAP2; eukaryotic initiation factor associated protein; p67;
 KW eIF-2; protein synthesis; antisense oligonucleotide; infection; human;
 KW inflammation; tumour; phosphorothioate; 2-methoxyethyl wing; ss.
 OS Homo sapiens.
 XX US6136604-A.
 FN 24-OCT-2000.
 PD 27-OCT-1999; 99US-00428584.
 PF 27-OCT-1999; 99US-00428584.
 PR 27-OCT-1999; 99US-00428584.
 XX (ISIS-) ISIS PHARM INC.
 PA Monia BP, Wyatt J;
 PI WPI; 2001-030942/04.
 DR New antisense compounds which specifically hybridize with and inhibit
 PT human methionine aminopeptidase 2 expression, useful for treating
 PT methionine aminopeptidase 2 related disorders and preventing inflammation
 PT or tumor formation.
 XX Claim 14; Col 39-40; 39pp; English.

CC Methionine aminopeptidase 2 (also known as MetAP2 and eukaryotic
 CC initiation factor [eIF-2] associated protein, p67) is a cellular
 CC glycoprotein that promotes protein synthesis in the presence of active
 CC eIF-2 kinases by protecting the eIF-2 alpha subunit from phosphorylation.
 CC The present invention relates to antisense oligonucleotides (AAC67690-
 CC C67767) which inhibit human methionine aminopeptidase 2 coding sequence
 CC expression (see AAC67683). The present sequence is one such antisense
 CC oligonucleotide. The present sequence may be used for treating a patient
 CC suspected of having or being prone to a disease or condition associated
 CC with expression of MetAP2. In addition, the present sequence can also be
 CC used as research reagents, diagnostics and to distinguish between
 CC functions of various members of a biological pathway. The antisense
 CC oligonucleotide may further be used prophylactically, e.g. to prevent or
 CC delay infection, inflammation or tumour formation. Note: the present
 CC sequence may have a phosphorothioate backbone and 2-methoxyethyl (2'-MOE)

CC wings
 SQ Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 TCGGAGACATGCGGCGGT 81
 |||||
 Db 20 TCGGGCAACATGCGGGTGT 1

RESULT 108
 AAF23345
 ID AAF23345 standard; DNA; 20 BP.
 AC AAF23345;
 DT 19-MAR-2001 (first entry)
 DE Oligonucleotide for detection of Mycobacterium diernhoferi.
 KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;
 KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
 KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
 KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
 KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
 XX Mycobacterium diernhoferi.
 OS WO200073436-A1.
 FN 07-DEC-2000.
 PD 16-MAY-2000; 2000WO-KR000477.
 PF 29-MAY-1999; 99KR-00019631.
 PR 29-MAY-1999; 99KR-00019632.
 PR 29-MAY-1999; 99KR-00019633.
 PR 29-MAY-1999; 99KR-00019634.
 PR 29-MAY-1999; 99KR-00019635.
 PR 07-APR-2000; 2000KR-00018189.
 XX (SJHI-) SJ HIGHTECH CO LTD.
 PA (KIMC/) KIM C M.
 PA (PARK/) PARK H K.
 PI Kim CM, Park HK, Jang HJ;
 PT WPI; 2001-061527/07.
 DR Novel oligonucleotide sequences of internal transcribing spacer region of
 PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
 PT detecting and identifying mycobacteria and distinguish TB complex from
 PT NTM.
 XX Claim 36; Page 82; 89pp; English.

CC The present sequence is an oligonucleotide developed using a
 CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
 CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
 CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
 CC diernhoferi genes were identified. The oligonucleotides derived from
 CC these sequences were used to develop PCR primers and hybridisation probes
 CC for detection and identification of Mycobacterium. ITS has a more
 CC polymorphic region than 16S rRNA and also has a conserved region. It is
 CC therefore highly effective as a target DNA for distinction of genotype.
 CC The oligonucleotide probes, attached to solid substrate, hybridise only
 CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
 CC can detect and identify the specific mycobacteria sensitively. The
 CC oligonucleotides can also detect and identify the specific mycobacteria
 CC by PCR amplification. Using the oligonucleotide primers or probes made

CC from ITS of mycobacteria, it is possible to detect mycobacteria,
 CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
 CC (NTM), and to identify mycobacteria species accurately and effectively
 XX
 SQ Sequence 20 BP; 9 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 998 TGCACATGAACTTTGAGAA 1017
 DB 1 TGCACAACTTTGAGAA 20
 RESULT 109
 AAD20131
 ID AAD20131 standard; DNA; 20 BP.
 AC
 XX AAD20131;
 DT
 XX 03-JAN-2002 (first entry)
 XX Human histone deacetylase antisense oligonucleotide, HDAC8 AS2.
 KW Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
 KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
 KW protozoal disease; fungal disease; infection; ss.
 XX
 OS Homo sapiens.
 XX WO200170675-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-IB000683.
 PF
 XX 24-MAR-2000; 2000US-0192151P.
 PR
 XX (METH-) METHYLGENE INC.
 PA
 XX Delorme D, Woo SH, Vaisburg A;
 PI
 XX WPI; 2001-639108/73.
 DR
 XX An inhibitor of histone deacetylase for the treatment of cell
 PT proliferation diseases and conditions such as cancer, restenosis or
 PT psoriasis or preventing protozoal or fungal disease or infections.
 XX
 PS Disclosure; Page 54; 241pp; English.
 CC The present invention relates to compounds and methods for inhibiting
 CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
 CC are used for the treatment of cell proliferative diseases and conditions
 CC such as cancer, restenosis or psoriasis. They are also used for treating
 CC or preventing protozoal or fungal disease or infections. The present
 CC sequence is antisense oligonucleotide, HDAC8 AS2 which is targeted to
 CC the 3' untranslated region (UTR) of human HDAC8 to inhibit its enzymatic
 CC activity
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 743 AGGCAGCTGCCACCTTATGC 762
 DB 1 AGCCAGCTGCCACTTGATGC 20
 RESULT 110
 AAF92365

ID
 .XX
 AC
 XX
 DT
 XX
 DE
 XX
 KW
 KW
 XX
 OS
 OS
 PN
 XX
 PD
 XX
 PF
 XX
 PR
 XX
 PA
 XX
 PI
 XX
 DR
 XX
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 SQ
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 105 TCAGTGGGGCTATTGGACTG 124
 DB 1 TCAGTGAGGCTGTGGATTG 20
 RESULT 111
 ABV73091
 ID ABV73091 standard; DNA; 20 BP.
 XX
 AC ABV73091;
 DT
 XX 08-JAN-2003 (first entry)
 XX Human HDAC-8 mRNA inhibiting antisense oligo HDAC8 AS2.
 DE
 XX Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation;
 KW HDAC-8; human; cancer; antisense; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX WO200269947-A2.
 PN
 XX 12-SEP-2002.
 PD
 XX 14-JAN-2002; 2002WO-IB002002.
 PF
 XX 12-JAN-2001; 2001US-0261522P.
 PR

```

PR 12-JAN-2001; 2001US-0261674P.
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Bonfils C, Woo SH, Vaisburg A, Delorme D;
XX Fournel M, Lavoie R, Li Z;
XX WPI; 2002-750436/81.
XX
XX Inhibition of HDAC-4 activity in a cell useful for treating e.g. cancer
XX involves contacting the cell with an antisense oligonucleotide or a small
XX molecule inhibitor of HDAC-4.
XX
XX Disclosure; Page 33; 124pp; English.
XX
XX The invention relates to inhibition of histone deacetylase (HDAC)-4
XX activity in a cell that involves contacting the cell with an antisense
XX oligonucleotide complementary to a region of RNA encoding a portion of
XX HDAC-4 or a small molecule inhibitor of HDAC-4. The method is useful for
XX inhibiting neoplastic cell proliferation in an animal (preferably human)
XX and for treating cancer. Sequences ABV73073-3091 represent HDAC isotype-
XX specific antisense and mismatch oligonucleotides
XX
XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      1.4%; Score 15.2; DB 1; Length 20;
    Best Local Similarity 85.0%; Pred. No. 1.2e+02;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGCGAGTCCACCTTATGC 762
DB 1 AGCCAGCTGCCACTTGATGC 20

RESULT 112
ABI93053/C
ID ABI93053 standard; DNA; 20 BP.
XX
XX AC ABI93053;
XX
XX 15-FEB-2002 (first entry)
XX
XX Capture oligonucleotide Zip IP#140 oligo #9.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US010958.
XX
XX 14-APR-2000; 2000US-0197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
XX Example 5; Fig 29; 300pp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary

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```

CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI92074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
SQ
    Query Match      1.4%; Score 15.2; DB 1; Length 20;
    Best Local Similarity 85.0%; Pred. No. 1.2e+02;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 CATCGAACCTTTGCTGG 786
DB 20 CATCGACACCGTTTGCTCG 1

RESULT 113
ABK87739
ID ABK87739 standard; DNA; 20 BP.
XX
XX AC ABK87739;
XX
XX 07-OCT-2002 (first entry)
XX
XX Human histone deacetylase isoform 8 antisense oligonucleotide AS2.
XX
XX Human; ss; histone deacetylase; HDAC-8; cancer; cytostatic; antisense;
XX tumour suppressor; cell proliferation; tumour; programmed cell death;
XX necrotic cell death.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..4
XX /tag= b
XX /mod_base= OTHER
XX /note= "These nucleotides have 2'-O-methyl groups
XX attached to their sugar residues"
XX modified_base 17..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "These nucleotides have 2'-O-methyl groups
XX attached to their sugar residues"
XX
XX US2002061860-A1.
XX
XX 23-MAY-2002.
XX
XX 06-AUG-2001; 2001US-00817913.
XX
XX 24-MAR-2000; 2000US-0192157P.
XX

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PN US2002137162-A1.
XX
PD 26-SEP-2002.
XX
PF 26-MAR-2001; 2001US-00817538.
XX
PR 24-MAR-2000; 2000US-0192157P.
XX
PR 12-JAN-2001; 2001US-0261522P.
XX
PA (L12Z/) LI Z.
PA (BONF/) BONFILS C.
PA (BEST/) BESTERMAN J M.
XX
PI Li Z, Bonfils C, Besterman JM;
XX
XX WPI; 2003-786641/74.
XX
XX New antisense oligonucleotide that inhibits one or more specific histone
PT deacetylase isoforms, is useful in modulating cell proliferation
PT especially neoplasia.
XX
PS Claim 21; SEQ ID NO 33; 52pp; English.
XX
XX The invention relates to an antisense oligonucleotide comprising a
CC nucleotide sequence of 13 to 15 nucleotides that inhibits one or more
CC specific histone deacetylase isoforms (HDAC-1 to HDAC-8), where the
CC oligonucleotide is complementary to a region of RNA or double stranded
CC DNA. The oligonucleotide is useful in inhibiting one or more histone
CC deacetylase isoforms in a cell comprising contacting the cell with the
CC oligonucleotide. Cell proliferation is inhibited in the contacted cell
CC which undergoes growth retardation and growth arrest. The contacted cell
CC undergoes programmed and necrotic cell death. The oligonucleotide is also
CC useful in inhibiting neoplastic cell proliferation in an animal,
CC preferably a human. The oligonucleotide is also useful in identifying a
CC histone deacetylase isoform that is required for the induction of cell
CC proliferation comprising contacting the histone deacetylase isoform with
CC the oligonucleotide where a decrease in induction of cell proliferation
CC indicates that the isoform is required for the induction of cell
CC proliferation. The above method is also applicable to identifying
CC isoforms required for cell proliferation. The oligonucleotide is useful
CC in identifying an isoform required for the induction of cell
CC differentiation, where an induction of cell differentiation indicates
CC that the isoform is required for differentiation. Also useful in
CC modulating cell proliferation especially neoplasia. The present sequence
CC an antisense oligonucleotide directed against an HDAC isoform containing
CC mismatched bases.
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 743 AGCGAGTGGCCACCTTATGC 762
DB 1 AGCCAGCTGCCACTTGTATGC 20
RESULT 116
ADC79289
ID ADC79289 standard; DNA; 20 BP.
XX
AC ADC79289;
XX
XX 01-JAN-2004 (first entry)
XX
DE 5'-RACE primer for amplifying fluorescent protein cDNA #SEQ ID 18.
XX
XX Fluorescent protein; label; protein function; protein distribution;
KW fungal; PCR; primer; ss; 5'RACE.
XX
XX Fungia sp.
OS
XX
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PN WO20003054191-A1.
XX
PD 03-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-JP013363.
XX
PR 20-DEC-2001; 2001JP-00387510.
XX
PA (RIKE ) RIKEN KK.
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Miyawaki A, Karasawa S;
XX
XX WPI; 2003-541818/51.
XX
XX Fluorescent proteins from Fungia species and DNA encoding them for
PT analysis of function and distribution of proteins in living systems.
XX
PS Example 1; Page 21; 59pp; Japanese.
XX
XX The invention relates to 4 fluorescent proteins originating from Fungia
CC species. Also disclosed are DNA sequences encoding the novel fluorescent
CC proteins, expression vectors containing this DNA, hosts transformed by
CC this vector, fluorescent fusion proteins containing the novel fluorescent
CC proteins fused to another protein, and a method for analysis of function
CC and distribution of another protein using the fluorescent fusion protein.
CC Novel proteins of the invention are useful for analysis of the
CC intracellular activity, function and localisation of proteins of
CC biological interest, using the fluorescent protein as a fluorescence
CC label. The fluorescent proteins have desirable fluorescence properties
CC and a low sensitivity to pH. The current sequence represents a 5'-RACE
CC (rapid amplification of cDNA ends) primer used to recover fungal
CC fluorescent protein terminal sequence from extracted cDNA.
XX
SQ Sequence 20 BP; 5 A; 6 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 497 TCTTAGAAGTCACTACTATCT 516
DB 1 TCTTCGAAGTCAAACTTTCT 20
RESULT 117
ABZ76492
ID ABZ76492 standard; DNA; 20 BP.
XX
AC ABZ76492;
XX
XX 23-JUN-2003 (first entry)
XX
DE Human HDAC8 mRNA targeting antisense oligo HDAC8 AS2.
XX
XX HDAC; histone deacetylase; cytostatic; vasotropic; antipsoriatic;
KW antisense; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003024448-A2.
XX
XX 27-MAR-2003.
XX
XX 12-SEP-2002; 2002WO-US029017.
XX
XX 14-SEP-2001; 2001US-0322402P.
XX
XX 26-JUN-2002; 2002US-0391728P.
XX
XX (METH-) METHYLGENE INC.
XX
XX Delorme D, Woo SH, Vaisburg A, Moradel O, Leit S, Raeppele S;
PI
```

PI Frechette S, Bouchain G;
 XX WPI; 2003-342612/32.
 XX
 XX New histone deacetylase inhibitors, useful for treatment of proliferative
 PT diseases or conditions e.g. cancer.
 PT
 XX Disclosure; Page 72; 347pp; English.
 XX
 XX The invention relates to histone deacetylase inhibitors of specified
 CC formulae and their salts. The compounds inhibit histone deacetylase
 CC (HDAC) enzymatic activity. They can be used for treating cell
 CC proliferative diseases or condition (e.g. cancer, restenosis and
 CC psoriasis). Sequences AB276476-492 represent antisense and mismatch
 CC oligonucleotides targeting the 5'- UTR (untranslated region) and 3'-UTRs
 CC of the human HDAC1-8 genes
 XX
 XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 SQ Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 743 AGCAGCTGCCACTTATGC 762
 DB |||||||||
 1 AGCCAGCTGCCACTTATGC 20
 RESULT 118
 ADH50696
 ID ADH50696 standard; DNA; 20 BP.
 XX
 XX
 AC ADH50696;
 XX
 XX 25-MAR-2004 (first entry)
 DT
 XX
 XX Human IRAK-1 DNA target sequence #18.
 DE
 XX Antisense therapy; human; interleukin-1 receptor-associated kinase-1;
 XX IL-1 receptor-associated kinase-1; IRAK-1;
 KW hyperproliferative disorder e.g.; cancer; autoimmune disorder;
 KW altered bone metabolism or inflammation; cytostatic; immunosuppressive;
 KW osteopathic; antiinflammatory; ds.
 KW
 XX Homo sapiens.
 OS
 XX US2003228690-A1.
 PN
 XX 11-DEC-2003.
 PD
 XX 10-JUN-2002; 2002US-00167034.
 PF
 XX 10-JUN-2002; 2002US-00167034.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Baker BF, Freier SM, Dobie KW;
 PI WPI; 2004-052028/05.
 XX
 XX New compound having a sequence targeted to a nucleic acid encoding IL-1
 XX receptor-associated kinase-1, useful for preparing a composition for
 PT treating hyperproliferative or autoimmune disorder or inflammation.
 PT
 XX Example 15; SEQ ID NO 103; 66pp; English.
 PS
 XX The present invention relates to antisense compounds targeted to a
 XX nucleic acid encoding interleukin-1 (il-1) receptor-associated kinase-1
 CC (IRAK-1). The antisense compound comprises an antisense oligonucleotide
 CC that specifically hybridizes with the nucleic acid and inhibits the
 CC expression of IRAK-1. The antisense oligonucleotide is a chimeric
 CC oligonucleotide. The antisense oligonucleotide comprises at least one
 CC modified internucleoside linkage, preferably a phosphorothioate linkage.

CC It also comprises at least one modified sugar moiety, preferably a 2'-O-
 CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
 CC comprises at least one modified nucleobase, preferably a 5-
 CC methylcytosine. The antisense oligonucleotides are useful for the
 CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
 CC autoimmune disorders, altered bone metabolism, and inflammation. The
 CC present sequence represents a human IRAK-1 DNA target sequence for an
 CC antisense oligonucleotide.
 XX
 XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 817 AGCAGGCTCTCATGACCCA 836
 DB |||||||||
 1 AGGAGGCTCTCATGACCCA 20
 RESULT 119
 ADH50625/C
 ID ADH50625 standard; DNA; 20 BP.
 XX
 XX
 AC ADH50625;
 XX
 XX 25-MAR-2004 (first entry)
 DT
 XX
 XX Human IRAK-1 DNA, antisense oligonucleotide #19.
 DE
 XX Antisense therapy; human; interleukin-1 receptor-associated kinase-1;
 XX IL-1 receptor-associated kinase-1; IRAK-1;
 KW hyperproliferative disorder e.g.; cancer; autoimmune disorder;
 KW altered bone metabolism or inflammation; cytostatic; immunosuppressive;
 KW osteopathic; antiinflammatory; phosphorothioate; ss.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "This oligonucleotide has a phosphorothioate
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
 FT and 3' ends, which are 5 nucleotides in length at each
 FT end. All cytidine residues are 5-methylcytidines"
 FT
 XX
 XX US2003228690-A1.
 PN
 XX 11-DEC-2003.
 PD
 XX 10-JUN-2002; 2002US-00167034.
 PF
 XX 10-JUN-2002; 2002US-00167034.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Baker BF, Freier SM, Dobie KW;
 PI WPI; 2004-052028/05.
 XX
 XX New compound having a sequence targeted to a nucleic acid encoding IL-1
 XX receptor-associated kinase-1, useful for preparing a composition for
 PT treating hyperproliferative or autoimmune disorder or inflammation.
 PT
 XX Example 15; SEQ ID NO 32; 66pp; English.
 PS
 XX The present invention relates to antisense compounds targeted to a
 XX nucleic acid encoding interleukin-1 (il-1) receptor-associated kinase-1
 CC (IRAK-1). The antisense compound comprises an antisense oligonucleotide
 CC that specifically hybridizes with the nucleic acid and inhibits the
 CC expression of IRAK-1. The antisense oligonucleotide is a chimeric
 CC oligonucleotide. The antisense oligonucleotide comprises at least one
 CC modified internucleoside linkage, preferably a phosphorothioate linkage.

CC modified internucleoside linkage, preferably a phosphorothioate linkage.
 CC It also comprises at least one modified sugar moiety, preferably a 2'-O-
 CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
 CC comprises at least one modified nucleobase, preferably a 5-
 CC methylcytosine. The antisense oligonucleotides are useful for the
 CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
 CC autoimmune disorders, altered bone metabolism, and inflammation. The
 CC present sequence represents an antisense oligonucleotide used in the
 CC examples of the present invention.
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCTCTCATGACCA 836
 ||||| |||||
 Db 20 AGGAGGCTCTCATGACCA 1

RESULT 120
 ADJ45254/c
 ID ADJ45254 standard; DNA; 20 BP.
 XX
 AC ADJ45254;

DT 06-MAY-2004 (first entry)

DE Hepatoma-derived growth factor antisense oligo seqid 24.

XX cytostatic; endocrine; hepatoma-derived growth factor inhibitor;
 KW hepatoma-derived growth factor; metabolic disorder; hyperproliferative;
 KW human; ss; antisense oligonucleotide.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= Phosphorothioate backbone. All cytidines
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 15..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

US2004023379-A1.

PN

PD 05-FEB-2004.

XX 31-JUL-2002; 2002US-00210429.

XX 31-JUL-2002; 2002US-00210429.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie KW;

XX WPI; 2004-142660/14.

XX New compound, particularly an antisense oligonucleotide targeted to a
 PT nucleic acid encoding a hepatoma-derived growth factor, useful for
 PT treating a hyperproliferative disorder e.g. cancer, or a metabolic
 PT disorder.

XX Example 15; SEQ ID NO 24; 61pp; English.

XX

CC The invention describes a compound 8-80 nucleobases in length targeted
 CC to, and which specifically hybridises with a nucleic acid molecule
 CC encoding hepatoma-derived growth factor, and inhibits the expression of
 CC hepatoma-derived growth factor. The compound, composition and methods are
 CC useful for treating a disease or condition associated with hepatoma-
 CC derived growth factor, such as a metabolic disorder, or a
 CC hyperproliferative disorder, e.g. cancer, which is selected from
 CC hepatoma, leiomyoma, esophageal cancer or ovarian cancer. They are also
 CC useful in research and diagnostics for modulating the expression of
 CC hepatoma-derived growth factor. This sequence represents a human hepatoma
 CC -derived growth factor antisense oligonucleotide.

SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 801 AGGCAGATAACGCTGAGCA 820
 ||||| |||||
 Db 20 AGGCAGATAACGCTGAGCA 1

RESULT 121
 ADJ45325
 ID ADJ45325 standard; DNA; 20 BP.
 XX
 AC ADJ45325;

DT 06-MAY-2004 (first entry)

DE Hepatoma-derived growth factor antisense oligo seqid 95.

XX cytostatic; endocrine; hepatoma-derived growth factor inhibitor;
 KW hepatoma-derived growth factor; metabolic disorder; hyperproliferative;
 KW human; ss; antisense oligonucleotide.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= Phosphorothioate backbone. All cytidines
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 15..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

US2004023379-A1.

PN

PD 05-FEB-2004.

XX 31-JUL-2002; 2002US-00210429.

XX 31-JUL-2002; 2002US-00210429.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie KW;

XX WPI; 2004-142660/14.

XX New compound, particularly an antisense oligonucleotide targeted to a
 PT nucleic acid encoding a hepatoma-derived growth factor, useful for
 PT treating a hyperproliferative disorder e.g. cancer, or a metabolic
 PT disorder.

XX

PS Example 15; SEQ ID NO 95; 61pp; English.

XX The invention describes a compound 8-80 nucleobases in length targeted

CC to, and which specifically hybridizes with a nucleic acid molecule

CC encoding hepatoma-derived growth factor, and inhibits the expression of

CC hepatoma-derived growth factor. The compound, composition and methods are

CC useful for treating a disease or condition associated with hepatoma-

CC derived growth factor, such as a metabolic disorder, or a

CC hyperproliferative disorder, e.g. cancer, which is selected from

CC hepatoma, leiomyoma, esophageal cancer or ovarian cancer. They are also

CC useful in research and diagnostics for modulating the expression of

CC hepatoma-derived growth factor. This sequence represents a human hepatoma

CC -derived growth factor antisense oligonucleotide.

XX

SQ Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 801 AGCAGATACGCTGAAGCA 820

||||| ||| |||||

Db 1 AGCAGAAACCTGAAGGA 20

RESULT 122

ADI34745

ID ADI34745 standard; DNA; 20 BP.

XX

AC ADI34745;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human HDAC8-specific oligo HDAC8AS2.

XX

XX HDAC; histone deacetylase; HDAC-7; HDAC-8; cell proliferation;

KW growth retardation; cytostatic; antisense therapy; apoptosis;

KW p21 transcription; antisense; ss.

XX

OS Synthetic.

XX

XX WO2004005513-A2.

PN

XX

XX 15-JAN-2004.

PD

XX

XX 12-JUN-2003; 2003WO-IB003052.

PF

XX

XX 03-JUL-2002; 2002US-00189818.

PR

XX

XX (METH-) METHYLGENE INC.

PA

XX

XX Besterman JM, Li Z, Delorme D, Bonfils C;

PI

XX

XX WPI; 2004-098393/10.

DR

XX

XX Inhibiting neoplastic cell proliferation in animals by administering an

XX antisense oligonucleotide complementary to region of RNA encoding portion

PT of histone deacetylase-7 (HDAC-7) or HDAC-8, or small molecule inhibitor

PT of HDAC-7 or HDAC-8.

PT

XX

XX Disclosure; Page 25; 98pp; English.

PS

XX

XX The invention relates to inhibiting neoplastic cell proliferation in an

XX animal by administering to the animal having at least one neoplastic cell

CC present in its body: an antisense oligonucleotide complementary to a

CC region of RNA that encodes a portion of histone deacetylase-7 (HDAC-7) or

CC HDAC-8; and/or a small molecule inhibitor of HDAC-7 or HDAC-8. Inhibition

CC of HDAC-7 or HDAC-8 activity in the contacted cell further leads to an

CC inhibition of cell proliferation, growth retardation and to necrotic cell

CC death, growth arrest, or programmed cell death of the contacted cell. The

CC method is useful for inhibiting neoplastic cell proliferation in an

CC animal, preferably human. The method further comprises administering an

CC antisense oligonucleotide complementary to a region of RNA that encodes a

CC

CC portion of HDAC-1, preferably chimeric or hybrid HDAC-1 antisense

CC oligonucleotide. Sequences ADI34722-ADI34746 represent HDAC isotype-

CC specific antisense and mismatch oligonucleotides.

XX

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 3 T; 1 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 1.2e+02;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGCAGCTGCCACCTTATGC 762

||||| ||| |||||

Db 1 AGCCAGCTGCCACTTGAUC 20

RESULT 123

ADJ96374

ID ADJ96374 standard; DNA; 20 BP.

XX

AC ADJ96374;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human breast cancer-1 antisense oligonucleotide #159144.

XX

XX Breast cancer-1; diagnosis; hyperproliferative disorder; cancer;

KW antisense therapy; human; antisense; ss.

XX

XX Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone where all cytidines are

FT 5'- methylcytidines"

FT modified_base 1..15

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'- methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'- methoxyethyl (2'-MOE) nucleotides"

XX

XX US2004014051-A1.

PN

XX

XX 22-JAN-2004.

PD

XX

XX 18-JUL-2002; 2002US-00199676.

PF

XX

XX 18-JUL-2002; 2002US-00199676.

PR

XX

XX (ISIS-) ISIS PHARM INC.

PA

XX

XX Brown-Driver VL, Dobie KW;

PI

XX

XX WPI; 2004-121557/12.

DR

XX

XX New antisense oligonucleotide compounds, useful for diagnosing,

PT preventing and/or treating conditions with aberrant activity of breast

PT cancer-1, such as breast, ovary, prostate and/or peritoneum cancers.

PT

XX

XX Example 15; Page 31; 175pp; English.

PS

XX

XX The present invention is directed to novel antisense compounds targetted

XX to breast cancer-1 proteins and their encoding nucleic acids. The

CC invention is useful for the diagnosis, prevention and/or treatment of

CC diseases and conditions associated with aberrant expression and activity

CC of breast cancer-1 such as a hyperproliferative disorder in particular

CC breast, ovary, prostate and peritoneum cancers. The invention is also

CC used in antisense therapy. The present sequence is human breast cancer-1

CC

CC antisense oligonucleotide. Note: This sequence given in example 15 of the
CC specification differs from that given in the sequence listing.

Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.48; Score 15.2; DB 1; Length 20;

Best Local Similarity 93.0%, Fied: NO: 1.2e+02,
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 224 GCCAAAGAGTCACCTATGA 243

Db 1 GGCAGAAGAGTCACTTATGA 20

RESULT 124

ADJ96440/C
ID ADJ96440 standard; DNA; 20 BP.

AC ADJ96440;

DT 06-MAY-2004 (first entry)

Human breast cancer-1 target oligonucleotide #25.

Breast cancer-1; diagnosis; hyperproliferative disorder; cancer;

KW antisense therapy; human; ss.

OS Homo sapiens.

PN US2004014051-A1.

22-JAN-2004.

18-JUL-2002;

PR 18-JUL-2002; 2002US-00199676.

PA (ISIS-) ISIS PHARM INC.

PI Brown-Driver VL, Dobie KW;

WPI; 2004-121557/12.

New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating conditions with aberrant activity of breast cancer-1, such as breast, ovary, prostate and/or peritoneum cancers.

PS Example 15: Page 32: 175pp: English.

The present invention is directed to novel antisense compounds targeted to breast cancer-1 proteins and their encoding nucleic acids. The invention is useful for the diagnosis, prevention and/or treatment of diseases and conditions associated with aberrant expression and activity of breast cancer-1 such as a hyperproliferative disorder in particular breast, ovary, prostate and peritoneum cancers. The invention is also used in antisense therapy. The present sequence is human breast cancer-1 target oligonucleotide.

Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;

BEST LOCAL SIMILARITY 85.0%; PRED. NO: 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 224 GCCAAAAGAGTCACCTATGA 243

Dbb 20 GGCAGAAGAGTCACTTATGA 1

RESULT 125

ADJ23397

XX

AC ADJ23397;
XX 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 1795.
XX
KW Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT FT /*tag= a
FT FT /mod base= OTHER
FT FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
FN WO2004009541-A2.
XX
XX 29-JAN-2004.
PD
XX 18-JUL-2003; 2003WO-US022410.
PF
XX 19-JUL-2002; 2002US-0397106P.
PR
XX (PHAA) PHARMACIA CORP.
PA
XX Bhat BG;
PI
XX WPI; 2004-132912/13.
DR
XX New antisense oligonucleotide for modulating endothelial lipase
FT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
PT
XX Claim 3; SEQ ID NO 1795; 1007pp; English.
PS
XX The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 865 TTGTAGTCCATGCTATTAA 884
Db 1 TTGTAGCCAATGCTATTACA 20

RESULT 126
ADJ23964
ID ADJ23964 standard; DNA; 20 BP.
XX
XX AC ADJ23964;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 2362.
XX

KW Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
 KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
 KW Cardiovascular disorder; metabolic syndrome X; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "this oligonucleotide has a phosphorothioate
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
 FT and 3' ends, which are 4 nucleotides in length. Also all
 FT cytidine residues are 5-methylcytidines"
 XX
 PN WO2004009541-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 18-JUL-2003; 2003WO-US022410.
 XX
 PR 19-JUL-2002; 2002US-0397106P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Bhat BG;
 XX
 DR WPI; 2004-132912/13.
 XX
 FT New antisense oligonucleotide for modulating endothelial lipase
 FT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
 FT high density lipoprotein or cardiovascular disorders.
 XX
 PS Claim 3; SEQ ID NO 2362; 1007pp; English.
 XX
 CC The present invention relates to antisense oligonucleotides (ADJ21603-
 CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
 CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
 CC with and inhibits the expression of EL. The antisense oligonucleotides
 CC are useful for modulating the expression of endothelial lipase in cells
 CC or tissues to treat diseases associated with EL expression, such as
 CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
 CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
 CC used for diagnostics, prophylaxis, or as research reagents or kits.
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 866 TGTAGTCCATGCTATTAAAA 885
 DB 1 TGTAGCCAATGCTATTACAA 20
 RESULT 127
 ADO07539
 ID ADO07539 standard; DNA; 20 BP.
 XX
 AC ADO07539;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human histone deacetylase coding sequence antisense oligonucleotide #17.
 XX
 KW histone deacetylase; HDAC; enzyme; benzamide derivative;
 KW cell proliferation; antisense; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035525-A1.

XX 29-APR-2004.
 PD 16-OCT-2003; 2003WO-CA001557.
 PF 17-OCT-2002; 2002US-0419688P.
 PR (METH-) METHYLGENE INC.
 PA Raeppeel S, Gaudette F, Paquin I, Vaisburg A, Delorme D;
 FI WPI; 2004-365141/34.
 XX
 DR New benzamide derivatives, useful to treat cell proliferative disease or
 XX conditions, are histone deacetylase inhibitors.
 FT Disclosures; Page 27; 73pp; English.
 XX
 PS The present invention relates to benzamide derivatives capable of
 XX inhibiting histone deacetylase (HDAC) enzymes. These are useful in the
 CC treatment of a cell proliferative disease or condition in a mammal
 CC (preferably human). The present sequence is an antisense oligonucleotide
 CC for use against a human histone deacetylase gene.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 743 AGGCGAGTGCACCTTATGC 762
 DB 1 AGCCAGCTGCCACTTGATGC 20
 RESULT 128
 ADR20736
 ID ADR20736 standard; DNA; 20 BP.
 XX
 AC ADR20736;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human histone deacetylase (HDAC8) gene-specific antisense oligo #2.
 XX
 KW histone deacetylase inhibitor; HDAC inhibitor; antisense oligonucleotide;
 KW proliferative disease; proliferative condition; ss; HDAC8.
 XX
 OS Homo sapiens.
 XX
 PN WO2004069823-A1.
 XX
 PD 19-AUG-2004.
 XX
 PF 04-FEB-2004; 2004WO-CA000139.
 XX
 PR 04-FEB-2003; 2003US-00358556.
 XX
 PA (METH-) METHYLGENE INC.
 XX
 PI Delorme D, Zhou Z;
 XX
 DR WPI; 2004-615556/59.
 XX
 DE New N-(2-Aminophenyl)-4-((4-pyridin-3-yl-pyrimidin-2-ylamino)-methyl)-
 XX benzamides histone deacetylase inhibitor useful to treat cell
 FT proliferative diseases.
 FT Disclosures; Page 77; 335pp; English.
 PS
 XX The invention comprises histone deacetylase (HDAC) inhibitors of the
 CC formula: N-(2-Amino-phenyl)-4-((4-pyridin-3-yl-pyrimidin-2-ylamino)-
 CC methyl)-benzamide. The invention also comprises a method of inhibiting

CC HDAC in a cell. The HDAC inhibitors of the invention are useful for
 CC treating cell proliferative diseases and conditions. The present DNA
 CC sequence represents a human HDAC gene-specific antisense oligonucleotide
 CC that was used in the exemplification of the invention.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 743 AGCGAGTGGCCACCTTATGC 762
 DB 1 AGCCAGTCCCACTTGATGC 20
 RESULT 129
 AAT66953
 ID AAT66953 standard; DNA; 21 BP.
 XX
 AC AAT66953;
 XX
 DT 23-NOV-1997 (first entry)
 XX
 DE Asialoglycoprotein receptor H1 PCR primer F1.5.
 XX
 KW Asialoglycoprotein receptor H1; AGPR; autoimmune hepatitis; autoantibody;
 KW liver; diagnosis; human; primer; PCR; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN EP773289-A2.
 XX
 PD 14-MAY-1997.
 XX
 PF 20-AUG-1996; 96EP-00113349.
 XX
 PR 21-AUG-1995; 95JP-00212118.
 XX
 PA (TOFU) TONEN CORP.
 XX
 PI Tanida E, Ohue C, Yagi S, Hasegawa A, Kiyosawa K, Yano A;
 XX WPI; 1997-261316/24.
 XX
 ASialo-glyco:protein receptor H1 and L-H2 soluble derivatives - comprise
 PT extracellular domains, optionally also with cytoplasmic domains, useful
 PT for autoimmune hepatitis diagnosis.
 XX
 PS Example 1; Page 6; 40pp; English.
 XX
 CC Primer F1.5 (AAT66953) corresponds to nucleotides 164-184 of a cDNA clone
 CC (see AAT66950) coding for human asialoglycoprotein receptor (AGPR) H1
 CC (AAW15245). It was used with other primers (see AAT66952 and AAT66954-55)
 CC to amplify AGPR H1 cDNA from human liver cDNA. The isolated clone can be
 CC used to produce soluble AGPR H1 derivatives (see AAW15249-50) useful in a
 CC claimed method for detecting or measuring anti-AGPR antibody. The
 CC appearance of autoantibodies against AGPR is an indicator of autoimmune
 CC hepatitis
 XX
 SQ Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 820 AGGCTCTCATGACCCAGGA 839
 DB 1 AGCCCTATCATGACCAAGGA 20
 RESULT 130
 AAF95925/c

AAF95925 standard; DNA; 21 BP.
 AAF95925;
 18-NOV-2004 (revised)
 06-JUN-2001 (first entry)
 Human gene single nucleotide polymorphism #696.
 Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 polymorphism; vascular disease; coronary artery disease; forensics;
 myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 pulmonary embolism; paternity test; ds.
 Homo sapiens.
 Unidentified.
 Key Location/Qualifiers
 variation ll
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 WO200118250-A2.
 15-MAR-2001.
 07-SEP-2000; 2000WO-US024503.
 10-SEP-1999; 99US-0153357P.
 26-JUL-2000; 2000US-0220947P.
 16-AUG-2000; 2000US-0225724P.
 (WHED) WHITEHEAD INST BIOMEDICAL RES.
 (MILL-) MILLENNIUM PHARM INC.
 Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 WPI; 2001-226749/23.
 Nucleic acids comprising single nucleotide polymorphisms, useful in
 applications such as forensics, paternity testing, medicine, genetic
 analysis and phenotype correlations to diseases such as diabetes and
 atherosclerosis.
 Example; Page 95; 242pp; English.
 The present invention provides a method of diagnosing a vascular disease
 in an individual, involving determining the sequence at various
 polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 genes. The sequences at a number of polymorphic sites are also provided
 in the specification. In particular, the method can be used in the
 diagnosis of atherosclerosis, myocardial infarction, coronary heart
 disease, stroke, peripheral vascular diseases, venous thromboembolism and
 pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 useful in forensics, paternity testing, genetic analysis and phenotype
 correlations to diseases. The present sequence is an example of one of
 the human gene SNPs shown in the specification
 Revised record issued on 18-NOV-2004 : The variantion feature was
 incorrectly given a captial V
 Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 733 GCAGTCTTTGTAGGCAGCTGC 752
 DB 20 GCAGTCATTGAGGCAGCTGC 1
 RESULT 131

```
AAF96968/c
ID AAF96968 standard; DNA; 21 BP.
XX AC AAF96968;
XX DT 18-NOV-2004 (revised)
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #1729.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT variation II
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX PN WO200118250-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JU;
XX XX WPI; 2001-226749/23.
XX XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis.
XX PS Example; Page 163; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification
XX CC Revised record issued on 18-NOV-2004 : The variation feature was
XX CC incorrectly given a capital V
XX CC Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CTGGCTTGGCGAGGCTGCC 22
DB 21 CTGCTGGGGCAGGCTGCC 2
```

```
RESULT 132
ABK82248
ID ABK82248 standard; DNA; 21 BP.
XX AC ABK82248;
XX DT 27-AUG-2002 (first entry)
XX DE Human ATP-binding cassette (ABC) transporter probe #86.
XX KW Human; ATP-binding cassette transporter; ABC transporter;
XX KW expression rate; drug development; biochemical kinetic; antihelminthic;
XX KW probe; ss.
XX OS Homo sapiens.
XX XX JP2002112775-A.
XX PN 16-APR-2002.
XX PD 03-OCT-2000; 2000JP-00303404.
XX PF 03-OCT-2000; 2000JP-00303404.
XX PR (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX PA WPI; 2002-458864/49.
XX DR Probes for determination of human ATP-binding cassette (ABC) transporters
XX FT capable of hybridization with 33 regions of genes.
XX PS Claim 8; Page 29; 36pp; Japanese.
XX CC The invention describes new probes for identification of human ATP-
XX CC binding cassette (ABC) transporters capable of hybridisation with 33
XX CC regions of genes. Elucidation of expression rate of ABC transporters is
XX CC useful for development of drugs and their biochemical kinetics. This
XX CC sequence represents a probe used to detect human ATP-binding cassette
XX CC (ABC) transporters
XX SQ Sequence 21 BP; 2 A; 4 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 295 TGGAAATTGTTGTTCTGCT 314
DB 1 TGGAGTTCTGTGCTGCT 20
RESULT 133
ABS98518/c
ID ABS98518 standard; DNA; 21 BP.
XX AC ABS98518;
XX DT 23-DEC-2002 (first entry)
XX DE Human acetyl choline muscarinic receptor 2 polymorphic sequence #1.
XX KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
XX KW cytochrome P450 A2; CYP4501A2; cytochrome P450 O2E; CYP45002E1; LTF;
XX KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
XX KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;
XX KW HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
XX KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
XX KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
```


KW 2'-O-methoxyethyl; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 XX
 FN WO2004010956-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 31-JUL-2003; 2003WO-US023994.
 XX
 PR 31-JUL-2002; 2002US-00210838.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Bhanot S, Dobie KW, Freier SM;
 XX
 DR WPI; 2004-143728/14.
 XX
 PT New compound comprises a sequence targeted to a nucleic acid encoding
 PT Leukocyte Antigen Related protein (LAR), useful for preparing a
 PT composition for treating metabolic or hyperproliferative disorders, e.g.
 PT cancer.
 XX
 PS Example 15; SEQ ID NO 82; 197pp; English.
 XX
 CC The present invention describes a compound (I) comprising a sequence
 CC comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding LAR
 CC (leukocyte antigen related protein), where (1) specifically hybridises
 CC with the nucleic acid and inhibits expression of LAR. Also described: (1)
 CC a composition comprising the compound (I) and a carrier or diluent; (2)
 CC inhibiting the expression of LAR in cells or tissues; (3) treating an
 CC animal having or suspected of having a disease or condition associated
 CC with LAR; and (4) screening for an antisense compound. (1) has cytostatic
 CC activity, and can be used in gene therapy. The antisense oligonucleotide
 CC compound (I) can be used for preparing a composition for treating
 CC metabolic or hyperproliferative disorders, particularly cancer. The
 CC present sequence represents a human LAR chimeric phosphorothioate
 CC antisense oligonucleotide, which is used in an example from the present
 CC invention.
 XX
 SQ Sequence 20 BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1079 CTTAACCTCTCTGGG 1093
 DB 20 CTTAACCTCTCTGGG 6
 RESULT 138
 AAH73748
 ID AAH73748 standard; DNA; 18 BP.
 XX
 AC AAH73748;
 XX
 DT 28-SEP-2001 (first entry)

XX PCR primer used to amplify murine Tspy pseudogene fragment.
 DE
 XX Sex determination; ratio; offspring; transgenic animal; PCR primer; tspy;
 KW testis specific protein Y-linked; ss.
 XX
 OS Mus sp.
 XX
 FN WO200147353-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 27-DEC-2000; 2000WO-US035275.
 XX
 PR 27-DEC-1999; 99US-0173096P.
 XX
 PA (LIUC/) LIU C.
 XX
 PI Liu C, Costantini F, Wang J;
 XX
 DR WPI; 2001-425551/45.
 XX
 PT Producing transgenic animals, involves creating transgene whose
 PT expression interfere with sperm's ability to undergo fertilization, and
 PT placing it under post-meiotic spermatogenesis-specific promoter control.
 XX
 PS Disclosure; Page 8; 20pp; English.
 XX
 CC This invention relates to a method for controlling the sex ratio of
 CC offspring. The invention involves producing transgenic animals with
 CC somatic/germ cells which contain a transgene whose expression can
 CC interfere with sperm's ability to undergo fertilisation. The transgene is
 CC placed under control of post-meiotic spermatogenesis-specific promoter,
 CC and is inserted on to one of the sex chromosomes. The present sequence
 CC represents a PCR primer used to amplify a fragment of murine tspy
 CC pseudogene (testis specific protein Y-linked). The DNA fragment is used
 CC in an example illustrating the method of the invention where the
 CC transgene is targeted to the tspy locus on the Y chromosome. The method
 CC is useful for producing transgenic animals having somatic/germ cells
 CC containing one or more transgenes whose expression results in alteration
 CC of the sex ratio of the offspring of the animals
 XX
 SQ Sequence 18 BP; 9 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 934 AAATGCACAAATCTGAAGC 951
 DB 1 AAATGCACAAATCTGAAGC 18
 RESULT 139
 ADE29652/c
 ID ADE29652 standard; RNA; 19 BP.
 XX
 AC ADE29652;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:274.
 XX
 KW short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiaesthetic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 XX
 OS Synthetic.

```

XX PN WO2003072590-A1.
XX PF 04-SEP-2003.
XX XX
XX XX 28-JAN-2003; 2003WO-US002510.
XX XX 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX XX (SIRN-) SIRNA THERAPEUTICS INC.
XX PA Mcswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
XX PI WPI; 2003-689980/65.
XX DR
XX XX New short interfering nucleic acid, useful e.g. for treatment and
XX PT diagnosis of cancer, downregulates expression of mitogen-activated
XX PT protein kinase genes.
XX PS Example 3; SEQ ID NO 274; 164pp; English.
XX CC The present invention describes a short interfering nucleic acid (siNA)
XX CC that downregulates expression of a mitogen-activated protein kinase
XX CC (MAPK) genes by RNA interference. Also described: (1) a method for
XX CC modulating expression of MAPK genes in cells, tissue explants or
XX CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
XX CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
XX CC vectors that express siNA and cells containing these vectors. MAPK siNAs
XX CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
XX CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
XX CC siNAs can be used to modulate the expression of MAPK genes, in cells,
XX CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
XX CC and II; a wide range of tumours, and inflammatory diseases (asthma,
XX CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
XX CC disease). They can also be used for drug screening; diagnosis; target
XX CC identification and validation; genetic engineering; pharmacogenomics;
XX CC studying gene function and gene mapping (e.g. of single-nucleotide
XX CC polymorphisms). The present sequence represents a MAPK siNA which is used
XX CC in the exemplification of the present invention.
XX SQ Sequence 19 BP; 7 A; 3 C; 2 G; 0 T; 7 U; 0 Other;
XX Query Match 1.3%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 1.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 382 AGGCAATGCAGTCATTTT 399
DB 18 AGAAATGCAGTCATTTT 1
RESULT 140
ADE29489
ID ADE29489 standard; RNA; 19 BP.
XX AC ADE29489;
XX XX
XX XX 29-JAN-2004 (first entry)
XX DT Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:111.
XX DE short interfering nucleic acid; siNA; downregulation; inhibition;
XX KW mitogen-activated protein kinase; MAP kinase; RNA interference;
XX KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiarthritic;
XX KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
XX KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
inflammatory disease; asthma; septic shock; rheumatoid arthritis;
psoriasis; inflammatory bowel disease; drug screening;
genetic engineering; pharmacogenomic; gene mapping; ss.
Synthetic.
WO2003072590-A1.
04-SEP-2003.
28-JAN-2003; 2003WO-US002510.
20-FEB-2002; 2002US-0358580P.
11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
(SIRN-) SIRNA THERAPEUTICS INC.
Mcswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
WPI; 2003-689980/65.
New short interfering nucleic acid, useful e.g. for treatment and
diagnosis of cancer, downregulates expression of mitogen-activated
protein kinase genes.
Example 3; SEQ ID NO 111; 164pp; English.
The present invention describes a short interfering nucleic acid (siNA)
that downregulates expression of a mitogen-activated protein kinase
(MAPK) genes by RNA interference. Also described: (1) a method for
modulating expression of MAPK genes in cells, tissue explants or
organisms by introduction of siNA; (2) kits for in vitro or in vivo
delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
vectors that express siNA and cells containing these vectors. MAPK siNAs
have cytostatic, anorectic, antidiabetic, antiinflammatory,
antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
siNAs can be used to modulate the expression of MAPK genes, in cells,
tissue explants or organisms, e.g. for treating obesity; diabetes types I
and II; a wide range of tumours, and inflammatory diseases (asthma,
septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
disease). They can also be used for drug screening; diagnosis; target
identification and validation; genetic engineering; pharmacogenomics;
studying gene function and gene mapping (e.g. of single-nucleotide
polymorphisms). The present sequence represents a MAPK siNA which is used
in the exemplification of the present invention.
Sequence 19 BP; 7 A; 2 C; 3 G; 0 T; 7 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 382 AGGCAATGCAGTCATTTT 399
DB 2 AGAAATGCAGTCATTTT 19
RESULT 141
ADQ27277
ID ADQ27277 standard; DNA; 19 BP.
XX AC ADQ27277;
XX XX
XX XX 26-AUG-2004 (first entry)
XX DT RNA interference target sequence #185.
XX DE RNA interference target sequence #185.
XX XX

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KW ss; detection; RNA interference; siRNA; gene silencing; gene expression;
 KW Cytotoxicity.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048566-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 21-NOV-2003; 2003WO-JP014893.
 XX
 PR 22-NOV-2002; 2002JP-00340053.
 XX
 PA (NATO/) NATORI Y.
 PA (SAIG/) SAIGO K.
 PA (TEIK/) TEI K.
 PA (NAIT/) NAITO Y.
 XX
 PI Saigo K, Tei K, Naito Y;
 XX
 DR WPI; 2004-487423/46.
 XX
 PT Detecting sequence of RNA interference useful for synthesizing siRNA, by
 PT detecting regions in sequence fulfilling specific criteria such as base
 PT at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
 PT guanine or cytosine.
 XX
 PS Disclosure; SEQ ID NO 199; 325pp; Japanese.
 XX
 CC The invention relates to a method of detecting the base sequence for RNA
 CC interference by detecting the regions in the DNA sequence fulfilling the
 CC following requirements such as: (i) the base at 3' terminal is adenine,
 CC thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine;
 CC (iii) the seven base sequence at 3' terminal is rich in adenine, thymine
 CC and uracil, and; (iv) there are bases in a such a number that it causes
 CC RNA interference without showing cytotoxicity. The method is used for
 CC designing and synthesizing siRNA causing RNA interference. This sequence
 CC corresponds to an RNA interference target sequence of the invention.
 XX
 SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 744 GGCAGCTGCCACTTATG 761
 Db 1 GACAGCTGGCACCCTATG 18
 RESULT 142
 ADR27528
 ID ADR27528 standard; DNA; 19 BP.
 XX
 AC ADR27528;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human single nucleotide polymorphism detection primer #618.
 XX
 KW ss; primer; single nucleotide polymorphism; SNP; diagnosis;
 KW disease association; linkage analysis; autoimmune disease;
 KW rheumatoid arthritis; diabetes; multiple sclerosis;
 KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
 KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
 KW glomerulonephritis; Graves' disease; myocarditis; Sjogren disease;
 KW primary systemic vasculitis; genotyping; gene therapy; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004067779-A2.
 XX
 PD 12-AUG-2004.

XX 30-JAN-2004; 2004WO-US002652.
 PF
 XX 30-JAN-2003; 2003US-0443566P.
 PR
 PR 18-MAR-2003; 2003US-0455444P.
 PR 25-APR-2003; 2003US-0455241P.
 PR 15-AUG-2003; 2003US-0495115P.
 PR 13-NOV-2003; 2003US-0519270P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Begovich AB, Carlton VE, Schrodli SJ, Alexander HC;
 XX
 DR WPI; 2004-594223/57.
 XX
 CC New single nucleotide polymorphisms (SNPs) associated with rheumatoid
 CC arthritis (RA), useful in identification of individuals at risk of
 CC developing RA or other autoimmune disease, and in development of
 CC therapeutic agents.
 XX
 PS Claim 21; SEQ ID NO 50200; 141pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule comprising at
 CC least 8 contiguous nucleotides where one of the nucleotides is a single
 CC nucleotide polymorphism (SNP) selected from any one of the nucleotide
 CC sequences of SEQ ID NOS:1-669 and 1339-49582, or their complements. The
 CC SNPs are useful as targets for the design of diagnostic reagents and the
 CC development of therapeutic agents, as well as for disease association and
 CC linkage analysis. In particular, the SNPs are useful for identifying an
 CC individual who is at an increased or decreased risk for developing an
 CC autoimmune disease such as rheumatoid arthritis, type 1 diabetes,
 CC multiple sclerosis, systemic lupus erythematosus, inflammatory bowel
 CC diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia,
 CC asthma, vitiligo, glomerulonephritis, Graves' disease, myocarditis,
 CC Sjogren disease, or primary systemic vasculitis. Methods associated with
 CC the SNPs are useful for early detection of the disease, for providing of
 CC clinically important information for the prevention and/or treatment of
 CC the autoimmune diseases particularly rheumatoid arthritis, and for
 CC screening and selecting therapeutic agents. The SNPs are useful for human
 CC identification applications. The genes containing the SNPs are useful for
 CC treating the diseases defined above. The nucleic acid molecules are
 CC useful as hybridization probes for genotyping SNPs in messenger RNA,
 CC cDNA, genomic DNA, and genomic clones. The nucleic acid molecules are
 CC useful for constructing host cells expressing a part or all of the
 CC nucleic acid molecules and variant peptides, for constructing transgenic
 CC animals, for assaying or screening drugs that modulate nucleic acid
 CC expression, or for gene therapy in patients whose cells have aberrant
 CC gene expression. This sequence corresponds to a PCR primer which
 CC hybridises to the nucleic acids of the invention to amplify the SNP
 CC containing region. (Note: SEQ ID NOS 1-49582 are claimed and stated as
 CC being provided in the specification, however these sequences are not
 CC provided in the printed specification).
 XX
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1064 CCAGTGGCTAACCACTT 1081
 Db 2 CCAGTGGCTCAACCACTT 19
 RESULT 143
 AAT36153/c
 ID AAT36153 standard; DNA; 20 BP.
 XX
 AC AAT36153;
 XX
 DT 15-MAY-1997 (first entry)
 XX
 DE PCR primer for detecting mutations in human Int6 gene homologue.

XX MMTV, mouse mammary tumour virus; Int6; breast cancer; neoplasia;
 KW diagnosis; treatment; immunotherapy; vaccine; probe; primer;
 KW polymerase chain reaction; PCR; ss.
 XX
 XX Synthetic.
 OS
 XX WO9624672-A1.
 PN
 XX
 XX 15-AUG-1996.
 PD
 XX
 XX 09-FEB-1996; 96WO-US001884.
 PF
 XX
 XX 09-FEB-1995; 95US-00385998.
 PR
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Marchetti A, Buttitta F, Smith GH, Callahan R;
 XX WPI; 1996-384444/38.
 XX
 XX DNA encoding Int6 tumour associated protein - and use of reagents derived
 XX from them in cancer gene therapy, vaccines, diagnosis and immunotherapy.
 XX
 XX Claim 16; Page 22; 93pp; English.
 PS
 XX
 XX AAT36149-T36174 are PCR primers derived from intronic sequences of human
 XX homologue of the murine Int6 gene located at chromosome 15 of a mouse
 XX genome. The primers are used for detecting mutations within the human
 XX Int6 gene. The Int6 gene is associated with MMTV (mouse mammary tumour
 XX virus) integration into a host genome during tumorigenesis. Primers and
 XX probes can be used in assays to diagnose MMTV infection, or any other
 XX Int6 gene integration. Antibodies against the Int6 protein can be used in
 XX the same way
 XX
 XX Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 926 CTTATTAGAAATGCAGAA 943
 DB |||||
 20 CTAATTAAATGCAGAA 3
 RESULT 144
 AAI72504/C
 ID AAI72504 standard; DNA; 20 BP.
 XX
 XX AAI72504;
 AC
 XX 21-MAY-2002 (first entry)
 DT
 XX Human Int6 exon 3 primer #1.
 DE
 XX PCR; murine; human; Int6; integration site; deregulation; neoplasia;
 KW mouse mammary tumour virus; MMTV; cancer; immunotherapy; gene therapy;
 KW prenatal screening; foetus; vaccine; primer; polymerase chain reaction;
 KW amplify; ss.
 XX
 XX Homo sapiens.
 OS
 XX US6342392-B1.
 PN
 XX 29-JAN-2002.
 PD
 XX 23-AUG-1999; 99US-00378842.
 PF
 XX 09-FEB-1995; 95US-00385998.
 PR
 XX 09-FEB-1996; 96WO-US001884.
 PR
 XX 25-SEP-1997; 97US-00875847.
 PR
 XX

(USSH) US DEPT HEALTH & HUMAN SERVICES.
 Marchetti A, Buttitta F, Smith GH, Callahan R;
 WPI; 1996-384444/38.
 DNA encoding Int6 tumour associated protein - and use of reagents derived
 from them in cancer gene therapy, vaccines, diagnosis and immunotherapy.
 Claim 11; Col 14; 45pp; English.
 The sequences given in AAI72500-23 are primers which were used to amplify
 the human Int6 coding sequence. The primers were derived from the
 intronic sequences which border the 5' and 3' ends of each exon of the
 human Int6 gene. Human Int6 is organised into 13 exons as is the murine
 Int6 gene, and contains a CA-repeat in the 7th intron. Human Int6 has
 been localised to chromosome 8, more specifically to 8q22-q24. Int6 is an
 integration site for mouse mammary tumour virus (MMTV), which causes
 deregulation of expression of cellular genes adjacent to the site of MMTV
 integration in mammary tumours. The Int6 protein has been found to be
 highly conserved across species, with Drosophila Int6 being 60% identical
 to human/mouse Int6. This indicates that Int6 is serving a basic life
 function. The method of the invention comprises assaying a sample to
 detect a human Int6 nucleic acid sequence, or its fragment, by contacting
 the sample with a sequence of at least 15 consecutive nucleotides of
 human Int6 cDNA or a conservative variant of it, where a disrupted
 expression or loss of expression of the variant is associated with
 neoplasia. The method is useful for prenatal screening of a foetus or to
 pre-symptomatically screen a subject at risk of having cancer. Detecting
 mutations in the Int6 gene can provide diagnostic and prognostic
 information. The nucleic acids and proteins are useful in immunotherapy,
 gene therapy or as vaccines for treating or preventing cancer. The
 nucleic acids are useful as probes for isolating homologues of Int6 gene
 or for detecting mutations in the Int6 gene
 Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 926 CTTATTAGAAATGCAGAA 943
 DB |||||
 20 CTAATTAAATGCAGAA 3
 RESULT 145
 AAZ03074
 ID AAZ03074 standard; DNA; 20 BP.
 XX
 XX AAZ03074;
 AC
 XX 07-OCT-1999 (first entry)
 DT
 XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
 DE
 XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 XX Synthetic.
 OS
 XX Chlamydia trachomatis.
 OS
 XX WO9928475-A2.
 PN
 XX 10-JUN-1999.
 PD
 XX 27-NOV-1998; 98WO-IB001939.
 PF
 XX 28-NOV-1997; 97FR-00015041.
 PR
 XX 17-DEC-1997; 97FR-00016034.
 PR
 XX 04-NOV-1998; 98US-0107077P.
 PR

XX (GEST) GENSET.
 XX Griffais R;
 XX WPI; 1999-371125/31.
 XX Genome sequence of Chlamydia trachomatis.
 XX Disclosure; Page 1577; 1755pp; English.
 XX PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,
 CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases
 XX SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 230 AGAGTCACCTATGACTCA 247
 |||||
 DB 3 AGAGTCACCTATGACTCA 20
 RESULT 146
 AAC73799
 ID AAC73799 standard; DNA; 20 BP.
 XX
 AC AAC73799;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Mouse IL-5R antisense oligonucleotide ISIS #23238.
 XX
 KW Mouse; interleukin-5; IL-5; signal transduction;
 KW antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;
 KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;
 KW inflammation; cancer; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PN WO200058512-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 17-MAR-2000; 2000WO-US007318.
 XX
 PR 26-MAR-1999; 99US-00280799.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Dean NM, Karras JG, McKay R;
 PI
 XX WPI; 2000-594648/56.
 XX
 XX Antisense oligonucleotide compound used to treat asthma and eosinophilic
 PT syndrome in humans modulates interleukin-5 signal transduction.
 XX
 PS Example 25; Page 77; 156pp; English.
 XX
 XX The present sequence is an oligonucleotide used for antisense modulation

CC of interleukin-5 (IL-5) signal transduction. Oligonucleotides were
 CC designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha.
 CC The antisense oligonucleotides may be used for the treatment of diseases
 CC associated with IL-5 signal transduction, IL-5 expression or IL-5
 CC receptor-alpha expression. Such diseases include asthma and eosinophilic
 CC syndrome. The oligonucleotides are also useful for research uses and to
 CC prevent or delay infection, inflammation or tumour formation
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1050 ACTTCCTATCTTCCAG 1067
 |||||
 DB 2 ACTTCCTATCTTCCAG 19
 RESULT 147
 AAS15166
 ID AAS15166 standard; DNA; 20 BP.
 XX
 AC AAS15166;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Mouse interleukin-5 receptor antisense oligonucleotide ISIS 23238.
 XX
 KW Mouse; antisense oligonucleotide; IL-5R; interleukin-5 receptor; ss;
 KW antiinfection; antiinflammatory; cytostatic; inflammation; infection;
 KW tumour; ISIS 23238; probe.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2, methoxyethoxy residues. All cytosines in this
 FT region are also 5-methyl-cytosine"
 XX
 PN WO200172765-A1.
 XX
 PD 04-OCT-2001.
 XX
 PF 28-MAR-2000; 2000WO-US008174.
 XX
 PR 28-MAR-2000; 2000WO-US008174.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Crooke ST, Manoharan M, Wyatt JR, Baker BF, Monia BP;
 PI Freier SM, McKay R, Karras JG;
 XX WPI; 2001-626250/72.
 DR
 XX Controlling cell behavior, useful e.g. for treatment of tumors, by
 PT modulating processing, e.g. splicing, of specific mRNA sequences with non
 PT -cleaving antisense agents.
 XX
 PS Example 8; Page 70; 121pp; English.
 XX
 XX The invention relates to controlling cell behaviour by modulating the
 CC processing of a selected wild-type mRNA target in the cell, is new. The
 CC mRNA is bound to a specific-binding antisense compound that does not
 CC cleave bound mRNA. The antisense oligonucleotides are useful as research
 CC reagents, diagnostic agents (in hybridisation assays), and for treatment

CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention

SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1010 TTGTGAGAGCATCATCAT 1027

DB 1 TTGTGAGAGCATCATCAT 18

RESULT 150

AAL42513/C

ID AAL42513 standard; DNA; 20 BP.

XX AAL42513;

AC AAL42513;

XX 28-JUN-2002 (first entry)

XX Alpha-V integrin-specific inhibitory antisense nucleic acid 2.

XX Antisense nucleic acid; ss; alpha-V integrin chain; antisense inhibition;
 KW cell adhesion modulation; platelet aggregation; immune function;
 KW tissue repair; cell proliferation; tumour invasion; cancer; gingivitis;
 KW chronic inflammatory disease; Chron's disease; rheumatoid arthritis;
 KW ocular neovascular disease; diabetic retinopathy; osteoporosis;
 KW excessive bone resorption; inflammatory skin disorder; psoriasis.

XX Unidentified.

OS EP1197553-A1.

PN 17-APR-2002.

XX 12-OCT-2000; 2000EP-00121394.

XX 12-OCT-2000; 2000EP-00121394.

XX (ATHR-) A3D GMBH ANTISENSE DESIGN & DRUG DEV.

PA Kronenwett R, Graef T, Haas R, Nedbal W;

PI WPI; 2002-364499/40.

XX Antisense nucleic acid against alpha V integrin for use in pharmaceutical
 PT compositions for the specific inhibition of the expression of alpha
 PT integrins in mammalian cells useful.

XX Claim 8; Page 3; 17pp; English.

XX The invention comprises antisense nucleic acids that are capable of
 CC binding to the transcription product of the gene coding for the alpha-V
 CC integrin chain, thereby inhibiting the expression of alpha-V integrins in
 CC mammalian cells. The antisense nucleic acids of the invention are useful
 CC for the treatment of pathological disorders by the modulation of cell
 CC adhesion which affects platelet aggregation, immune functions, tissue
 CC repair, cell proliferation, tumour invasion, inflammation and inherited
 CC diseases. Disorders which can be treated include: cancer; restenosis
 CC after angioplasty; stenosis to vein bypass; chronic inflammatory diseases
 CC (e.g. Chron's disease and rheumatoid arthritis); ocular neovascular
 CC diseases (e.g. diabetic retinopathy); disorders associated with excessive
 CC bone resorption (e.g. osteoporosis); disorders of mammalian oral cavity
 CC (e.g. gingivitis); and inflammatory skin disorders (e.g. psoriasis). The
 CC present DNA sequence represents an antisense nucleic acid of the
 CC invention used to inhibit alpha-V integrin expression

XX Sequence 20 BP; 10 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 417 TTTTCCTTATATTGGAA 434

DB 18 TTTTCCTTATATTCCAA 1

RESULT 151

ABT05772/C

ID ABT05772 standard; DNA; 20 BP.

XX ABT05772;

XX 16-OCT-2002 (first entry)

XX Nod2 related oligonucleotide SEQ ID No 52.

XX Intracellular signaling polypeptide; Nod2; Crohn's disease; mutation;
 KW cytosine residue insertion; nuclear factor; NF-B activation; NF-kappa B;
 KW RICK signaling; gene therapy; transgenic plant; plant; ds.

XX Unidentified.

XX WO200244426-A2.

XX 06-JUN-2002.

XX 26-OCT-2001; 2001WO-US051068.

XX 30-OCT-2000; 2000US-0244266P.

XX 25-APR-2001; 2001US-0286316P.

XX 26-OCT-2001; 2001US-00286316.

XX (UNMI) UNIV MICHIGAN.

XX (UYCH-) UNIV CHICAGO.

XX Nunez G, Inohara N, Ogura Y, Cho J, Nicolae DL, Bonen D;

XX WPI; 2002-547704/58.

XX New isolated intracellular signaling polypeptide, termed Nod2, useful for
 PT producing an antibody that recognizes Nod2, and as a target for screening
 PT drugs.

XX Example 9; Page 231; 316pp; English.

XX The invention relates to an isolated intracellular signaling polypeptide,
 CC termed Nod2, comprising a sequence of 1007 or 1040 amino acids, given in
 CC the specification. The nucleic acid encoding the isolated protein is
 CC useful for identifying subjects at risk of developing Crohn's disease by
 CC providing a nucleic acid from the subject, where the nucleic acid
 CC comprises a Nod2 gene, and detecting the presence or absence of one or
 CC more variations in the Nod2 gene. Detecting comprises comparing the
 CC sequence of the nucleic acid to the sequence of a wild-type Nod2 nucleic
 CC acid. Detection is accomplished by hybridisation analysis. The method
 CC further comprises determining if the subject is at risk of developing
 CC Crohn's disease based on the presence or absence of the variations, and
 CC determining a genotype relative risk or a population attributable risk
 CC for the subject. The variation is a polymorphism or a mutation,
 CC preferably a cytosine residue insertion, where the mutation causes a
 CC deletion of a Leu-Arg-Arg repeat of Nod2. The variation results in
 CC increased nuclear factor (NF)-B activation. The variation is selected
 CC from the sequences of the Nod2 gene. The isolated protein is useful as a
 CC target for screening drugs that can alter, for example, RICK signaling,
 CC and thus the physiological effects of NF-kappa B. The Nod2 gene is useful
 CC for producing the isolated protein by recombinant techniques, as starting
 CC nucleic acids for directed evolution, for gene therapy, or to decrease
 CC the level of Nod2 protein or mRNA in transgenic plants, plant tissues, or
 CC plant cells as compared to wild-type plants, plant tissues or plant
 CC cells. This polynucleotide represents a Nod2 gene related DNA sequence of
 CC the invention

XX Sequence 20 BP; 5 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 784 TGGGATGCTTGGAGA 801
 DB 18 TGGGATGCTTGAAGA 1

RESULT 152
 ABX04453
 ID ABX04453 standard; DNA; 20 BP.
 AC ABX04453;
 XX
 DT 13-JAN-2003 (first entry)
 DE Mouse Interleukin 5 receptor antisense oligonucleotide ISIS 23238.
 XX
 KW Mouse; ss; antisense; interleukin 5; IL-5; IL-5 receptor; antiasthmatic;
 KW immunosuppressant; eosinophilic syndrome; asthma.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PN US2002128216-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 07-MAR-2001; 2001US-00800629.
 XX
 PR 26-MAR-1999; 99US-00280799.
 PR 17-MAR-2000; 2000WO-US007318.
 XX
 PA (DEAN/) DEAN N M.
 PA (KARR/) KARRAS J G.
 PA (MCKA/) MCKAY R.
 PA (MANO/) MANOHARAN M.
 XX
 PI Dean NM, Karras JG, McKay R, Manoharan M;
 XX WPI; 2003-039602/03.
 DR

Novel antisense compound for treating disease/condition e.g. eosinophilic
 syndrome or asthma associated with interleukin-5 or IL-5 receptor
 expression or IL-5 signal transduction, modulates IL-5 signal
 transduction.
 XX
 PS Example 25; Page 24; 77pp; English.

XX The invention relates to an antisense compound of 8-30 nucleobases in
 CC length, which modulates interleukin (IL)-5 signal transduction. Also
 CC include are a pharmaceutical composition comprising the antisense
 CC oligonucleotide and a pharmaceutically acceptable carrier or diluent, and
 CC a diagnostic kit for detecting the expression level of the membrane form
 CC versus soluble form of IL-5 receptor a. The antisense compound is useful
 CC for modulating IL-5 signal transduction, modulating expression of
 CC mammalian IL-5 or modulating the expression of mammalian IL-5 receptor a,
 CC in cells or tissues, for altering the ratio of the isoforms of mammalian
 CC IL-5 receptor a in mammalian cells or tissues, treating a mammalian
 CC having a disease or condition associated with IL-5 signal transduction,
 CC IL-5 expression or IL-5 receptor a expression, where the disease or
 CC condition include eosinophilic syndrome or asthma. An antisense compound
 CC which alters splicing of an RNA encoding IL-5 receptor a is also useful
 CC for treating a mammal having a disease or condition. The present sequence
 CC is an antisense oligonucleotide targeting mouse IL-5 receptor
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTCCAG 1067
 DB 2 ACTTCCTTACCTTCTCG 19
 RESULT 153
 ABZ81557
 ID ABZ81557 standard; DNA; 20 BP.
 XX
 AC ABZ81557;
 XX
 DT 26-AUG-2003 (first entry)
 DE PKA regulatory subunit RII beta antisense oligonucleotide ISIS #114487.
 XX
 KW Human; cytostatic; antidiabetic; antisense therapy; phosphorothioate;
 KW protein kinase inhibitor; protein kinase A; PKA;
 KW regulatory subunit RII beta; cAMP-dependent protein kinase; diabetes;
 KW cancer; infection; inflammation; tumour; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /mod_base= a
 FT /note= "Oligonucleotide has phosphorothioate backbone and
 FT all cytidine nucleotides are 5-methylcytidine. Optionally
 FT some nucleotides with 2'-methoxyethyl (2'-MOE wings)
 FT modification"
 XX
 PN WO2003010283-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 15-JUL-2002; 2002WO-US022629.
 XX
 PR 25-JUL-2001; 2001US-00915485.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Wyatt JR;
 XX WPI; 2003-239434/23.
 DR

New antisense oligonucleotides targeted to nucleic acid encoding protein
 kinase A regulatory subunit RII beta, useful in treating diseases e.g.
 cancer associated with the aberrant expression of the protein kinase.
 XX
 PS Claim 3; Page 74; 98pp; English.

XX The present invention relates to novel antisense oligonucleotides
 CC (ABZ81522-ABZ81593) which are targeted to human protein kinase A (PKA)
 CC regulatory subunit RII beta nucleotide sequence (ABZ81513), and which
 CC specifically hybridize with and inhibit the expression of the PKA
 CC regulatory subunit RII beta (PKA is also known as cAMP-dependent protein
 CC kinase). The antisense oligonucleotides are useful for modulating the
 CC expression of PKA regulatory subunit RII beta and for treating diseases
 CC or conditions associated with aberrant expression of PKA regulatory
 CC subunit RII beta, e.g. diabetes or cancer. The antisense compounds are
 CC also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent
 CC or delay infection, inflammation or tumour formation, as research
 CC reagents and kits, and in distinguishing between functions of various
 CC members of a biological pathway
 XX

SQ Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 663 TATGTTACTCAAAATG 680


```

Db      3  TATGTTACTGACATTATG 20
|||||
RESULT 154
AAD57723/c
ID  AAD57723 standard; DNA; 20 BP.
XX
AC  AAD57723;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human PLSCR4 antisense oligonucleotide, ISIS #196336.
XX
KW  Human; phospholipid scramblase 4; autoimmune disorder; gene therapy;
KW  neurodegenerative disease; hyperproliferative disorder; HuPLSCR4;
KW  MuPLSCR4; PLSCR4; LOC57088; antisense; phosphorothioate; ss.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FH  modified_base 1..20 /tag= a
FH  /mod_base= OTHER
FH  /note= "Phosphorothioate backbone; All cytidine residues
FH  are 5-methylcytidines"
FH  modified_base 1..5 /tag= b
FH  /mod_base= OTHER
FH  /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FH  modified_base 16..20 /tag= c
FH  /mod_base= OTHER
FH  /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN  WO2003048331-A2.
XX
PD  12-JUN-2003.
XX
PF  04-DEC-2002; 2002WO-US038619.
XX
PR  04-DEC-2001; 2001US-00012984.
XX
PA  (ISIS-) ISIS PHARM INC.
XX
PI  Dobie K;
XX
DR  WPI; 2003-569054/53.
XX
PT  New compound, useful for preparing a composition for treating
PT  hyperproliferative or autoimmune disorders, comprises a sequence targeted
PT  to a nucleic acid encoding human phospholipid scramblase 4.
XX
PS  Example 15; Page 78; 166pp; English.
XX
CC  The invention relates to novel antisense compounds targetted to a nucleic
CC  acid encoding human phospholipid scramblase 4 (also known as PLSCR4,
CC  HuPLSCR4, MuPLSCR4 and LOC57088) to inhibit its expression. Antisense
CC  compounds of the invention are useful for preparing compositions for
CC  treating neurodegenerative diseases, e.g. hyperproliferative or
CC  autoimmune disorders. The invention is also useful in gene therapy. The
CC  present sequence is an antisense oligo targetted to human PLSCR4 DNA
XX
SQ  Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
PT  PT
PT  PT
PT  PT
XX
PS  Example 15; Page 78; 166pp; English.
XX
CC  The invention relates to novel antisense compounds targetted to a nucleic
CC  acid encoding human phospholipid scramblase 4 (also known as PLSCR4,
CC  HuPLSCR4, MuPLSCR4 and LOC57088) to inhibit its expression. Antisense
CC  compounds of the invention are useful for preparing compositions for
CC  treating neurodegenerative diseases, e.g. hyperproliferative or
CC  autoimmune disorders. The invention is also useful in gene therapy. The
CC  present sequence is an antisense oligo targetted to human PLSCR4 DNA
XX
SQ  Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy  418 TTTCCTTATATTGGAAG 435
|||
Db  18 TTGCCTTATATTGGAAG 1
|||||
RESULT 155
ADE25541/c
ID  ADE25541 standard; DNA; 20 BP.
XX
AC  ADE25541;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Human TLR1 related PCR primer SEQ ID NO 7.
XX
KW  Human; TLR1; cancer; cytostatic; primer; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
PN  WO2003061697-A1.
XX
PD  31-JUL-2003.
XX
PF  26-DEC-2002; 2002WO-JP013642.
XX
PR  27-DEC-2001; 2001JP-00398165.
XX
PA  (TAKE ) TAKEDA CHEM IND LTD.
XX
PI  Hikichi Y, Katsuyama R, Kakoi Y, Nishizawa S;
XX
DR  WPI; 2003-598709/56.
XX
PT  Treatment and prevention for cancer of the e.g. digestive system, liver
PT  and lung.
XX
PS  Example 2; Page 89; 98pp; Japanese.
XX
CC  The invention relates to the treatment and prevention of cancer
CC  comprising a compound that inhibits the activity of protein or peptide
CC  fragment of a fully defined amino acid sequence TLR1 given as SEQ ID NO
CC  1. TLR1 is useful in the treatment and prevention of cancers of the large
CC  intestine, mammary glands, lung, prostate, digestive tract, stomach and
CC  liver. TLR1 gene expression is detected in breast cancer tissue. The
CC  present sequence is that of a human TLR1 related PCR primer used in
CC  examples of the invention.
XX
SQ  Sequence 20 BP; 10 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy  305 GTTTCCTGCTTTGGATT 322
|||
Db  19 GTTCTGCTTTGGATT 2
|||||
RESULT 156
ABZ93663
ID  ABZ93663 standard; DNA; 20 BP.
XX
AC  ABZ93663;
XX
DT  17-OCT-2003 (first entry)
XX
DE  Human oligonucleotide sequence.
XX
KW  Human; antisense; lung dysfunction; nasal airway dysfunction;
KW  antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW  antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW  antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW  adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW  lung inflammation; respiratory disease; ds.
XX

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Fri Aug 19 11:00:00 2005

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OS Homo sapiens.
PN WO200285308-A2.
PD 31-OCT-2002.
PF 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
PR (EPITG-) EPIGENESIS PHARM INC.
PA
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
DR
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8905; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiallergic, immunosuppressive,
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing levels of adenosine
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 8 A; 6 C; 2 G; 2 T; 0 U; 2 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 936 ATGCAGAAATCTGAAGCCCCA 955
DB 1 ATGNAGAAATCAAAACCCCA 20
RESULT 157
ABD29893
ID ABD29893 standard; DNA; 20 BP.
XX
AC ABD29893;
XX
DT 29-JUL-2004 (first entry)
XX
DE T74688-derived oligonucleotide SEQ ID 8905.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiasthmatic; antiallergic; antiinflammatory;
KW analgesic; hypotensive; immunosuppressive; cytoskeletal; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
```

```
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
PN WO200285309-A2.
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPITG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
DR
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 8905; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine, (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiasthmatic, antiinflammatory, antiallergic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.
CC Transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 8 A; 6 C; 2 G; 2 T; 0 U; 2 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 936 ATGCAGAAATCTGAAGCCCCA 955
DB 1 ATGNAGAAATCAAAACCCCA 20
RESULT 158
ADJ86050
ID ADJ86050 standard; DNA; 20 BP.
XX
AC ADJ86050;
```

```

XX 06-MAY-2004 (first entry)
DT
XX
XX Nucleic acid analysis-related Tag probe SeqID1118.
DE
XX
XX restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
KW T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
KW assay development; product development; product validation;
KW quality control; probe; ss.
XX
XX Synthetic.
OS Unidentified.
XX
XX WO2004007684-A2.
FN
XX
XX 22-JAN-2004.
PD
XX
XX 14-JUL-2003; 2003WO-US021990.
PF
XX
XX 12-JUL-2002; 2002US-0395530P.
PR
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
XX Christians FC;
PI
XX
XX WPI; 2004-122923/12.
DR
XX
XX New DNA molecules made by annealing and extending overlapping 60mer
PT oligonucleotides, useful in producing synthetic Tag genes useful as assay
PT controls, in assay development, product development and for quality
PT control.
XX
XX Disclosure; SEQ ID NO 1118; 91pp; English.
XX
XX This invention relates to a novel DNA molecule which comprises a DNA
CC molecule made up of the following elements in a 5' to 3' direction: a
CC first restriction endonuclease site; a T3 promoter site; at least one Tag
CC gene comprising at least 5 20mer Tag sequences; a Poly A site having at
CC least 21 consecutive A residues; a second restriction endonuclease site
CC which may be the same or different than the first restriction
CC endonuclease site; or a T7 promoter on the opposite strand as the T3
CC promoter. The invention may be useful in nucleic acid analysis, in
CC particular to synthetic Tag genes useful as assay controls, in assay
CC development, product development and validation and for quality control.
CC The present sequence is that of a Tag oligonucleotide probe which may be
CC used during the creation of the novel DNA molecule of the invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 697 TCATGTACTCAGCGTCT 714
Db 2 TCATGTACTGACAGTCT 19
RESULT 159
ADJ54494/C
ID ADJ54494 standard; DNA; 20 BP.
XX
XX AC ADJ54494;
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human B7-2 DNA antisense oligonucleotide #109.
DE
XX
XX Airway hyperresponsiveness; pulmonary inflammation;
KW antisense oligonucleotide; human; B7 protein; B7-2; asthma;
KW antiasthmatic; antiinflammatory; ss.
XX
XX Homo sapiens.
OS

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```

XX US2004023917-A1.
PN
XX
XX 05-FEB-2004.
PD
XX
XX 23-MAY-2003; 2003US-00444206.
PF
XX
XX 31-DEC-1996; 96US-00777266.
PR
XX 04-JUN-1999; 99US-00326186.
PR
XX 25-MAY-2000; 2000WO-US014471.
PR
XX 09-MAY-2001; 2001US-00851871.
PR
XX (BENN/) BENNETT C F.
PA (VICK/) VICKERS T A.
PA (KARR/) KARRAS J G.
XX
XX Bennett CF, Vickers TA, Karras JG;
PI
XX WPI; 2004-132608/13.
DR
XX
XX Treating airway hyperresponsiveness or pulmonary inflammation comprises
PT administering an antisense compound targeted to a nucleic acid molecule
PT encoding a human B7 protein to the individual.
PT
XX
XX Example 27; SEQ ID NO 314; 182pp; English.
PS
XX
XX The invention relates to a method for treating airway hyperresponsiveness
CC or pulmonary inflammation in an individual comprising administering an
CC antisense compound targeted to a nucleic acid molecule encoding a human
CC B7 protein. The invention also relates to a method of inhibiting
CC expression of a nucleic acid molecule encoding B7-1 or B7-2. The
CC antisense compound is an antisense oligonucleotide which has a modified
CC sugar moiety and nucleobase. The human B7 protein is human B7-1 or B7-2
CC protein or both. The compound is useful for treating airway
CC hyperresponsiveness or pulmonary inflammation, which is associated with
CC asthma, by inhibiting expression of human B7 protein. This sequence
CC represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 7 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 640 AAATAGACCTCTCAATT 657
Db 20 AAATAGACCTCTCAATT 3
RESULT 160
ADJ23824
ID ADJ23824 standard; DNA; 20 BP.
XX
XX AC ADJ23824;
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 2222.
DE
XX
XX Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key... Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 4 nucleotides in length. Also all
FT

```

FT cytidine residues are 5-methylcytidines"

XX WO2004009541-A2.

XX 29-JAN-2004.

XX 18-JUL-2003; 2003WO-US022410.

XX 19-JUL-2002; 2002US-0397106P.

XX (PHAA) PHARMACIA CORP.

XX Bhat BG;

XX WPI; 2004-132912/13.

XX New antisense oligonucleotide for modulating endothelial lipase

XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low

XX high density lipoprotein or cardiovascular disorders.

XX Claim 3; SEQ ID NO 2222; 1007pp; English.

XX The present invention relates to antisense oligonucleotides (ADJ21603-

XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence

XX (ADJ25517), where the antisense oligonucleotide specifically hybridises

XX with and inhibits the expression of EL. The antisense oligonucleotides

XX are useful for modulating the expression of endothelial lipase in cells

XX or tissues to treat diseases associated with EL expression, such as

XX dyslipidaemia, low high density lipoprotein (HDL), cardiovascular

XX disorder or metabolic syndrome X. In addition, the oligonucleotides are

XX used for diagnostics, prophylaxis, or as research reagents or kits.

XX Sequence 20 BP; 3 A; 4 C; 12 G; 1 T; 0 U; 0 Other;

XX

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 CGGGCCGTGCAGGAGC 39

Db 1 CGGGCCGTGCAGGAGC 18

RESULT 161

ADJ22770

ID ADJ22770 standard; DNA; 20 BP.

XX

XX ADJ22770;

XX 20-MAY-2004 (first entry)

XX Human endothelial lipase antisense oligonucleotide, SEQ ID 1168.

XX Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;

XX Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;

XX cardiovascular disorder; metabolic syndrome X; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1. .20

FT /tag= a

FT /mod_base= OTHER

FT /note= "This oligonucleotide has a phosphorothioate

FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'

FT and 3' ends, which are 4 nucleotides in length. Also all

FT cytidine residues are 5-methylcytidines"

XX WO2004009541-A2.

XX 29-JAN-2004.

XX

PF 18-JUL-2003; 2003WO-US022410.

XX

PR 19-JUL-2002; 2002US-0397106P.

XX

XX (PHAA) PHARMACIA CORP.

XX Bhat BG;

XX WPI; 2004-132912/13.

XX New antisense oligonucleotide for modulating endothelial lipase

XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low

XX high density lipoprotein or cardiovascular disorders.

XX Claim 3; SEQ ID NO 1168; 1007pp; English.

XX The present invention relates to antisense oligonucleotides (ADJ21603-

XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence

XX (ADJ25517), where the antisense oligonucleotide specifically hybridises

XX with and inhibits the expression of EL. The antisense oligonucleotides

XX are useful for modulating the expression of endothelial lipase in cells

XX or tissues to treat diseases associated with EL expression, such as

XX dyslipidaemia, low high density lipoprotein (HDL), cardiovascular

XX disorder or metabolic syndrome X. In addition, the oligonucleotides are

XX used for diagnostics, prophylaxis, or as research reagents or kits.

XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

XX

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 865 TTGTAGTCCATGCTATTA 882

Db 3 TTGTAGTCCATGCTATTA 20

RESULT 162

ADJ23294

ID ADJ23294 standard; DNA; 20 BP.

XX

XX ADJ23294;

XX 20-MAY-2004 (first entry)

XX Human endothelial lipase antisense oligonucleotide, SEQ ID 1692.

XX Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;

XX Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;

XX cardiovascular disorder; metabolic syndrome X; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1. .20

FT /tag= a

FT /mod_base= OTHER

FT /note= "This oligonucleotide has a phosphorothioate

FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'

FT and 3' ends, which are 4 nucleotides in length. Also all

FT cytidine residues are 5-methylcytidines"

XX WO2004009541-A2.

XX 29-JAN-2004.

XX

XX 18-JUL-2003; 2003WO-US022410.

XX

XX 19-JUL-2002; 2002US-0397106P.

XX

XX (PHAA) PHARMACIA CORP.

XX

PI Bhat BG;
 XX WPI; 2004-132912/13.
 XX
 XX New antisense oligonucleotide for modulating endothelial lipase
 PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
 PT high density lipoprotein or cardiovascular disorders.
 XX
 XX Claim 3; SEQ ID NO 1692; 1007pp; English.
 XX
 XX The present invention relates to antisense oligonucleotides (ADJ21603-
 CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
 CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
 CC with and inhibits the expression of EL. The antisense oligonucleotides
 CC are useful for modulating the expression of endothelial lipase in cells
 CC or tissues to treat diseases associated with EL expression, such as
 CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
 CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
 CC used for diagnostics, prophylaxis, or as research reagents or kits.
 XX
 XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 865 TTGTAGTCCATGCTATTA 882
 ||||| |||||
 Db 2 TTGTAGCCATGCTATTA 19
 ||||| |||||
 RESULT 163
 ADK19749/c
 ID ADK19749 standard; DNA; 20 BP.
 XX
 XX AC ADK19749;
 XX
 XX 03-JUN-2004 (first entry)
 XX
 XX Mouse cDNA clone C630041L24 RT-PCR primer #2.
 XX
 KW Mouse; ss; PCR; cancer; prostate cancer; neuroblastoma; leukaemia;
 KW inflammation; arthritis; inflammatory skin disorder;
 KW insulin dependent diabetes; adult respiratory distress syndrome;
 KW cell death-related disorder; Alzheimer's disease; Parkinson's disease;
 KW multiple sclerosis; AIDS; septic shock; stroke; osteoporosis; ischaemia;
 KW reperfusion injury; myocardial infarction; appetite; immune response;
 KW antigen; anaphylaxis; primer; RT-PCR; reverse transcriptase PCR.
 XX
 OS Mus musculus.
 XX
 XX US2004053306-A1.
 XX
 XX 18-MAR-2004.
 XX
 XX 17-JUN-2003; 2003US-00462691.
 XX
 XX 17-JUN-2002; 2002US-0389145P.
 XX
 XX (HAYA/) HAYASHIZAKI Y.
 PA (KAMI/) KAMIYA M.
 XX
 XX Hayashizaki Y, Kamiya M;
 PI
 XX WPI; 2004-247724/23.
 DR
 XX New polynucleotides encoding short polypeptides, for preventing and
 PT treating disease conditions associated with the activity of the
 PT polypeptide, e.g. inflammation, cancer, arthritis, insulin-dependent
 PT diabetes or osteoporosis.
 XX
 XX Example 1; SEQ ID NO 67; 122pp; English.
 PS
 XX

CC The invention relates to an isolated mouse polynucleotide having a
 CC nucleotide sequence of a clone consisting of 110005117, 170007F22,
 CC 170001J22, 1700056N09, 2310014H11, 2310031C01, 4930563B01, 9130004I05,
 CC 9230110A19, 9230111007, A030004E11, A430045L05, A530065I17, A830010B16,
 CC B230114Q10, B230352020, C230071E12, C630041L24 or D630020P16. is new. The
 CC clones 110005117, 170007F22, 170001J22, 1700056N09, 2310014H11,
 CC 2310031C01, 4930563B01, 9130004I05, 9230110A19, 9230111007, A030004E11,
 CC A430045L05, A530065I17, A830010B16, B230114Q10, B230352020, C230071E12,
 CC C630041L24 and D630020P16, appearing as ADK19683-ADK19701 encoding the
 CC proteins appearing as ADK19702-ADK19720. The polynucleotides and
 CC polypeptides are useful in research, diagnostic and therapeutic agent
 CC screening applications, and prevention and treatment of disease
 CC conditions associated with the activity of the polypeptide, e.g.
 CC inflammation, cancer (e.g. prostate cancer, neuroblastoma and leukaemia),
 CC multiple sclerosis, arthritis, chronic inflammatory conditions of the
 CC skin, insulin-dependent diabetes, adult respiratory distress syndrome, or
 CC disorders relating cell death, such as Alzheimer's disease, Parkinson's
 CC disease, septic shock, stroke, osteoporosis, ischaemia, reperfusion
 CC injury, AIDS or myocardial infarction. The polypeptides are also useful
 CC in modulating appetite and modulating an immune response, including
 CC increasing antibody production in response to an antigen, inhibiting
 CC anaphylaxis, and reducing inflammation. The present sequence is a reverse
 CC transcriptase PCR (RT)-PCR primer used to isolate a mouse polynucleotide
 CC of the invention.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 56 CCCAGTTCGGAGACATG 73
 ||||| |||||
 Db 18 CCCAGTTTGGAGACAGG 1
 ||||| |||||
 RESULT 164
 ADO56167/c
 ID ADO56167 standard; DNA; 20 BP.
 XX
 XX AC ADO56167;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 XX Cyclin-dependent kinase 6, antisense oligonucleotide #231.
 DE
 XX antisense therapy; cyclin-dependent kinase 6;
 KW hyperproliferative disorder; cancer; bacterial infection;
 KW viral infection; apoptosis; ss; probe; human.
 XX
 XX Homo sapiens.
 OS
 XX US2004087523-A1.
 XX
 XX 06-MAY-2004.
 XX
 XX 31-JUL-2002; 2002US-00210802.
 XX
 XX 31-JUL-2002; 2002US-00210802.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Freier SM, Dobie KW;
 PI
 XX WPI; 2004-356241/33.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding cyclin-dependent kinase 6, useful for treating
 PT cancer, bacterial/viral infection or conditions involving aberrant
 PT apoptosis.
 XX
 XX Example 15; Page 34; 68pp; English.
 PS
 XX

Fri Aug 19 11:00:00 2005

CC The invention relates to antisense oligonucleotides targeted to cyclin-
CC dependent kinase 6, and which inhibit the expression of cyclin-dependent
CC kinase 6. The antisense oligonucleotides are useful for treating a
CC disease or condition associated with cyclin-dependent kinase 6, such as a
CC hyperproliferative disorder (e.g. cancer), or conditions arising from
CC bacterial or viral infections, or involving aberrant apoptosis. They are
CC also useful in research and diagnostics for modulating the expression of
CC cyclin-dependent kinase 6. The present sequence represents a cyclin-
CC dependent kinase 6 antisense oligonucleotide. Note: Seqid 15-134 are also
CC used in the sequence listing but these sequences do not match seqid 15-
CC 134 displayed in Tables 1 and 2 (page 30-34).
XX
SQ Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 602 AAAGACTTCATAGTAGG 619
||| ||||| |||||
Db 18 AAACACTTCAGAGTAGG 1

RESULT 165

AD056108
ID AD056108 standard; DNA; 20 BP.

AC AD056108;

XX 29-JUL-2004 (first entry)

XX Cyclin-dependent kinase 6, antisense oligonucleotide #172.

XX antisense therapy; cyclin-dependent kinase 6;
KW hyperproliferative disorder; cancer; bacterial infection;
KW viral infection; apoptosis; ss; probe; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX modified_base 1..20

XX /tag= b

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone. All cytidines are 5-

XX methylcytidines."

XX modified_base 1..5

XX /tag= a

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX modified_base 16..20

XX /tag= c

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

PN US2004087523-A1.

XX 06-MAY-2004.

PD 31-JUL-2002; 2002US-00210802.

XX 31-JUL-2002; 2002US-00210802.

PR (ISIS-) ISIS PHARM INC.

XX Freier SM, Dobie KW;

XX WPI; 2004-356241/33.

XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding cyclin-dependent kinase 6, useful for treating
XX cancer, bacterial/viral infection or conditions involving aberrant
XX apoptosis.

PS Example 15; Page 32; 68pp; English.

XX The invention relates to antisense oligonucleotides targeted to cyclin-
CC dependent kinase 6, and which inhibit the expression of cyclin-dependent
CC kinase 6. The antisense oligonucleotides are useful for treating a
CC disease or condition associated with cyclin-dependent kinase 6, such as a
CC hyperproliferative disorder (e.g. cancer), or conditions arising from
CC bacterial or viral infections, or involving aberrant apoptosis. They are
CC also useful in research and diagnostics for modulating the expression of
CC cyclin-dependent kinase 6. The present sequence represents a cyclin-
CC dependent kinase 6 antisense oligonucleotide. Note: Seqid 15-134 are also
CC used in the sequence listing but these sequences do not match seqid 15-
CC 134 displayed in Tables 1 and 2 (page 30-34).
XX

SQ Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 602 AAAGACTTCATAGTAGG 619
||| ||||| |||||
Db 3 AAACACTTCAGAGTAGG 20

RESULT 166

ADN31001/c

ID ADN31001 standard; DNA; 20 BP.

XX ADN31001;

XX 29-JUL-2004 (first entry)

XX Human Int6 cDNA PCR primer #5.

XX Human; Int6; PCR; ss; mammary epithelial cellular growth; cancer;

KW cytostatic; primer.

XX Homo sapiens.

XX US6737251-B2.

XX 18-MAY-2004.

XX 14-MAY-2001; 2001US-00858152.

XX 09-FEB-1995; 95US-00385998.

XX 09-FEB-1996; 96US-00875847.

XX 09-FEB-1996; 96WO-US001884.

XX 23-AUG-1999; 99US-00378842.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Marchetti A, Buttitta F, Smith GH, Callahan R;

XX WPI; 2004-387097/36.

XX Novel tumor Int6 recombinant protein that deregulates mammary epithelial
XX cellular growth, useful for treating cancer.
XX Example 13; SEQ ID NO 9; 44pp; English.
XX The invention relates to the Int6 protein and the cDNA encoding it. The
XX Int6 protein deregulates mammary epithelial cellular growth. The cDNA and
XX protein are useful as vaccines for treating cancer. This sequence
XX represents a PCR primer used to amplify cDNA encoding the human Int6
XX protein of the invention.
XX Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 1.3%; Score 14.8; DB 1; Length 20;

CC asthma. This sequence represents a murine IL-5 receptor a DNA antisense oligonucleotide of the invention.

CC CC

XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

SQ Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 748 GCTGCCACCTTATGCAGT 765
1 GCTGCCACCTGTCAGT 18

Db

RESULT 169
ADRI12130
ID ADRI12130 standard; DNA; 20 BP.
XX AC
ADRI12130;
XX AC
DT 23-SEP-2004 (first entry)
XX DE Murine interleukin-5 (IL-5) receptor a DNA antisense oligonucleotide #72.
XX KW Mouse; interleukin-5; IL-5; ss; antisense oligonucleotide;
XX IL-5 receptor a; phosphorothioate; 2'-O-methoxyethyl sugar moiety;
KW 5-methylcytosine; IL-5 signal transduction; apoptosis;
KW eosinophilic syndrome; asthma; antiasthmatic; cytostatic.
XX KW
OS Mus musculus.
XX US2004121376-A1.
XX 24-JUN-2004.
XX 06-OCT-2003; 2003US-00679532.
XX 26-MAR-1999; 99US-00280799.
PR 17-MAR-2000; 2000WO-US007318.
PR 07-MAR-2001; 2001US-00800629.
XX (DEAN/) DEAN N M.
PA (KARR/) KARRAS J G.
PA (MCKA/) MCKAY R.
PA (MANO/) MANOHARAN M.
XX Dean NM, Karraas JG, McKay R, Manoharan M;
PI WPI; 2004-479669/45.
XX New antisense compound modulating interleukin-5 signal transduction, useful in promoting apoptosis and in treating eosinophilic syndrome or asthma.
XX Example 25; SEQ ID NO 152; 77pp; English.
XX The invention relates to an antisense compound that modulates interleukin-5 (IL-5) signal transduction. The antisense compound is an antisense oligonucleotide targeted to a nucleic acid molecule encoding a mammalian IL-5 or IL-5 receptor a, where the antisense compound modulates the expression of mammalian IL-5 or IL-5 receptor a. The antisense oligonucleotide comprises at least one modified internucleoside linkage, i.e. a phosphorothioate linkage, or a peptide nucleic acid, at least one modified sugar moiety, i.e. a 2'-O-methoxyethyl sugar moiety, and at least one modified nucleobase, i.e. 5-methylcytosine. Altering the ratio of the isoforms of mammalian IL-5 receptor a in mammalian cells or tissues comprises contacting the cells or tissues with an antisense compound so that the ratio of the mammalian IL-5 receptor a isoforms is altered. Treating a mammal having a disease or condition associated with IL-5 signal transduction or IL-5 or IL-5 receptor a expression, or a disease or condition characterised by a reduction in apoptosis comprises administering to the mammal a therapeutic or prophylactic amount of an antisense compound so that IL-5 signal transduction, IL-5 or IL-5 receptor a expression, or that IL-5 receptor a is modulated, the ratio of IL-5 receptor a isoforms is altered, or expression of membrane IL-5 receptor a is modulated. The antisense compounds, methods and compositions are useful in promoting apoptosis and in treating eosinophilic syndrome and

CC CC

XX Sequence 21 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 1 Other;

SQ Query Match 1.3%; Score 14.8; DB 1; Length 21;

Best Local Similarity 80.0%; Pred. No. 1.5e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 1;

QY 331 TCTTGTCTGTGGTGTGCA 350
||||| : : : : :
Db 2 TCTTGTATGGGCTGTGCA 21

RESULT 171
ABS66964
ID ABS66964 standard; DNA; 21 BP.
AC ABS66964;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human MRP-1 polymorphic DNA region #229.
XX
XX Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX WO200259142-A2.
PN
XX 01-AUG-2002.
PD
XX 25-JAN-2002; 2002WO-EP000796.
PF
XX 26-JAN-2001; 2001EP-00101651.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
PA
XX Brinkmann U, Hoffmeyer S, Mornhinweg E;
PI
XX WPI; 2002-657475/70.
DR
XX Novel multidrug resistance-associated protein 1 polymnucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
XX Example 2; Page 82; 198pp; English.
PS
XX The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polymnucleotide. The polymnucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
||||| : : : : :
Db 4 AATCACTCAACCTCTCTG 21

RESULT 172
ABS66965/c
ID ABS66965 standard; DNA; 21 BP.
XX
XX ABS66965;
AC
XX
XX 29-NOV-2002 (first entry)
XX

DE Human MRP-1 polymorphic DNA region #230.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX WO200259142-A2.
PN
XX 01-AUG-2002.
PD
XX 25-JAN-2002; 2002WO-EP000796.
PF
XX 26-JAN-2001; 2001EP-00101651.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
PA
XX Brinkmann U, Hoffmeyer S, Mornhinweg E;
PI
XX WPI; 2002-657475/70.
DR
XX Novel multidrug resistance-associated protein 1 polymnucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
XX Example 2; Page 82; 198pp; English.
PS
XX The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polymnucleotide. The polymnucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
||||| : : : : :
Db 18 AATCACTCAACCTCTCTG 1

RESULT 173
ABS66968
ID ABS66968 standard; DNA; 21 BP.
XX
AC ABS66968;
XX
XX 29-NOV-2002 (first entry)
DT
XX Human MRP-1 polymorphic DNA region #233.
DE
XX Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX WO200259142-A2.
PN
XX 01-AUG-2002.
PD
XX 25-JAN-2002; 2002WO-EP000796.
PF
XX 26-JAN-2001; 2001EP-00101651.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
PA

XX Brinkmann U, Hoffmeyer S, Mornhinweg E;
 XX WPI; 2002-657475/70.
 XX Novel multidrug resistance-associated protein 1 polynucleotide useful for
 PT diagnosis and treatment of cancer and multidrug resistance related
 PT diseases, and for identifying single nucleotide polymorphisms.
 XX
 XX Claim 1; Page 82; 198pp; English.
 XX The invention relates to a multidrug resistance-associated protein 1 (MRP
 CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
 CC for identifying a single nucleotide polymorphism and for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
 CC of the activity of a molecular variant of MRP-1. The sequences are useful
 CC for diagnosing a disorder related to the presence of a molecular variant
 CC of MRP-1 or susceptibility to such a disorder, where the disorder is
 CC cancer (particularly renal cancer) or a disease related to multidrug
 CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
 XX
 XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 Db 4 AATCACTMAACCTCTCTG 21
 RESULT 174
 ABS66966
 ID ABS66966 standard; DNA; 21 BP.
 AC ABS66966;
 XX 29-NOV-2002 (first entry)
 DT Human MRP-1 polymorphic DNA region #231.
 DE Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
 XX renal cancer; cytostatic; single nucleotide polymorphism.
 KW Homo sapiens.
 OS WO200259142-A2.
 PN 01-AUG-2002.
 PD 25-JAN-2002; 2002WO-EP000796.
 PF 26-JAN-2001; 2001EP-00101651.
 PR (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
 PA Brinkmann U, Hoffmeyer S, Mornhinweg E;
 XX WPI; 2002-657475/70.
 XX Novel multidrug resistance-associated protein 1 polynucleotide useful for
 PT diagnosis and treatment of cancer and multidrug resistance related
 PT diseases, and for identifying single nucleotide polymorphisms.
 XX
 XX Example 2; Page 82; 198pp; English.
 XX The invention relates to a multidrug resistance-associated protein 1 (MRP
 CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
 CC for identifying a single nucleotide polymorphism and for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
 CC of the activity of a molecular variant of MRP-1. The sequences are useful
 CC for diagnosing a disorder related to the presence of a molecular variant
 CC of MRP-1 or susceptibility to such a disorder, where the disorder is
 CC cancer (particularly renal cancer) or a disease related to multidrug
 CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
 XX
 XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 Db 4 AATCACTMAACCTCTCTG 21

CC of the activity of a molecular variant of MRP-1. The sequences are useful
 CC for diagnosing a disorder related to the presence of a molecular variant
 CC of MRP-1 or susceptibility to such a disorder, where the disorder is
 CC cancer (particularly renal cancer) or a disease related to multidrug
 CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
 XX
 XX Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 Db 4 AATCACTMAACCTCTCTG 21
 RESULT 175
 ABS66967/c
 ID ABS66967 standard; DNA; 21 BP.
 XX ABS66967;
 AC ABS66967;
 XX 29-NOV-2002 (first entry)
 DT Human MRP-1 polymorphic DNA region #232.
 DE Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
 XX renal cancer; cytostatic; single nucleotide polymorphism.
 KW Homo sapiens.
 OS WO200259142-A2.
 PN 01-AUG-2002.
 PD 25-JAN-2002; 2002WO-EP000796.
 PF 26-JAN-2001; 2001EP-00101651.
 PR (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
 PA Brinkmann U, Hoffmeyer S, Mornhinweg E;
 XX WPI; 2002-657475/70.
 XX Novel multidrug resistance-associated protein 1 polynucleotide useful for
 PT diagnosis and treatment of cancer and multidrug resistance related
 PT diseases, and for identifying single nucleotide polymorphisms.
 XX
 XX Example 2; Page 82; 198pp; English.
 XX The invention relates to a multidrug resistance-associated protein 1 (MRP
 CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
 CC for identifying a single nucleotide polymorphism and for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
 CC of the activity of a molecular variant of MRP-1. The sequences are useful
 CC for diagnosing a disorder related to the presence of a molecular variant
 CC of MRP-1 or susceptibility to such a disorder, where the disorder is
 CC cancer (particularly renal cancer) or a disease related to multidrug
 CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
 XX
 XX Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 Db 18 AATCACTMAACCTCTCTG 1

```

RESULT 176
ABS66969/c
ID ABS66969 standard; DNA; 21 BP.
XX
AC ABS66969;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #234.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
WP1; 2002-657475/70.
XX
Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Claim 1; Page 82; 198pp; English.
XX
The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db ||||| ||||| |||||
18 AATCACTTAACCTCTCTG 1

RESULT 177
ACF62467/c
ID ACF62467 standard; DNA; 21 BP.
XX
AC ACF62467;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:296.
XX
KW Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO2003013534-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008219.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.

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XX WO2003013534-A2.
XX 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008219.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
WP1; 2003-268144/26.
XX
New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
PS Disclosure; Page 40; 86pp; English.
XX
The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db ||||| ||||| |||||
18 AATCACTTAACCTCTCTG 1

RESULT 178
ACF62464
ID ACF62464 standard; DNA; 21 BP.
XX
AC ACF62464;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:293.
XX
KW Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO2003013534-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008219.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.

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Fri Aug 19 11:00:00 2005

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX Disclosure; Page 40; 86pp; English.
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTTAACCTCTCTG 21
RESULT 179
ACF62465/C
ID ACF62465 standard; DNA; 21 BP.
XX ACF62465;
XX 08-OCT-2003 (first entry)
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:294.
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX Synthetic.
XX WO2003013534-A2.
PN
XX 20-FEB-2003.
PD
XX 23-JUL-2002; 2002WO-EP008219.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,

PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX Disclosure; Page 40; 86pp; English.
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTTAACCTCTCTG 1
RESULT 180
ACF62466
ID ACF62466 standard; DNA; 21 BP.
XX ACF62466;
XX 08-OCT-2003 (first entry)
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:295.
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX Synthetic.
XX WO2003013534-A2.
PN
XX 20-FEB-2003.
PD
XX 23-JUL-2002; 2002WO-EP008219.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX Disclosure; Page 40; 86pp; English.
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTTAACCTCTCTG 1

CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
 CC cytosolic activity. The therapeutic applications of (I) is improved,
 CC since it is possible to individually treat a subject with an appropriate
 CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
 CC harmful or toxic effects are efficiently avoided. Unnecessary and
 CC potentially harmful treatment of those subjects who do not respond to the
 CC treatment with substances (nonresponders), as well as the development of
 CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
 CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
 CC exemplification of the present invention

XX SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
 |||||
 Db 4 AATCACTTAACCTCTCTG 21

RESULT 181

ADB21135
 ID ADB21135 standard; DNA; 21 BP.

AC ADB21135;

XX 20-NOV-2003 (first entry)

XX MRP1 based cancer related nucleic acid SEQ ID NO:293.

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
 KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
 KW variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene;
 KW ds.

XX Unidentified.

OS WO2003013533-A2.

PN 20-FEB-2003.

PD 23-JUL-2002; 2002WO-EP008200.

PF 23-JUL-2001; 2001EP-00117608.

PR 24-MAY-2002; 2002EP-00011710.

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PA Heinrich G, Kerb R;

PI WPI; 2003-354397/33.

DR Use of irinotecan or its derivative for preparation of a pharmaceutical
 XX composition for treating cancer in a subject having a genome with a
 PT variant allele comprising a multidrug resistance protein 1
 PT polynucleotide.

XX Claim 8; Page 49; 100pp; English.

XX The present invention describes a method for the use of irinotecan (I) or
 CC its derivative for the preparation of a pharmaceutical composition for
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
 CC cancer, or malignant glioma in a subject having a genome with a variant
 CC allele which comprises a multidrug resistance protein 1 (MRP1)
 CC polynucleotide (II). (I) has cytosolic activity. (I) or its derivative
 CC can be used for the preparation of a pharmaceutical composition for
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
 CC cancer, or malignant glioma in a subject, where the subject is a human
 CC (preferably African or Asian) or a mouse. The present sequence represents
 CC a sequence which is used in the exemplification of the present invention.

XX

SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091

|||||
 Db 4 AATCACTTAACCTCTCTG 21

RESULT 182

ADB21136/C

ID ADB21136 standard; DNA; 21 BP.

AC ADB21136;

XX 20-NOV-2003 (first entry)

XX MRP1 based cancer related nucleic acid SEQ ID NO:294.

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
 KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
 KW variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene;
 KW ds.

XX Unidentified.

OS WO2003013533-A2.

PN 20-FEB-2003.

PD 23-JUL-2002; 2002WO-EP008200.

PF 23-JUL-2001; 2001EP-00117608.

PR 24-MAY-2002; 2002EP-00011710.

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PI Heinrich G, Kerb R;

XX WPI; 2003-354397/33.

DR Use of irinotecan or its derivative for preparation of a pharmaceutical
 XX composition for treating cancer in a subject having a genome with a
 PT variant allele comprising a multidrug resistance protein 1
 PT polynucleotide.

XX Claim 8; Page 49; 100pp; English.

XX The present invention describes a method for the use of irinotecan (I) or
 CC its derivative for the preparation of a pharmaceutical composition for
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
 CC cancer, or malignant glioma in a subject having a genome with a variant
 CC allele which comprises a multidrug resistance protein 1 (MRP1)
 CC polynucleotide (II). (I) has cytosolic activity. (I) or its derivative
 CC can be used for the preparation of a pharmaceutical composition for
 CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
 CC cancer, or malignant glioma in a subject, where the subject is a human
 CC (preferably African or Asian) or a mouse. The present sequence represents
 CC a sequence which is used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091

|||||
 Db 18 AATCACTTAACCTCTCTG 1

```

RESULT 183
ADB21138/c
ID ADB21138 standard; DNA; 21 BP.
XX
AC ADB21138;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:296.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008200.
PF
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008200.
PF
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008200.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
PR
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-354397/33.
XX
XX Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
XX Disclosure; Page 49; 100pp; English.
XX
XX The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.
XX
XX Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
XX
XX Query Match 1.3%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 1.5e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1074 AACCACTTAACCTCTCTG 1091
DB ||||| ||||| |||||
4 AATCACTTAACCTCTCTG 21
XX
RESULT 185
ADB88225/c
ID ADB88225 standard; DNA; 21 BP.
XX
AC ADB88225;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:266.
XX
XX ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW ovarian cancer; pancreatic cancer; malignant glioma;
KW uridine diphosphate glycosyltransferase1 member A1.
XX
OS Homo sapiens.
XX
PN WO2003013536-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008217.
PF

```


CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTTAACCTCTCTG 21
RESULT 188
ADB88226
ID ADB88226 standard; DNA; 21 BP.
XX
AC ADB88226;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:267.
XX
as; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW ovarian cancer; pancreatic cancer; malignant glioma;
KW uridine diphosphate glycosyltransferase1 member A1.
XX
XX Homo sapiens.
XX WO2003013536-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008217.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX WPI; 2003-289896/28.
XX
XX Use of irinotecan to treat cancer patient by determining if patient has
XX variant alleles of UGT1A1 gene, administering increased/decreased amounts
XX of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX Disclosure; Page 53; 107pp; English.
XX
XX The invention relates to the novel use of irinotecan to treat a patient
XX suffering from cancer. This involves determining if the patient has one
XX or more variant alleles of the UGT1A1 gene, and if the patient has one or
XX more of such variant alleles, irinotecan is administered in an increased
XX or decreased amount in comparison to the amount that is administered
XX without regard to the patient's alleles in the UGT1A1 gene. The invention
XX has cytostatic activity. A composition of the invention acts as a
XX topoisomerase I inhibitor. The method is useful for treating a patient,
XX an animal e.g. mouse or a human, preferably African or Asian, suffering
XX from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
XX pancreatic cancer or malignant glioma. The present sequence is udes in
XX the exemplification of the invention.
XX
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTTAACCTCTCTG 21
RESULT 189
ADB97207
ID ADB97207 standard; DNA; 21 BP.
XX
XX ADB97207;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:293.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; ds; CYP3A5; MRP1;
KW TOP1.
XX
XX Homo sapiens.
XX WO2003013537-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
XX treating cancer in subject having genome with variant allele comprising
XX multidrug resistance 1 polynucleotide.
XX
XX Claim 2; Page 77; 130pp; English.
XX
XX The invention relates to the novel use of irinotecan or its derivative
XX for the preparation of pharmaceutical compositions for treating
XX colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
XX malignant glioma in a subject having a genome with a variant allele which
XX comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
XX of the invention has cytostatic activity. The invention is useful for the
XX preparation of pharmaceutical compositions for treating colorectal,
XX cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
XX glioma in a subject (preferably human, more preferably African or Asian)
XX or a mouse. The present sequence is used in the exemplification of the
XX invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTTAACCTCTCTG 21
RESULT 190
ADB97210/c
ID ADB97210 standard; DNA; 21 BP.
XX
XX ADB97210;
XX


```

XX 04-DEC-2003 (first entry)
XX Human MRP1 variant allele sequence fragment SEQ ID NO:296.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX multidrug resistance 1; MDR1; cytosstatic; human; ds; Cyp3A5; MRP1; MDR1;
XX TOPI.
XX
XX Homo sapiens.
XX
XX WO2003013537-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX
XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
XX treating cancer in subject having genome with variant allele comprising
XX multidrug resistance 1 polynucleotide.
XX
XX Disclosure; Page 77; 130pp; English.
XX
XX The invention relates to the novel use of irinotecan or its derivative
XX for the preparation of pharmaceutical compositions for treating
XX colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
XX malignant glioma in a subject having a genome with a variant allele which
XX comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
XX of the invention has cytostatic activity. The invention is useful for the
XX preparation of pharmaceutical compositions for treating colorectal,
XX cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
XX glioma in a subject (preferably human, more preferably African or Asian)
XX or a mouse. The present sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
XX
XX Query Match 1.3%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 1.5e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1074 AACCACTTAACCTCTCTG 1091
XX ||||| ||||| ||||| |||||
XX Db 18 ATCACTTAACCTCTCTG 1
XX
XX RESULT 191
XX ADB97209
XX ID ADB97209 standard; DNA; 21 BP.
XX
XX AC ADB97209;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human MRP1 variant allele sequence fragment SEQ ID NO:295.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX multidrug resistance 1; MDR1; cytosstatic; human; ds; Cyp3A5; MRP1; MDR1;
XX TOPI.
XX
XX Homo sapiens.
XX
XX

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PN WO2003013537-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX
XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
XX treating cancer in subject having genome with variant allele comprising
XX multidrug resistance 1 polynucleotide.
XX
XX Disclosure; Page 77; 130pp; English.
XX
XX The invention relates to the novel use of irinotecan or its derivative
XX for the preparation of pharmaceutical compositions for treating
XX colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
XX malignant glioma in a subject having a genome with a variant allele which
XX comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
XX of the invention has cytostatic activity. The invention is useful for the
XX preparation of pharmaceutical compositions for treating colorectal,
XX cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
XX glioma in a subject (preferably human, more preferably African or Asian)
XX or a mouse. The present sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
XX
XX Query Match 1.3%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 1.5e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1074 AACCACTTAACCTCTCTG 1091
XX ||||| ||||| ||||| |||||
XX Db 4 ATCACTTAACCTCTCTG 21
XX
XX RESULT 192
XX ADB97208/c
XX ID ADB97208 standard; DNA; 21 BP.
XX
XX AC ADB97208;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human MRP1 variant allele sequence fragment SEQ ID NO:294.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX multidrug resistance 1; MDR1; cytosstatic; human; ds; Cyp3A5; MRP1; MDR1;
XX TOPI.
XX
XX Homo sapiens.
XX
XX WO2003013537-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX

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XX WPI; 2003-268145/26.
 XX New use of irinotecan for preparation of pharmaceutical compositions for
 PT treating cancer in subject having genome with variant allele comprising
 PT multidrug resistance 1 polynucleotide.
 XX Claim 2; Page 77; 130pp; English.
 XX The invention relates to the novel use of irinotecan or its derivative
 CC for the preparation of pharmaceutical compositions for treating
 CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
 CC malignant glioma in a subject having a genome with a variant allele which
 CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
 CC of the invention has cytostatic activity. The invention is useful for the
 CC preparation of pharmaceutical compositions for treating colorectal,
 CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
 CC glioma in a subject (preferably human, more preferably African or Asian)
 CC or a mouse. The present sequence is used in the exemplification of the
 CC invention.
 XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 DB 18 AATCACTTAACCTCTCTG 1
 RESULT 193
 ADB92401/c
 ID ADB92401 standard; DNA; 21 BP.
 XX
 AC ADB92401;
 XX
 DT 04-DEC-2003 (first entry)
 XX Human MRP1 variant allele sequence fragment SEQ ID NO:296.
 XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
 KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
 KW multidrug resistance 1; MDR1; cytosstatic; ds; human; UGT1A1; MRP1; TOP1.
 XX Homo sapiens.
 OS
 XX WO2003013535-A2.
 PN
 XX 20-FEB-2003.
 PD
 XX 23-JUL-2002; 2002WO-EP008220.
 PF
 XX 23-JUL-2001; 2001EP-00117608.
 PR
 XX 24-MAY-2002; 2002EP-00011710.
 XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 PA
 XX Heinrich G, Kerb R;
 PI
 XX WPI; 2003-342400/32.
 XX
 XX New use of irinotecan for preparation of pharmaceutical compositions for
 PT treating cancer in subject having genome with variant allele comprising
 PT multidrug resistance 1 polynucleotide.
 XX Disclosure; Page 48; 104pp; English.
 XX The invention relates to a novel use of irinotecan or its derivative for
 CC the preparation of a pharmaceutical composition for treating colorectal,
 CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
 CC glioma in a subject having a genome with a variant allele which comprises
 CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
 CC invention has cytostatic activity. The present sequence is used in the
 CC exemplification of the invention.
 XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 DB 18 AATCACTTAACCTCTCTG 1
 RESULT 195
 ADB92398

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
 CC invention has cytostatic activity. The present sequence is used in the
 CC exemplification of the invention.
 XX Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 DB 18 AATCACTTAACCTCTCTG 1
 RESULT 194
 ADB92399/c
 ID ADB92399 standard; DNA; 21 BP.
 XX
 AC ADB92399;
 XX
 DT 04-DEC-2003 (first entry)
 XX Human MRP1 variant allele sequence fragment SEQ ID NO:294.
 XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
 KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
 KW multidrug resistance 1; MDR1; cytosstatic; ds; human; UGT1A1; MRP1; TOP1.
 XX Homo sapiens.
 OS
 XX WO2003013535-A2.
 PN
 XX 20-FEB-2003.
 PD
 XX 23-JUL-2002; 2002WO-EP008220.
 PF
 XX 23-JUL-2001; 2001EP-00117608.
 PR
 XX 24-MAY-2002; 2002EP-00011710.
 XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 PA
 XX Heinrich G, Kerb R;
 PI
 XX WPI; 2003-342400/32.
 XX
 XX New use of irinotecan for preparation of pharmaceutical compositions for
 PT treating cancer in subject having genome with variant allele comprising
 PT multidrug resistance 1 polynucleotide.
 XX Disclosure; Page 48; 104pp; English.
 XX The invention relates to a novel use of irinotecan or its derivative for
 CC the preparation of a pharmaceutical composition for treating colorectal,
 CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
 CC glioma in a subject having a genome with a variant allele which comprises
 CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
 CC invention has cytostatic activity. The present sequence is used in the
 CC exemplification of the invention.
 XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1074 AACCACTTAACCTCTCTG 1091
 DB 18 AATCACTTAACCTCTCTG 1
 RESULT 195
 ADB92398

CC further relates to: an oligonucleotide containing single nucleotide
CC polymorphisms; a PCR primer set chosen from the combination of two DNA
CC fragments from any one of 1220 fully defined sequences as given in
CC specification; a labelling probe containing the SNP containing oligo; and
CC a microarray equipped with the SNP containing oligo. The isolated human
CC gene of the invention is useful for detecting the single nucleotide
CC polymorphisms in human gene. The isolated human gene is also useful for
CC diagnosis of disease and determination of side effect to a medical agent.
CC The isolated human gene is also effective in detecting single nucleotide
CC polymorphisms in a human gene. This polynucleotide sequence represents
CC one of the PCR primers used in the single nucleotide polymorphism
CC detection method of the invention.

XX Sequence 21 BP; 3 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
SQ

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 899 ACCAAGAGCTCAACATT 916
DB 19 ACCAAGGAGCTCAACATT 2

RESULT 198
ADP46739/c
ID ADP46739 standard; DNA; 21 BP.
XX
AC ADP46739;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human c-Cbl siRNA sense strand, SEQ ID 75.
XX
KW Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour;
KW fat deposition; metabolic rate; lean muscle mass; body fat; Cbl;
KW multi-adaptor protein; feeding disorder; glucose uptake disorder;
KW metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl;
KW siRNA; short interfering RNA; ds; RNA interference; gene silencing.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004055181-A1.
XX
XX 01-JUL-2004.
XX
XX 16-DEC-2003; 2003WO-AU001676.
XX
XX 16-DEC-2002; 2002AU-00953393.
XX
XX 14-NOV-2003; 2003AU-00906285.
XX
XX (GARV-) GARVAN INST MEDICAL RES.
XX
XX Molero JC, James D;
XX
XX WPI; 2004-488065/46.
XX
XX Identifying compounds capable of modulating feeding behavior, fat
XX deposition, metabolic rate, or the ratio of lean muscle mass to body fat
XX by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity
XX and hypolipidemia.

PS Claim 86; SEQ ID NO 75; 213pp; English.

CC The present invention relates to a method for identifying a compound that
CC is capable of modulating feeding behaviour, fat deposition, metabolic
CC rate, or the ratio of lean muscle mass to body fat in a subject. The
CC method comprises performing an assay to measure a metabolism-associated
CC phenotype that has been determined for a genetically modified non-human
CC animal that comprises a genetic modification within an allele of its Cbl
CC locus, and determining the effect of the compound on the phenotype. The
CC genetic modification reduces or prevents expression of a functional
CC endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
CC protein that is involved in ligand-induced down regulation of receptor
CC tyrosine kinases. The method of the invention is useful in the treatment
CC of feeding disorders or disorders of glucose uptake and metabolism, such
CC as diabetes, obesity and hyperlipidaemia. The present sequence is the

CC endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
CC protein that is involved in ligand-induced down regulation of receptor
CC tyrosine kinases. The method of the invention is useful in the treatment
CC of feeding disorders or disorders of glucose uptake and metabolism, such
CC as diabetes, obesity and hyperlipidaemia. The present sequence is the
CC sense strand for a human c-Cbl siRNA. The siRNA is useful in modulating a
CC metabolism-associated phenotype in a cell, tissue or animal subject.

XX Sequence 21 BP; 0 A; 7 C; 5 G; 9 T; 0 U; 0 Other;
SQ

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 AGGAAGCGGAGCAGCC 50
DB 18 AGGAGCGAGAGCAGCC 1

RESULT 199
ADP46857
ID ADP46857 standard; DNA; 21 BP.
XX
AC ADP46857;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human c-Cbl siRNA antisense strand, SEQ ID 193.
XX
KW Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour;
KW fat deposition; metabolic rate; lean muscle mass; body fat; Cbl;
KW multi-adaptor protein; feeding disorder; glucose uptake disorder;
KW metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl;
KW siRNA; short interfering RNA; ds; RNA interference; gene silencing.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004055181-A1.
XX
XX 01-JUL-2004.
XX
XX 16-DEC-2003; 2003WO-AU001676.
XX
XX 16-DEC-2002; 2002AU-00953393.
XX
XX 14-NOV-2003; 2003AU-00906285.
XX
XX (GARV-) GARVAN INST MEDICAL RES.
XX
XX Molero JC, James D;
XX
XX WPI; 2004-488065/46.
XX
XX Identifying compounds capable of modulating feeding behavior, fat
XX deposition, metabolic rate, or the ratio of lean muscle mass to body fat
XX by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity
XX and hypolipidemia.

PS Claim 86; SEQ ID NO 193; 213pp; English.

CC The present invention relates to a method for identifying a compound that
CC is capable of modulating feeding behaviour, fat deposition, metabolic
CC rate, or the ratio of lean muscle mass to body fat in a subject. The
CC method comprises performing an assay to measure a metabolism-associated
CC phenotype that has been determined for a genetically modified non-human
CC animal that comprises a genetic modification within an allele of its Cbl
CC locus, and determining the effect of the compound on the phenotype. The
CC genetic modification reduces or prevents expression of a functional
CC endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
CC protein that is involved in ligand-induced down regulation of receptor
CC tyrosine kinases. The method of the invention is useful in the treatment
CC of feeding disorders or disorders of glucose uptake and metabolism, such
CC as diabetes, obesity and hyperlipidaemia. The present sequence is the

```

CC antisense strand for a human c-Cbl siRNA. The siRNA is useful in
CC modulating a metabolism-associated phenotype in a cell, tissue or animal
CC subject.
XX
SQ Sequence 21 BP; 7 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
    Query Match      1.3%; Score 14.8; DB 1; Length 21;
    Best Local Similarity 88.9%; Pred. No. 1.5e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 AGGAGCGCGAGGAGCGCC 50
DB 2 AGGGAGCGAGAGCGCGCC 19

RESULT 200
ID ADR18488 standard; DNA; 21 BP.
AC ADR18488;
XX
DT 18-NOV-2004 (first entry)
DE Human GOBLIN siRNA antisense strand oligonucleotide SEQ ID NO:269.
XX
KW cancer; GOBLIN; micrometastasis; metastasis; cytostatic; gene therapy;
KW squamous cell carcinoma; hepatocellular carcinoma; melanoma;
KW head and neck cancer; adenocarcinoma; gastrointestinal cancer;
KW renal cell cancer; bladder cancer; prostate cancer;
KW non-squamous carcinoma; glioblastoma; medullablastoma; ovarian cancer;
KW basal cell carcinoma; clear cell carcinoma; endometrioid ovarian cancer;
KW mucinous ovarian cancer; breast cancer; lobular lesion; stromal lesion;
KW ductal carcinoma; ductal adenocarcinoma;
KW proliferative fibrocystic change; epitheliosis; intraductal papilloma;
KW atypical ductal hyperplasia; hyperproliferative disease; human;
KW small interfering RNA; siRNA; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT misc_feature 1..19
FT /tag= a
FT /note= "human GOBLIN mRNA target sequence"
FT misc_feature 20..21
FT /tag= b
FT /note= "3'-extension dinucleotide TT overhang"
XX
PN WO2004072285-A1.
XX
PD 26-AUG-2004.
XX
PP 12-FEB-2004; 2004WO-AU000169.
XX
PR 14-FEB-2003; 2003US-0447697P.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Stanford P, Harris J, Ormandy C;
XX
DR WPI; 2004-625877/60.
XX
PT Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises
PT determining the level of expression of a GOBLIN gene in a sample.
XX
PS Claim 93; SEQ ID NO 269; 217pp; English.
XX
CC The present invention describes a method for detecting a cancer cell in a
CC subject. The method comprises determining the level of expression of a
CC GOBLIN gene in a sample of the subject where elevated expression of the
CC gene is indicative of a primary cancer or its micrometastasis or
CC metastasis. Also described: (1) an isolated GOBLIN nucleic acid molecule;
CC (2) a vector comprising the isolated nucleic acid of (1); (3) a

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```

CC monoclonal or polyclonal antibody that binds specifically to a GOBLIN
CC polypeptide; (4) an isolated GOBLIN polypeptide, or its immunogenic
CC epitope; (5) a fusion protein comprising the isolated polypeptide of (4);
CC (6) a method of identifying a compound that reduces or antagonises
CC expression of a GOBLIN gene; (7) a process for identifying or determining
CC and producing a compound; (8) an isolated nucleic acid that antagonises
CC expression of a GOBLIN gene, where the nucleic acid comprises a
CC nucleotide sequence comprising any of the 21 bp sequences of SEQ ID
CC NOS:46-353; (9) an isolated antisense nucleic acid that antagonises
CC expression of a GOBLIN gene, where the nucleic acid comprises a
CC nucleotide sequence capable of selectively hybridising to mRNA encoded by
CC the isolated nucleic acid of (1); and (10) a process for monitoring the
CC efficacy of treatment of a cancer in a subject. GOBLIN sequences have
CC cytotostatic activity, and can be used in gene therapy. An isolated GOBLIN
CC nucleic acid molecule can be used for detecting a cancer cell. An
CC isolated GOBLIN polypeptide can be used for producing an antibody. The
CC method, nucleic acid molecules and the encoded polypeptides, and
CC antibodies can be used for detecting a cancer, e.g. squamous cell
CC carcinoma, hepatocellular carcinoma, melanoma, head and neck cancer,
CC adenocarcinoma, gastrointestinal cancer (e.g. gastric, colon, or
CC pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer,
CC non-squamous carcinoma, glioblastoma, medullablastoma, ovarian cancer
CC (e.g. basal cell carcinoma, clear cell carcinoma, endometrioid ovarian
CC cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular
CC lesion, stromal lesion, ductal carcinoma, ductal adenocarcinoma,
CC proliferative fibrocystic change, epitheliosis, intraductal papilloma, or
CC atypical ductal hyperplasia) in a subject. The antagonist of GOBLIN
CC function, method, and compound are useful for treating hyperproliferative
CC disease, like cancer. The present sequence represents a small interfering
CC RNA (siRNA) oligonucleotide targeted to human GOBLIN, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
    Query Match      1.3%; Score 14.8; DB 1; Length 21;
    Best Local Similarity 88.9%; Pred. No. 1.5e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 828 CATGACCCAGGAGGCGCG 845
DB 1 CTTGACCGGAGGAGGCGG 18

RESULT 201
ID ADR18487/C
XX ADR18487 standard; DNA; 21 BP.
AC ADR18487;
XX
DT 18-NOV-2004 (first entry)
DE Human GOBLIN siRNA sense strand oligonucleotide SEQ ID NO:268.
XX
KW cancer; GOBLIN; micrometastasis; metastasis; cytostatic; gene therapy;
KW squamous cell carcinoma; hepatocellular carcinoma; melanoma;
KW head and neck cancer; adenocarcinoma; gastrointestinal cancer;
KW renal cell cancer; bladder cancer; prostate cancer;
KW non-squamous carcinoma; glioblastoma; medullablastoma; ovarian cancer;
KW basal cell carcinoma; clear cell carcinoma; endometrioid ovarian cancer;
KW mucinous ovarian cancer; breast cancer; lobular lesion; stromal lesion;
KW ductal carcinoma; ductal adenocarcinoma;
KW proliferative fibrocystic change; epitheliosis; intraductal papilloma;
KW atypical ductal hyperplasia; hyperproliferative disease; human;
KW small interfering RNA; siRNA; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT misc_feature 1..19
FT /tag= a
FT /note= "human GOBLIN mRNA target sequence"
FT misc_feature 20..21
FT /tag= b
FT /note= "3'-extension dinucleotide TT overhang"
XX
PN WO2004072285-A1.
XX
PD 26-AUG-2004.
XX
PP 12-FEB-2004; 2004WO-AU000169.
XX
PR 14-FEB-2003; 2003US-0447697P.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Stanford P, Harris J, Ormandy C;
XX
DR WPI; 2004-625877/60.
XX
PT Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises
PT determining the level of expression of a GOBLIN gene in a sample.
XX
PS Claim 93; SEQ ID NO 269; 217pp; English.
XX
CC The present invention describes a method for detecting a cancer cell in a
CC subject. The method comprises determining the level of expression of a
CC GOBLIN gene in a sample of the subject where elevated expression of the
CC gene is indicative of a primary cancer or its micrometastasis or
CC metastasis. Also described: (1) an isolated GOBLIN nucleic acid molecule;
CC (2) a vector comprising the isolated nucleic acid of (1); (3) a

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Fri Aug 19 11:00:00 2005

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FT /*tag= b
XX /note= "3'-extension dinucleotide TT overhang"
PN WO2004072285-A1.
XX
XX 26-AUG-2004.
XX
XX 12-FEB-2004; 2004WO-AU0000169.
XX
XX 14-FEB-2003; 2003US-0447697P.
XX (GARV-) GARVAN INST MEDICAL RES.
XX
XX Stanford P, Harris J, Ormandy C;
XX WPI; 2004-625877/60.
XX
XX Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises
XX determining the level of expression of a GOBLIN gene in a sample.
XX
XX Claim 93; SEQ ID NO 268; 217pp; English.
XX
XX The present invention describes a method for detecting a cancer cell in a
XX subject. The method comprises determining the level of expression of a
XX GOBLIN gene in a sample of the subject where elevated expression of the
XX gene is indicative of a primary cancer or its micrometastasis or
XX metastasis. Also described: (1) an isolated GOBLIN nucleic acid molecule;
XX (2) a vector comprising the isolated nucleic acid of (1); (3) a
XX monoclonal or polyclonal antibody that binds specifically to a GOBLIN
XX polypeptide; (4) an isolated GOBLIN polypeptide, or its immunogenic
XX epitope; (5) a fusion protein comprising the isolated polypeptide of (4);
XX (6) a method of identifying a compound that reduces or antagonises
XX expression of a GOBLIN gene; (7) a process for identifying or determining
XX and producing a compound; (8) an isolated nucleic acid that antagonises
XX expression of a GOBLIN gene, where the nucleic acid comprises a
XX nucleotide sequence comprising any of the 21 bp sequences of SEQ ID
XX NOS:46-353; (9) an isolated antisense nucleic acid that antagonises
XX expression of a GOBLIN gene, where the nucleic acid comprises a
XX nucleotide sequence capable of selectively hybridising to mRNA encoded by
XX the isolated nucleic acid of (1); and (10) a process for monitoring the
XX efficacy of treatment of a cancer in a subject. GOBLIN sequences have
XX cytostatic activity, and can be used in gene therapy. An isolated GOBLIN
XX nucleic acid molecule can be used for detecting a cancer cell. An
XX isolated GOBLIN polypeptide can be used for producing an antibody. The
XX method, nucleic acid molecules and the encoded polypeptides, and
XX antibodies can be used for detecting a cancer, e.g. squamous cell
XX carcinoma, hepatocellular carcinoma, melanoma, head and neck cancer,
XX pancreatic cancer, renal cell cancer, bladder cancer, prostate cancer,
XX non-squamous carcinoma, glioblastoma, medullablastoma, ovarian cancer
XX (e.g. basal cell carcinoma, clear cell carcinoma, endometrioid ovarian
XX cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular
XX lesion, atypical ductal hyperplasia) in a subject. The antagonist of GOBLIN
XX proliferative fibrocystic change, epitheliosis, intraductal papilloma, or
XX atypical ductal hyperplasia) in a subject. The antagonist of GOBLIN
XX function, method, and compound are useful for treating hyperproliferative
XX disease, like cancer. The present sequence represents a small interfering
XX RNA (siRNA) oligonucleotide targeted to human GOBLIN, which is used in
XX the exemplification of the present invention.
XX
XX Sequence 21 BP; 2 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 1.5e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 828 CATGACCCAGGAGGCCG 845
XX Db 19 CTTGACCCAGGAGGCCG 2
XX
XX RESULT 202
XX ABL52014
```

```
ABL52014 standard; DNA; 15 BP.
ABL52014;
11-JUL-2002 (first entry)
Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:62.
Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
single nucleotide polymorphism; antiinflammatory; neuroleptic;
haplotyping; genotyping; respiratory inflammatory disease;
neuropsychiatric disorder; monoaminergic brain system; primer; ss.
Homo sapiens.
Key Location/Qualifiers
misc_feature 14
/*tag= a
/!note= "polymorphic site indicated by an ambiguity base"
WO200222652-A2.
21-MAR-2002.
17-SEP-2001; 2001WO-US042217.
15-SEP-2000; 2000US-0232895P.
(GENA-) GENAISANCE PHARM INC.
Anastasio AE, Han J, Kliem SE, Sausker EA;
WPI; 2002-393942/42.
Novel genetic variants of soluble carrier family 18 (vesicular
monoamine), member 2 gene useful for screening drugs to treat diseases
e.g. neuropsychiatric disorders involving monoaminergic brain systems.
Claim 17; Page 15; 183pp; English.
The present invention describes an isolated polynucleotide (I) having a
sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a
sequence (SS) of 40023 bp (see ABL51954), and defined by a corresponding
set of polymorphisms whose locations and identities are given in the
specification; or a sequence (S2) complementary to (S1). (I) has
antiinflammatory and neuroleptic activities, and can be used in gene
therapy. Methods from the present invention can be used for haplotyping
and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known
as the vesicular monoamine transporter (VMAT2). (I) is useful in studying
the expression and function of SLC18A2, and in expressing the SLC18A2
protein for use in screening for candidate drugs to treat diseases
related to SLC18A2 activity and in studying the effect of the variation
on the biological activity of SLC18A2 as well as on the binding affinity
of candidate drugs targeting SLC18A2 for the treatment of respiratory
inflammatory diseases such as neuropsychiatric disorders involving
monoaminergic brain systems. The present sequence represents an allele
specific oligonucleotide (ASO) primer for human SLC18A2, which is given
in the present invention
Sequence 15 BP; 0 A; 3 C; 3 G; 8 T; 0 U; 1 Other;
XX
XX Query Match 1.3%; Score 14.6; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 1.4e+02;
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 303 TTGTTTCTGCCTTG 317
XX Db 1 TTGTTTCTGCCTTG 15
XX
XX RESULT 203
```

```

ABK27525
ID  ABK27525 standard; DNA; 15 BP.
XX
AC  ABK27525;
XX
XX
DT  09-APR-2002 (first entry)
XX
DE  Human CTLA4 gene allele-specific oligonucleotide sequencing primer #2.
XX
KW  Human; cytotoxic T-lymphocyte-associated protein 4; CTLA4; haplotyping;
KW  haplotype pair; single nucleotide polymorphism; autoimmune disorder; ss;
KW  genotyping; gene therapy; drug screening; antisense gene therapy; primer;
KW  immunosuppressive; sequencing; PCR; probe.
XX
OS  Homo sapiens.
XX
XX
PN  WO200190122-A2.
XX
XX
PD  29-NOV-2001.
XX
XX
PF  23-MAY-2001; 2001WO-US016905.
XX
XX
PR  23-MAY-2000; 2000US-0206353P.
XX
XX
PA  (GENA-) GENAISSANCE PHARM INC.
XX
XX
PI  Chew A, Choi JY, Messer C;
XX
XX
WPI; 2002-089914/12.
XX
XX
New genetic variants of human cytotoxic T-lymphocyte-associated protein
PT  4, CTLA4 gene for studying expression, function of the gene and
PT  expressing CTLA4 protein useful in identifying drugs to treat autoimmune
PT  disorder.
XX
PS  Claim 17; Page 13; 62pp; English.
XX
XX
The invention relates to single nucleotide polymorphisms in the gene
CC  encoding the human cytotoxic T-lymphocyte-associated protein 4 or CTLA4
CC  protein. A method for haplotyping the CTLA4 gene in an individual
CC  comprises identifying the nucleotide at one or more polymorphic sites and
CC  determining whether one of the copies of the gene is defined by one of
CC  the CTLA4 haplotypes given in the specification or whether both copies
CC  are defined by a haplotype pair. This method is useful in genotyping,
CC  whereby all possible haplotype pairs can be assigned to specific
CC  genotypes. An association between a trait and a haplotype or haplotype
CC  pair of the CTLA4 gene can be identified by comparing the frequency of
CC  the haplotype or haplotype pair in a population exhibiting the trait with
CC  the frequency of the haplotype or haplotype pair in a reference
CC  population, where a higher haplotype frequency in the trait population
CC  indicates the trait is associated with the haplotype or haplotype pair.
CC  CTLA4 and its corresponding DNA are used for studying the expression and
CC  function of CTLA4, for use in screening for candidate drugs to treat
CC  diseases related to CTLA4 activity, such as autoimmune disorders. The
CC  sequences are also useful for studying the effect of variation on the
CC  biological activity of CTLA4 as well as on the binding affinity of
CC  candidate drugs targeting CTLA4. Sequences ABK27518-ABK27549 represent
CC  allele-specific oligonucleotide probes, sequencing primers and PCR
CC  primers used to detect CTLA4 gene polymorphisms
XX
SQ  Sequence 15 BP; 3 A; 3 C; 1 G; 7 T; 0 U; 1 Other;

Query Match      1.3%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  586 TCATGTTCACTTTAA 600
DB  1 TCATGTTCACTTTA 15
|||||

RESULT 204
ABQ78935

ABQ78935 standard; DNA; 16 BP.
XX
AC  ABQ78935;
XX
XX
DT  04-NOV-2002 (first entry)
XX
DE  Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
XX
KW  Mouse; intermediate-conductance potassium channel; dermatological;
KW  antiinflammatory; keratolytic; vulnery; antipsoriatic; atopic eczema;
KW  contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose;
KW  hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIK1;
KW  PCR; primer; ss.
XX
OS  Mus musculus.
XX
XX
PN  WO200253171-A2.
XX
XX
PD  11-JUL-2002.
XX
XX
PF  27-DEC-2001; 2001WO-EP015317.
XX
XX
PR  28-DEC-2000; 2000DE-01065475.
XX
XX
PR  20-MAR-2001; 2001US-0277453P.
XX
XX
PA  (SWIT-) SWITCH BIOTECH AG.
XX
PA  (UYLU-) UNIV LUDWIG MAXIMILIANS.
XX
XX
PI  Goppelt A, Alzheimer C, Koegel H;
XX
XX
WPI; 2002-643295/69.
XX
XX
Use of intermediate-conductance potassium channel proteins for the
PT  diagnosis, prevention and treatment of disorders associated with
PT  disturbed keratinocyte activity, especially psoriasis.
XX
PS  Example 3; Page 119; 121pp; German.
XX
XX
The invention relates to a novel use of intermediate-conductance
CC  potassium channel proteins. The proteins of the invention have
CC  dermatological, antiinflammatory, keratolytic, vulnery, and
CC  antipsoriatic activity. The method is used especially in the field of
CC  damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo,
CC  hyperkeratosis, actinic keratosis, hypertrophic scars, keloids, lentigo,
CC  aged skin, ulcers and especially psoriasis. The sequence represents a PCR
CC  primer for the mouse potassium channel protein mIK1 of the invention
XX
SQ  Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      1.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  265 CTGTCGGGAACCTGGCA 280
DB  1 CTGTCGGGAACCTGGCA 16
|||||

RESULT 205
AAA18571
ID  AAA18571 standard; RNA; 17 BP.
XX
XX
AC  AAA18571;
XX
XX
DT  19-JUN-2000 (first entry)
XX
XX
DE  Human TIE-2 substrate sequence SEQ ID NO:1797.
XX
XX
Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW  integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW  hammerhead ribozyme; angiogenic factor; cycostatic; antidiabetic;
KW  ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW  dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;

```

KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 56; Page 103; 305pp; English.
XX
XX The present invention describes enzymatic cleavage of RNA molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA1767 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA1768 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 9 A; 1 C; 3 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 75.0%; Pred. No. 1.6e+02;
XX Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1023 ATCATAGAGAGTAAA 1038
XX :||:|||||:
XX 2 AUCAUAGAGUAGAAA 17
XX
XX RESULT 206
XX ABN02574/C
XX ID ABN02574 standard; DNA; 17 BP.
XX
XX AC ABN02574;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2566.
XX
XX

KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 2566; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterize and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The sequence in the exemplification of the present invention. N.B.
XX hGDMPLP-1 sequence in this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCTT 758
|||
Db 16 AGGCAGCTGCCACCTT 1

RESULT 207
 ABN02573/c
 ID ABN02573 standard; DNA; 17 BP.
 AC ABN02573;
 XX
 DT 29-MAY-2002 (first entry)
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2565.
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (ABOM-) ABOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 2565; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised in chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 743 AGGCAGCTGCCACCTT 758
 DB 17 AGGCAGCTGCCGCGCTT 2
 RESULT 208
 ABK19407
 ID ABK19407 standard; RNA; 17 BP.
 XX
 AC ABK19407;
 XX
 DT 09-APR-2002 (first entry)
 DE Human ERG Amberzyme target sequence Seq ID No 2054.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberosus scleriosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200188124-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX
 DR WPI; 2002-082995/11.
 XX
 PT Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 PS Claim 4; Page 128; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus scleriosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and

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CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 1.6e+02;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 959 TGGACCCAGGACATT 974
 Db 1 UGGACUCAGGACAUU 16
 RESULT 209
 ABK17677
 ID ABK17677 standard; RNA; 17 BP.
 XX
 AC ABK17677;
 XX
 DT 09-APR-2002 (first entry)
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 324.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO200188124-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 16-MAY-2001; 2001WO-US015866.
 XX
 XX 16-MAY-2000; 2000US-00572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082995/11.
 XX
 DR Novel polynucleotide which down regulates expression of Ets-related gene,
 FT useful for treating cancer, diabetic retinopathy, macular degeneration,
 FT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 XX Claim 4; Page 64; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration, verruca
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 4 G; 0 T; 4 U; 0 Other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 958 CTGGACCCAGGACATT 973
 Db 2 CUGGACUCAGGACAUU 17
 RESULT 210
 ACD52117
 ID ACD52117 standard; RNA; 17 BP.
 XX
 AC ACD52117;
 XX
 DT 24-SEP-2003 (first entry)
 DE HBV inozyme substrate sequence #247.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 XX WO200281494-A1.
 XX
 XX 17-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 XX
 XX 26-MAR-2001; 2001US-00817879.
 XX 08-JUN-2001; 2001US-00877478.
 XX 08-JUN-2001; 2001US-0296876P.
 XX 24-OCT-2001; 2001US-0335059P.
 XX 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MACE/) MACEJAK D.
 XX (MCSW/) MCSWIGGEN J.
 XX (MORR/) MORRISSEY D.
 XX (PANC/) PAVCO P.
 XX (LEEP/) LEE P.
 XX (DRAP/) DRAPER K.
 XX (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 XX Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR

CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules.
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 839 AAGCGCGGGTGGATC 854

Db 16 AAGCGCTGGGTGGATC 1

RESULT 213

AD30660
 ID ADE30660 standard; DNA; 17 BP.

AC ADE30660;

XX 29-JAN-2004 (first entry)

XX Cholesterol homeostasis/adipogenesis related DNA seq id 47.

XX expression vector; anorectic; antiarteriosclerotic; cardiant;
 KW antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;
 KW obesity; atherosclerosis; diabetes mellitus;
 KW coronary artery heart disease; cholesterol homeostasis; ss;
 KW differential expression.

XX Homo sapiens.

XX US2003180764-A1.

XX 25-SEP-2003.

XX 08-JAN-2003; 2003US-00339793.

XX 09-JAN-2002; 2002US-0347286P.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Shang J, Bowen B;

XX WPI; 2003-830986/77.

XX Polynucleotides differentially regulated in response to cholesterol and
 PT adipogenesis are useful to detect and treat associated conditions such as
 PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart
 PT disease.

XX Claim 8; SEQ ID NO 47; 59pp; English.

XX The invention describes a composition comprising at least one expression
 CC vector comprising a polynucleotide of the invention. The composition has
 CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.
 CC The invention is used to detect and treat conditions associated with
 CC elevated cholesterol and lipid or during adipogenesis, particularly
 CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart
 CC disease. This sequence represents a polynucleotide differentially
 CC expressed during cholesterol homeostasis and adipogenesis.

XX Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGTTGT 996

Db 1 GATCCAAAGGAGTTGT 16

RESULT 214

ADI50064/c
 ID ADI50064 standard; DNA; 17 BP.

XX ADI50064;

XX 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SeqID2567.

XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosstatic; virucide; neuroprotective; nectropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

XX Homo sapiens.

XX WO2003025177-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.

XX 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Tellerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

XX Disclosure; SEQ ID NO 2567; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nectropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration.
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpat_sequences

XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 839 AAGCGCGGGTGGATC 854

Db 16 AAGCGCTGGGTGGATC 1

RESULT 215

ACC53731/c
 ID ACC53731 standard; DNA; 17 BP.

ngs.res

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PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUYX//) GU Y.
PA (JIYX//) JI Y.
PA (PENN//) PENN S G.
PA (HANKZ//) HANZEL D K.
PA (RANK//) RANK D.
PA (CHEN//) CHEN W.
PA (SHAN//) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
XX Disclosure; SEQ ID NO 2565; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63102
XX
XX Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
DB 17 AGGCAGCTGCCACCTT 2
RESULT 218
ACN65664/c
ID ACN65664 standard; DNA; 17 BP.
XX
XX ACN65664;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMLP-1 probe SEQ ID NO:2566.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
XX hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX skeletal muscle function.
XX
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OS Homo sapiens.
XX US20041137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX 25-MAY-2001; 2001US-00866108.
XX
XX (GUYX//) GU Y.
XX (JIYX//) JI Y.
XX (PENN//) PENN S G.
XX (HANKZ//) HANZEL D K.
XX (RANK//) RANK D.
XX (CHEN//) CHEN W.
XX (SHAN//) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
XX Disclosure; SEQ ID NO 2566; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63102
XX
XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
DB 16 AGGCAGCTGCCACCTT 1
RESULT 219
AAA85722/c
ID AAA85722 standard; DNA; 19 BP.
XX
XX AAA85722;
XX
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DT 04-DEC-2000 (first entry)
XX Cyclin B1 ribozyme binding site #51.
DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KW Mammalia.
XX WO200032765-A2.
XX 08-JUN-2000.
XX 06-DEC-1999; 99WO-US028772.
XX 04-DEC-1999; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX Disclosure; Page 96; 109pp; English.
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
XX Sequence 19 BP; 4 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 791 GTGCTTGGAGGCGCAG 806
Db 19 GGGCTTGGAGGCGCAG 4

RESULT 220
AAH60884/c
ID AAH60884_standard; DNA; 19 BP.
XX AAH60884;
AC
XX 10-SEP-2001 (first entry)
XX
XX Cyclin B1 ribozyme binding site SEQ ID NO:3308.
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200130362-A2.
PN

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XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-US029500.
XX 26-OCT-1999; 99US-0161532P.
XX (IMMU-) IMMUSOL INC.
XX Robbins JM, Tritz R;
XX WPI; 2001-300427/31.
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX Example 1; Page 312; 408pp; English.
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 4 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 791 GTGCTTGGAGGCGCAG 806
Db 19 GGGCTTGGAGGCGCAG 4

RESULT 221
ABA82563
ID ABA82563_standard; DNA; 19 BP.
XX ABA82563;
AC
XX 25-JAN-2002 (first entry)
XX
XX Zmax1 gene region physical map preparation STS marker #522.
XX Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisenase therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200177327-A1.
PN
XX 18-OCT-2001.
PD
XX 21-JUN-2000; 2000WO-US016951.
PF

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Fri Aug 19 11:00:00 2005

XX 05-APR-2000; 2000US-00543771.
 PR 05-APR-2000; 2000US-00544398.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA Carulli JP, Little RD, Recker RR, Johnson ML;
 XX WPI; 2001-657171/75.
 XX New high bone mass (HBM) and Zmax1 genes and proteins useful for
 PT modulating bone mass for the treatment of e.g. osteoporosis.
 XX Disclosure; Page 37; 443pp; English.
 XX The present invention describes the human Zmax1 gene and the high bone
 CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
 CC genes have osteopathic activities. The genes can be used in gene therapy,
 CC antisense therapy and in the production of vaccines. They can be used in
 CC the diagnosis and treatment of bone disorders including osteoporosis,
 CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
 CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 295 TGGAAATGTTGTTCT 310
 DB 1 TGGAAATGTTGTTCT 16
 RESULT 222
 ABK23360
 ID ABK23360 standard; DNA; 19 BP.
 XX AC ABK23360;
 XX 09-APR-2002 (first entry)
 DE Human Zmax1 cDNA reverse PCR primer #261.
 XX Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
 KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
 KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
 KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
 KW bone development disorder; antiarteriosclerotic; cardiovascular;
 KW osteopathic; cerebroprotective.
 XX Homo sapiens.
 OS WO200192891-A2.
 PN 06-DEC-2001.
 PD 25-MAY-2001; 2001WO-US016946.
 PF 26-MAY-2000; 2000US-00578900.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
 XX Carulli JP, Little RD, Recker RR, Johnson ML;
 XX WPI; 2002-097784/13.
 XX Identifying molecules involved in lipid regulation, useful for
 PT diagnosing, treating or preventing e.g. arteriosclerosis, comprises
 PT identifying a molecule that binds to high bone mass gene or its
 PT corresponding wild type gene.

XX Disclosure; Page 42; 409pp; English.
 PS The invention relates to a method for identifying a molecule involved in
 CC lipid regulation comprising identifying a molecule that binds to or
 CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
 CC gene, Zmax1. Compounds identified by the method are useful for treating,
 CC diagnosing, preventing or screening for normal and abnormal lipid-
 CC associated conditions including arteriosclerosis, cardiovascular
 CC disease, stroke, and osteoporosis. The compounds may also be used in the
 CC treatment or prevention of diabetic atherosclerosis, neurovascular
 CC conditions caused by plaque build-up, poor circulation due to plaque
 CC build-up and associated poor wound healing. The methods may be used in
 CC gene therapy, pharmaceutical development, and diagnostic assays for bone
 CC development disorders. Molecules identified by comparison of Zmax1 and
 CC HBM systems can be used as surrogate markers in pharmaceutical
 CC development, in diagnosis of human or animal bone disease, and in the
 CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
 CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
 CC and adapters of the invention
 XX Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 295 TGGAAATGTTGTTCT 310
 DB 1 TGGAAATGTTGTTCT 16
 RESULT 223
 ACC45943
 ID ACC45943 standard; DNA; 19 BP.
 XX AC ACC45943;
 XX 02-JUN-2003 (first entry)
 DE Human HBM STS marker reverse primer #261.
 XX Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
 KW gene therapy; bone density modulation; bone strength; trabecular number;
 KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
 KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
 XX Homo sapiens.
 OS WO200292764-A2.
 PN 21-NOV-2002.
 PD 13-MAY-2002; 2002WO-US014876.
 PF 11-MAY-2001; 2001US-0290071P.
 PR 17-MAY-2001; 2001US-0291311P.
 PR 01-FEB-2002; 2002US-0353058P.
 PR 04-MAR-2002; 2002US-0361293P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 XX Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
 XX WPI; 2003-129278/12.
 XX New transgenic animals (e.g. mice), useful as models for studying bone
 PT density modulation, developing drugs for treating or preventing bone
 PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
 PT reduced bone density.
 XX Disclosure; Page 58; 603pp; English.
 PS

XX The invention relates to novel transgenic animals expressing the high
 CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
 CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
 CC an LRP5 that is modulated by an altered gene control sequence introduced
 CC by homologous or non-homologous recombination. The transgenic animals are
 CC for the study of bone density modulation or bone mass modulation. The
 CC invention has osteopathic and cytostatic activity. The polynucleotides of
 CC the invention may have a use in gene therapy. The transgenic animals and
 CC nucleic acids are for the study of bone density modulation, where the
 CC bone mass is modulated relative to non-transgenic animals of the same
 CC species in more than one parameter selected from bone density, bone
 CC strength, trabecular number, bone size, or bone tissue connectivity. The
 CC transgenic animals, nucleic acids and methods are useful for identifying
 CC molecules involved in bone development, and for developing pharmaceutical
 CC compositions, which may be employed for treating or preventing bone
 CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
 CC neoplasms of the bone. The transgenic animals and nucleic acids are also
 CC useful in methods for diagnosing diseases involved in bone development, is
 CC or characterised by reduced bone density or mass. The present sequence is
 CC used in the exemplification of the invention

SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TGGAAATGTTGTTCT 310
 |||||
 Db 1 TGGAAATGTTGTTCT 16

RESULT 224

ADB98641
 ID ADB98641 standard; DNA; 19 BP.

XX AC ADB98641;

XX DT 04-DEC-2003 (first entry)

XX DE Sequence tagged site #522 used to prepare Zmax1 (LRP5) gene region map.

XX KW Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
 XX KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.

XX OS Homo sapiens.

XX FN WO200292000-A2.

XX PD 21-NOV-2002.

XX PF 13-MAY-2002; 2002WO-US014877.

XX PR 11-MAY-2001; 2001US-0290071P.

XX PR 17-MAY-2001; 2001US-0291311P.

XX PR 01-FEB-2002; 2002US-0353058P.

XX PR 04-MAR-2002; 2002US-0361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.

XX PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;

XX DR WPI; 2003-129214/12.

XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
 PT diagnosing a HBM-like phenotype in a subject and for preparing a
 PT composition for modulating bone mass and/or lipid levels in a subject
 PT suffering from e.g. osteoporosis.

XX Example 2; Page 65; 629pp; English.

XX

CC The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
 CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
 CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
 CC level modulation. The invention is useful for diagnosing a HBM-like
 CC phenotype in a subject and for preparing a composition for modulating
 CC bone mass and/or lipid levels in a subject suffering from e.g.
 CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)
 CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
 CC region.

SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TGGAAATGTTGTTCT 310
 |||||
 Db 1 TGGAAATGTTGTTCT 16

RESULT 225

ADRL17506

ID ADRL17506 standard; DNA; 19 BP.

XX AC ADRL17506;

XX DT 04-NOV-2004 (first entry)

XX DE Human chromosome 11 Zmax1 region reverse mapping primer #261.

XX KW Human; high bone mass; Zmax1; ss; primer; HBM; osteoporosis; osteopathic;
 XX KW LDL receptor; bone development; metabolic bone disease; PCR.

XX OS Homo sapiens.

XX FN US6780609-B1.

XX PD 24-AUG-2004.

XX PF 05-APR-2000; 2000US-00543771.

XX PR 13-JAN-1998; 98US-0071449P.

XX PR 23-OCT-1998; 98US-0105511P.

XX PR 13-JAN-1999; 99US-00229319.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX PI Carulli JP, Little RD, Recker RR, Johnson ML;

XX DR WPI; 2004-623529/60.

XX New high bone mass gene of chromosome 11Q13.3, encoding protein useful
 PT for treating, diagnosing, preventing, or screening for normal and
 PT abnormal conditions of bone, including metabolic bone diseases, e.g.
 PT osteoporosis.

XX Disclosure; SEQ ID NO 588; 284pp; English.

XX The invention relates to an isolated amino acid protein sequence selected
 CC from an amino acid sequence appearing as ADRL16922 or an amino acid
 CC sequence comprising or consisting of the extracellular domain of
 CC ADRL16922(amino acids 23-1385). ADRL16922 is encoded by the HBM (high bone
 CC mass) allele of the human Zmax1 gene and has sequence similarity to LDL
 CC receptors. Also disclosed are nucleic acids, proteins, cloning vectors,
 CC expression vectors, transformed hosts, methods of developing
 CC pharmaceutical compositions, methods of identifying molecules involved in
 CC bone development, and methods of diagnosing and treating diseases
 CC involved in bone development. Specifically disclosed is the Zmax1 gene
 CC and the high bone mass (HBM) allele on chromosome 11q13.3 encoding
 CC ADRL16922. The protein is useful for treating, diagnosing, preventing, or
 CC screening for normal and abnormal conditions of bone, including metabolic
 CC bone diseases, e.g. osteoporosis. The present sequence is a PCR primer

CC used in the mapping of the Zmax1/HBM gene.
 XX Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTCT 310
 |||||
 DB 1 TCGAATTGTTGTTCT 16

RESULT 226
 ADR48157 ID ADR48157 standard; DNA; 19 BP.
 XX AC ADR48157;
 XX 02-DEC-2004 (first entry)
 XX Human chromosome 11 Zmax1 region reverse mapping primer #261.
 DE Human; ss; PCR; high bone mass; Zmax1; HBM; bone modulation;
 KW bone development disorder; osteoporosis; chromosome 11; gene therapy;
 KW primer.
 XX Homo sapiens.
 OS US2004176582-A1.
 PN 09-SEP-2004.
 PD 10-DEC-2003; 2003US-00731739.
 XX 13-JAN-1998; 98US-0071449P.
 PR 23-OCT-1998; 98US-0105511P.
 PR 13-JAN-1999; 99US-00229319.
 PR 05-APR-2000; 2000US-00544398.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (UYCR-) UNIV CREIGHTON.
 PA Carulli JP, Little RD, Recker RR, Johnson ML;
 XX WFI; 2004-661408/64.
 XX New nucleic acid sequence encoding high bone mass, useful in diagnosing,
 PT treating and/or preventing osteoporosis.
 PT Disclosure; SEQ ID NO 588; 303pp; English.

CC The invention relates to an isolated nucleic acid sequence encoding a
 CC high bone mass protein (HBM). The gene exists in two alleles, Zmax1, the
 CC notional wild-type (the cDNA for which appears as ADR47570 encoding
 CC ADR47572) and the HBM allele (the cDNA for which appears as ADR47571
 CC encoding ADR47573). The two alleles differ by a single nucleotide
 CC polymorphism (G to T at position 582 of ADR47570) causing a Gly to Val
 CC change at position 171 of the protein. Also included are a replicative
 CC cloning vector comprising HBM/Zmax1 (and a replicon operative in an
 CC isolated host cell), an expression vector comprising HBM/Zmax1 operably
 CC linked to a transcription regulatory region, an isolated host cell
 CC transformed with the vector(s), a method for testing a substance as a
 CC therapeutic agent for bone modulation in a host, a method of identifying
 CC a molecule involved in bone modulation, a method for identifying a
 CC (candidate) protein involved in bone modulation, a method of testing for
 CC HBM activity, a method of developing a pharmaceutical for the treatment
 CC of bone development disorders, a method for treating a bone development
 CC disorder in an animal, a method of altering bone development in a host, a
 CC method for diagnostic screening for a genetic predisposition to a bone
 CC development disorder, a diagnostic assay for bone development disorders,
 CC a method of expressing the HBM protein in bone tissue, a bacterial
 CC artificial chromosome comprising HBM/Zmax1 sequence (appearing as

CC ADR47574-ADR47580), a method for amplifying a nucleotide polymorphism in
 CC the Zmax1 or HBM gene, a method for identifying a regulatory element of a
 CC HBM gene and an isolated nucleic acid segment of at least 15 contiguous
 CC nucleotides including a polymorphic site from HBM/Zmax1. The nucleic acid
 CC molecule and the encoded polypeptide, composition, and methods are useful
 CC in diagnosing, treating and preventing a bone development disorder, i.e.
 CC osteoporosis. The gene for HBM/Zmax1 is located on chromosome 11q13.3.
 CC The present sequence is a primer used in the mapping of the HBM/Zmax1
 CC gene.
 XX Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTCT 310
 |||||
 DB 1 TCGAATTGTTGTTCT 16

RESULT 227
 AAX92502/c ID AAX92502 standard; DNA; 20 BP.
 XX AC AAX92502;
 XX 13-SEP-1999 (first entry)
 XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.
 XX Synthetic.
 OS Chlamydothila pneumoniae.
 XX WO9927105-A2.
 XX 03-JUN-1999.
 XX 20-NOV-1998; 98WO-IB001890.
 XX 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX (GEST) GENSET.
 PA Griffais R;
 XX WPI; 1999-357842/30.
 XX Genome sequence of Chlamydia pneumoniae.
 XX Page 1516; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 287 TTCACTACTGGAATTG 302
 Db 19 TTCACTACGGGAATTG 4

RESULT 228
 AAA96394
 ID AAA96394 standard; DNA; 20 BP.

XX AAA96394;

XX 08-FEB-2001 (first entry)

XX Primer used to amplify a sara25/26 polymorphic microsatellite repeat.

XX Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
 KW ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus;
 KW insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;
 KW Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma;
 KW thyroiditis; postpartum thyroiditis; rheumatoid arthritis;
 KW Hashimoto's disease; coeliac disease; PCR primer; ss.

XX Homo sapiens.

OS WO200056856-A2.

XX 28-SEP-2000.

PF 24-MAR-2000; 2000WO-US007938.

PR 25-MAR-1999; 99US-0126215P.

XX (GENY) GENETICS INST INC.

XX Ling V, Wu P, Gray GS;

PI WPI; 2000-628257/60.

XX Determining predisposition of humans to develop autoimmune disease
 PT involves detecting polymorphic microsatellite repeat sequence within
 PT human costimulatory receptor gene locus.

PS Claim 18; Page 151; 160pp; English.

XX PCR primers AAA96393-94 were used to amplify polymorphic microsatellite
 CC repeat (PMR) sequences from the human costimulatory receptor gene locus
 CC (hCGR). The primers are used in the method of the invention. The
 CC specification describes a method for determining the predisposition of a
 CC human subject to develop autoimmune disease. The method comprises
 CC detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the
 CC human costimulatory receptor gene locus (hCGR). PMR sequences vary in
 CC length among individuals and can be amplified to generate products that
 CC differ in size. These products can then be detected by rapid and
 CC convenient high resolution processes. The method is useful for
 CC determining the predisposition of insulin-dependent diabetes mellitus
 CC (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism,
 CC myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis,
 CC rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy.
 CC PMR sequences within hCGR are useful as markers in a variety of assays
 CC and in the field of forensic medicine, disease diagnosis and human genome
 CC mapping

XX Sequence 20 BP; 9 A; 3 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 721 AAATATATTAACGCAG 736

Db 5 AAATATATTAACCCAG 20

RESULT 229
 AAZ72439
 ID AAZ72439 standard; DNA; 20 BP.

XX AAZ72439;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:6795.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

PD 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

PR 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.

XX Claim 9; Page 1679; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 218 TTCATTGCCAAAAGAG 233

Db 5 TTCATTGCCAAAAGAG 20

RESULT 230
 AAA47500

ID AAA47500 standard; cDNA; 20 BP.

XX AAA47500;

XX

Fri Aug 19 11:00:00 2005

DT 20-OCT-2000 (first entry)
XX Primer for amplifying CCR2 chemokine.
DE
XX
XX Secondary lymphoid chemokine; SLC; cancer; hyperproliferative disorders;
KW prostatic hyperplasia; proliferative breast disease;
KW proliferative retinopathy; melanoma; breast cancer; cancer; metastases;
KW suppression; angiogenesis; tumorigenesis; inflammation; immune response;
KW chemotaxis; graft rejection; autoimmune disease; primer; ss.
XX
XX Synthetic.
OS
XX WO200038706-A2.
XX
XX 06-JUL-2000.
XX
XX 28-DEC-1999; 99WO-US031096.
XX
XX 31-DEC-1998; 98US-0114498P.
PR
XX (CHIR) CHIRON CORP.
XX
XX Keting C, Xin H, Chan VWF, Kothakota S, Williams LT, Winter JA;
PI
XX WPI; 2000-465631/40.
XX
XX Treating cancer or hyperproliferative disorder and modulating dendritic
PT cell function in a mammal involves administering secondary lymphoid
PT chemokine to the mammal.
XX
XX Disclosure; Page 28; 53pp; English.
PS
XX Secondary lymphoid chemokines (SLC's), variants, fragments, and the
CC polynucleotides encoding the chemokines, variants and fragments, anti-SLC
CC antibodies or ligands for the CCR7 receptor can be used to modulate
CC dendritic cell function in a mammal which results in a decreased primary
CC immune response. SLC can be used to treat cancer or hyperproliferative
CC disorders such as prostatic hyperplasia, proliferative breast diseases,
CC proliferative retinopathy or pigmented skin lesions. SLC is also useful
CC for treating solid tumours such as melanoma, breast cancer, tumours of
CC the head and neck, cancers or metastases of ovary, endometrium, urinary
CC tract, stomach, testicle, prostate, lung, bladder, pancreas, bone, liver,
CC colon or rectum, or metastases of unknown primary origin. SLC can also be
CC used to suppress angiogenesis particularly angiogenesis involved in
CC cancer, tumorigenesis, metastases and tumour growth, and for mediating
CC recruitment of leukocytes into sites of inflammation and immune
CC responses, particularly, the chemotaxis of dendritic and other cells. SLC
CC is also useful in preventing graft rejection, prevention and treatment of
CC the autoimmune diseases and for enhancing an immune response. Two primers
CC (AAA47499, AAA47500) were used to amplify the sequence encoding the
CC chemokine CCR2
XX
SQ Sequence 20 BP; 1 A; 4 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 781 GCTTGGGATGTGCTT 796
DB 2 GCTTGGTGTGCTT 17
RESULT 231
ABK85315
ID ABK85315 standard; DNA; 20 BP.
XX
AC ABK85315;
XX
XX 13-AUG-2002 (first entry)
XX
XX Human PTP1B antisense oligonucleotide ISIS 142070.
DE
XX

KW Antisense; protein phosphatase 1B; PTP1B; ss; probe; human;
KW type 2 diabetes; obesity; ovarian cancer; chronic myeloid leukaemia;
KW hyperproliferative disease; antidiabetic; anorectic; cytostatic;
KW blood glucose; gene therapy.
XX
XX Homo sapiens.
OS
XX US2002055479-A1.
XX
XX 09-MAY-2002.
XX
XX 14-MAY-2001; 2001US-00854883.
XX
XX 18-JAN-2000; 2000US-00487368.
PR
XX 31-JUL-2000; 2000US-00629644.
XX
XX (COWS/) COWSERT L M.
PA (WYAT/) WYATT J.
PA (FREI/) FREIER S M.
PA (MONI/) MONIA B P.
PA (BUTL/) BUTLER M M.
PA (MCKA/) MCKAY R.
XX
XX Cowsert LM, Wyatt J, Freier SM, Monia BP, Butler MM, Mckay R;
PI
XX WPI; 2002-462914/49.
XX
XX Compound for inhibiting the expression of protein phosphatase 1B (PTP1B)
PT and for treating diabetes, cancer, or obesity, comprises an antisense
PT oligonucleotide targeted to nucleic acid encoding PTP1B.
XX
XX Claim 3; Page 27; 133pp; English.
PS
XX The invention relates to a compound of 8-50 nucleobases in length
CC targeted to a nucleic acid encoding protein phosphatase 1B (PTP1B), where
CC the compound specifically hybridises with and inhibits the expression of
CC PTP1B (e.g. an antisense oligonucleotide). Also included are (1) a
CC compound of 8-50 nucleobases in length which specifically hybridises with
CC an 8 nucleobase portion of an active site on a nucleic acid encoding
CC PTP1B; (2) inhibiting the expression of PTP1B in cells or tissues
CC comprising contacting the cells or tissues with the compound; treating an
CC animal having or suspected of having a disease or condition associated
CC with PTP1B comprising administering the compound; (4) decreasing blood
CC sugar levels in an animal comprising administering the compound; (5)
CC preventing or delaying the onset of a disease or condition associated
CC with PTP1B in an animal comprising administering the compound; and (6)
CC preventing or delaying the onset of an increase in blood glucose levels
CC in an animal comprising administering the compound. The compound is used
CC to inhibit the expression of PTP1B in cells or tissues, to treat or
CC prevent or delay the onset of a disease or condition associated with
CC PTP1B, such as type 2 diabetes, obesity, cancer (especially ovarian
CC cancer, chronic myeloid leukaemia and hyperproliferative diseases in an
CC animal having or suspected of having the disease or condition, and for
CC decreasing blood sugar levels or preventing or delaying the onset of an
CC increase in blood glucose levels in an animal. The compound is also used
CC in diagnostics, therapeutics, prophylaxis, and in research reagents and
CC kits. The present sequence is an antisense compound of the invention
CC targeting human PTP1B
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 343 GGCTGTGATCAATGG 358
DB 1 GGCTGTGATCAATGG 16
RESULT 232
ACCS86742
ID ACC86742 standard; DNA; 20 BP.

XX ACC86742;
 XX
 XX
 DT 04-AUG-2003 (first entry)
 XX
 XX Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:37.
 DE
 XX Vascular endothelial growth factor receptor 1; VEGF receptor; VEGFR;
 KW inhibitor; cytostatic; antirheumatic; antiarthritic; angiogenic;
 KW antinflammatory; antisense gene therapy; hyperproliferative disorder;
 KW cancer; rheumatoid arthritis; angiogenesis; infection; inflammation;
 KW tumour formation; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "This oligonucleotide has a phosphorothioate
 FT backbone and 2'-O-methoxyethyl (2'-MOE) wings at the 5'
 FT and 3' ends, which are 5 nucleotides in length. Also all
 FT cytidine residues are 5-methylcytidines"
 XX
 XX WO2003022227-A2.
 PN
 XX
 XX 20-MAR-2003.
 XX
 XX 12-SEP-2002; 2002WO-US029148.
 XX
 XX 13-SEP-2001; 2001US-00953318.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Watt AT;
 XX
 XX WPI; 2003-301004/29.
 DR
 XX New antisense oligonucleotide targeted to a nucleic acid encoding
 PT vascular endothelial growth factor receptor-1, useful for diagnosing or
 PT treating cancer, rheumatoid arthritis, or diseases or conditions
 PT involving angiogenesis.
 XX
 XX Claim 3; Page 82; 150pp; English.
 PS
 XX The present invention describes a compound (C) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding vascular endothelial growth
 CC factor receptor-1 (VEGFR-1), where the compound inhibits the expression
 CC of VEGFR-1 and specifically hybridises with the nucleic acid encoding
 CC VEGFR-1 or with an 8-nucleobase portion of an active site on the nucleic
 CC acid molecule encoding VEGFR-1. Also described: (1) a composition
 CC comprising (C) and a carrier or diluent; (2) inhibiting the expression of
 CC VEGFR-1 in cells or tissues by contacting the cells or tissues with (C)
 CC so that the expression of VEGFR-1 is inhibited; and (3) treating an
 CC animal having a disease or condition associated with VEGFR-1 by
 CC administering (C) to the animal so that the expression of VEGFR-1 is
 CC inhibited. (C) has antiangiogenic, antirheumatic, antiarthritic,
 CC cytostatic and antiinflammatory activities, and can be used in antisense
 CC gene therapy. The antisense compounds are useful for modulating the
 CC expression of VEGFR-1 and for treating diseases or conditions associated
 CC with the expression of VEGFR-1, such as hyperproliferative disorders
 CC (e.g. cancer), rheumatoid arthritis, or diseases or conditions involving
 CC angiogenesis. The antisense compounds are also useful for diagnostics,
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation, as research reagents and kits, and in
 CC distinguishing between functions of various members of a biological
 CC pathway. The present sequence represents a human VEGFR-2 chimeric
 CC phosphorothioate antisense oligonucleotide, which is used in an example
 CC from the present invention
 XX
 XX Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 626 GTTTTATCTCAGCAA 641
 DB 4 GTTTTATCTCAGCAA 19
 RESULT 233
 ADB68675/c
 ID ADB68675 standard; DNA; 20 BP.
 XX
 XX AC ADB68675;
 XX
 XX DT 04-DEC-2003 (first entry)
 XX
 XX DE Microsomal triglyceride transfer protein antisense oligonucleotide #91.
 XX
 KW microsomal triglyceride transfer protein; antisense oligonucleotide;
 KW hybridisation; microsomal triglyceride transfer protein inhibitor;
 KW cardiant; antiarteriosclerotic; antilipemic; antisense gene therapy;
 KW abnormal lipid metabolism; abnormal cholesterol metabolism;
 KW atherosclerosis; cardiovascular disease; mouse; phosphorothioate; ss;
 KW 2'-O-methoxyethyl.
 XX
 XX OS Synthetic.
 OS Mus musculus.
 XX
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages, and all cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 XX
 XX WO2003018600-A2.
 PN
 XX
 XX 06-MAR-2003.
 XX
 XX 17-JUL-2002; 2002WO-US022799.
 XX
 XX 30-JUL-2001; 2001US-00917963.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Crooke RM, Graham MJ;
 XX WPI; 2003-300705/29.
 XX
 XX New antisense oligonucleotide compounds, useful for diagnosing,
 PT preventing and/or treating conditions with aberrant activity of the
 PT microsomal triglyceride transfer protein, such as atherosclerosis and
 PT heart disease.
 XX
 XX Claim 3; Page 97; 135pp; English.
 PS
 XX The present invention describes compounds (I) comprising 8-50 nucleobases
 CC in length targeted to a nucleic acid molecule encoding a microsomal
 CC triglyceride transfer protein, where the compounds specifically hybridise
 CC with and inhibit the expression of the microsomal triglyceride transfer
 CC protein. Also described: (1) a compound 8-50 nucleobases in length which
 CC specifically hybridises with at least an 8-nucleobase portion of an
 CC active site on a nucleic acid molecule encoding microsomal triglyceride
 CC transfer protein; (2) a composition comprising (I) and a carrier or

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CC diluent; (3) inhibiting the expression of microsomal triglyceride
 CC transfer protein in cells or tissues, comprising contacting the cells or
 CC tissues with (1) so that expression of microsomal triglyceride transfer
 CC protein is inhibited; and (4) treating an animal having a disease or
 CC condition associated with microsomal triglyceride transfer protein,
 CC comprising administering (1) to the animal so that expression of
 CC microsomal triglyceride transfer protein is inhibited. (1) have cardiant,
 CC antiarteriosclerotic and antilipemic activities, and can be used in
 CC antisense gene therapy. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC diseases or conditions associated with aberrant expression or activity of
 CC microsomal triglyceride transfer protein, such as an abnormal lipid or
 CC cholesterol metabolism condition like atherosclerosis and cardiovascular
 CC disease. The present sequence represents a mouse microsomal triglyceride
 CC transfer protein chimeric phosphothioate antisense oligonucleotide,
 CC which is used in an example from the present invention.

XX Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 130 TCTTATGCTGGGATGT 145
 DB 18 TCTTATGCTGGGATGT 3

RESULT 234
 ACF36599/C
 ID ACF36599 standard; DNA; 20 BP.
 XX ACF36599;
 XX 18-DEC-2003 (first entry)
 XX
 XX Coll1a2 cDNA amplifying RT-PCR primer COL-2.
 XX
 XX KRAB; repressor fusion protein; Kruppel-associated box; KAP1; Coll1a2;
 KW cloned cell production; drug screening; luciferase; RT-PCR; primer; ss.
 XX Synthetic.
 OS
 XX WO2003072788-A1.
 XX
 XX 04-SEP-2003.
 XX
 XX 20-FEB-2003; 2003WO-US005347.
 XX
 XX 21-FEB-2002; 2002US-0358599P.
 XX
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PA
 XX Rauscher FJ, Ayyanathan K, Schultz DC;
 XX
 XX WPI; 2003-712733/67.
 DR
 XX Producing a cloned cell containing a stably silenced target gene, useful
 PT in research and drug screening, comprises introducing a nucleic acid
 PT molecule expressing a chimeric repressor fusion protein into a parent
 PT cell.
 XX
 XX Example 7; Page 54; 113pp; English.
 PS
 XX The invention relates to producing a cloned cell containing a stably
 CC silenced target gene. The method involves introducing a nucleic acid
 CC molecule expressing a chimeric repressor fusion protein into a parent
 CC cell. The repressor fusion protein comprises a first amino acid sequence
 CC comprising a Kruppel-Associated Box (KRAB) domain or its variant that
 CC binds to the protein KAP1 and has DNA-dependent repressor activity fused
 CC to a second amino acid targeting sequence that binds to the target gene,
 CC fused to a switch component that, in the presence of a ligand or
 CC inducer, permits the second amino acid sequence to bind to the target

CC gene, where the fusion protein is under the control of regulatory
 CC sequences capable of directing its expression in the parent cell. The
 CC methods are useful for producing cloned cells that are particularly
 CC useful in research and drug screening, e.g. identifying a test molecule
 CC that activates the expression of a stably silenced target gene, or
 CC manipulating expression of target gene in a cell. Sequences ACF36598-99
 CC represent primers used in a RT-PCR assay for detecting levels of Coll1a2
 CC mRNA in NIH3T3 cells

XX Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 600 AGAAGACTTCATAAG 615
 DB 18 AGCAAGACTTCATAAG 3

RESULT 235
 ADI14044
 ID ADI14044 standard; DNA; 20 BP.
 XX ADI14044;
 XX 22-APR-2004 (first entry)
 XX
 XX Antisense DNA oligo to target human PTP1B DNA SeqID 297.
 XX
 XX human; ss; antisense; PTP1B; protein phosphatase 1B; PTPN1;
 KW phosphothioate backbone; hyperproliferative condition; cancer;
 KW cytostatic; antidiabetic; anorectic; type 2 diabetes; obesity.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2, methoxyethyl nucleotides. All cytidine
 FT nucleobases are 5' methylcytidine."
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2, methoxyethyl nucleotides. All cytidine
 FT nucleobases are 5' methylcytidine."
 XX
 XX US2003220282-A1.
 XX
 XX 27-NOV-2003.
 XX
 XX 07-FEB-2003; 2003US-00360510.
 XX
 XX 18-JAN-2000; 2000US-00487368.
 XX 31-JUL-2000; 2000US-00629644.
 XX 14-MAY-2001; 2001US-00854883.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bhanot S, Cowser LM, Wyatt JR, Monia BP, Butler WM, McKay R;
 PI Freier SM;
 XX
 XX WPI; 2004-051719/05.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding PTP1B, useful for treating a disease/condition
 PT associated with PTP1B, such as cancer, diabetes or obesity.
 PT

```

XX Claim 3; SEQ ID NO 297; 143pp; English.
XX
XX This invention relates to novel compositions and methods for modulating
CC the expression of PTP1B (also known as protein phosphatase 1B and PTPN1).
CC Specifically, it refers to antisense compounds that can target and
CC hybridise with a nucleic acid molecule encoding PTP1B, as well as splice
CC variants thereof and inhibit expression accordingly. PTP1B is a tyrosine
CC phosphatase that plays an essential regulatory role in signalling
CC mediated by the insulin receptor and as such is useful for treating
CC diseases such as type 2 diabetes and obesity. Furthermore, PTP1B can
CC suppress transformation of oncogenic genes, such that compositions of
CC this invention can also be used to treat hyperproliferative conditions
CC including cancer. Accordingly, these compounds can be described as having
CC cytostatic, antidiabetic and anorectic activities. This oligonucleotide
CC sequence is an antisense DNA oligo that targets human PTP1B DNA, and
CC which has a phosphorothioate backbone and 2'-O-methoxyethyl wings, used
CC in an exemplification of the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
SQ
    Query Match      1.3%; Score 14.4; DB 1; Length 20;
    Best Local Similarity 93.8%; Pred. No. 1.7e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 GGCTGTGATCAATGG 358
Db 1 GGCTGTGATCAAGG 16

RESULT 236
ADJ25024
ID ADJ25024 standard; DNA; 20 BP.
XX
XX ADJ25024;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 3422.
DE
XX
XX Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX WO2004009541-A2.
PN
XX
XX 29-JAN-2004.
PD
XX
XX 18-JUL-2003; 2003WO-US022410.
PP
XX
XX 19-JUL-2002; 2002US-0397106P.
PR
XX
XX (PHAA ) PHARMACIA CORP.
PA
XX
XX Bhat BG;
PI
XX
XX WPI; 2004-132912/13.
DR
XX
XX New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidaemia, low
PT high density lipoprotein or cardiovascular disorders.

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XX Claim 3; SEQ ID NO 3422; 1007pp; English.
XX
XX The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of EL. The antisense oligonucleotides
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
XX Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 U; 0 Other;
SQ
    Query Match      1.3%; Score 14.4; DB 1; Length 20;
    Best Local Similarity 93.8%; Pred. No. 1.7e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GCCCGGGCGGTGGCAG 34
Db 5 GCCCGGGCGGTGGCAG 20

RESULT 237
ADN61693/C
ID ADN61693 standard; DNA; 20 BP.
XX
XX ADN61693;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Corn chromosome 6 SSR marker bnlg 2249 6.04 PCR primer 1 SEQ ID:23.
DE
XX
XX Corn; plant; transmissible; introgression; chromosomal locus;
KW bin 6.02-6.04; bin 10.04-10.06; bin 1.03-1.06; bin 1.08-1.11;
KW bin 3.05-3.07; corn seed; plant breeding; transgenic plant; chromosome 6;
KW SSR marker; marker assisted breeding; PCR; primer; ss.
XX
XX Zea mays.
OS
XX
XX WO2003103377-A2.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 05-JUN-2003; 2003WO-US017626.
PP
XX
XX 06-JUN-2002; 2002US-0386522P.
PR
XX
XX (MONS ) MONSANTO TECHNOLOGY LLC.
PA
XX
XX Lowe BA, Chomet P;
PI
XX
XX WPI; 2004-062179/06.
DR
XX
XX Producing a transformable corn line comprises introgressing at least one
PT chromosomal locus mapping to bin 6.02-6.04 or 10.04-10.06, where the
PT locus is introgressed from a more transformable corn line into a less
PT transformable corn line.
XX
XX Example 3; SEQ ID NO 23; 77pp; English.
XX
XX The invention relates to a method of producing a transformable corn line
CC by introgressing at least one chromosomal locus mapping to bin 6.02-6.04
CC or bin 10.04-10.06, where the locus is introgressed from a more
CC transformable corn line into a less transformable corn line. The
CC invention also relates to corn variety 178-187-20 seed (ATCC accession
CC no. PTA-5183) and corn variety 178-74-25 seed (ATCC accession no. PTA-
CC 5182); progeny of a plant grown from the seed cited above, where the
CC progeny comprises loci mapping to chromosomal bins 1.03-1.06, 1.08-1.11,
CC 3.05-3.07, and 6.02-6.04; a transgenic corn plant produced by
CC transforming the progeny cited above; and hybrid corn seed and plants
CC produced by crossing a corn line with the progeny cited above. Because

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CC more transformable lines are typically agronomically poor, while lines
 CC with superior or desired agronomic traits tend to be less transformable,
 CC the methods of the invention provide a means of testing for the effects
 CC of an introduced gene on traits such as yield, kernel quality and plant
 CC phenotype in earlier plant generations in a breeding programme. Sequences
 CC ADN61671-ADN61702 represent PCR primers used in an example of the
 CC invention to amplify corn SSR markers useful in marker assisted breeding.
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 775 CCTTTGCTGGGGAT 790
 Db 19 CCTTTGCTAGGGAT 4

RESULT 238
 ADN01882
 ID ADN01882 standard; cDNA; 20 BP.
 AC ADN01882;
 XX
 XX 29-JUL-2004 (first entry)
 DE Human HIP1 antisense target sequence ISIS168127.
 XX
 XX Human; antisense; ss; Huntington interacting protein 1; HIP1;
 KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
 KW
 XX Homo sapiens.
 OS
 XX US2004092465-A1.
 PN 13-MAY-2004.
 XX
 XX 11-NOV-2002; 2002US-00293864.
 XX
 XX 11-NOV-2002; 2002US-00293864.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Dobie KW;
 XX
 XX WPI; 2004-374983/35.
 XX
 XX New compound that modulates huntingtin interacting protein 1 expression,
 PT useful in treating an animal having a disease or condition involving
 PT dysregulation of cellular apoptosis.
 XX
 XX Example 15; SEQ ID NO 120; 85pp; English.
 XX
 XX The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
 CC nucleobases in length, is an antisense oligonucleotide, where the
 CC compound specifically hybridises with the nucleic acid molecule encoding
 CC huntingtin interacting protein 1 comprising a sequence appearing as
 CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
 CC Also included are inhibiting the expression of huntingtin interacting
 CC protein 1 in cells or tissues, screening for a modulator of huntingtin
 CC interacting protein 1, a diagnostic method for identifying a disease
 CC state, a kit or assay device comprising the compound and treating an
 CC animal having a disease or condition associated with huntingtin
 CC interacting protein 1 is inhibited. The compound and the methods are
 CC useful in treating an animal having a disease or condition involving
 CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
 CC gene is located on chromosome 7q11.23. The present sequence is an
 CC antisense target region from the HIP1 cDNA.
 XX
 XX Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 GCTGAAGCAGGCTCT 827
 Db 5 GCTGCAGCAGGCTCT 20

RESULT 239
 ADN01807/c
 ID ADN01807 standard; DNA; 20 BP.
 XX
 XX ADN01807;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 XX Human HIP1 antisense oligonucleotide ISIS251612.
 XX
 XX Human; antisense; ss; Huntington interacting protein 1; HIP1;
 KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages and all cytidines are 5
 FT -methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 XX
 XX US2004092465-A1.
 XX
 XX 13-MAY-2004.
 XX
 XX 11-NOV-2002; 2002US-00293864.
 XX
 XX 11-NOV-2002; 2002US-00293864.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Dobie KW;
 XX
 XX WPI; 2004-374983/35.
 XX
 XX New compound that modulates huntingtin interacting protein 1 expression,
 PT useful in treating an animal having a disease or condition involving
 PT dysregulation of cellular apoptosis.
 XX
 XX Example 15; SEQ ID NO 45; 85pp; English.
 XX
 XX The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
 CC nucleobases in length, is an antisense oligonucleotide, where the
 CC compound specifically hybridises with the nucleic acid molecule encoding
 CC huntingtin interacting protein 1 comprising a sequence appearing as
 CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
 CC Also included are inhibiting the expression of huntingtin interacting
 CC protein 1 in cells or tissues, screening for a modulator of huntingtin
 CC interacting protein 1, a diagnostic method for identifying a disease
 CC state, a kit or assay device comprising the compound and treating an
 CC animal having a disease or condition associated with huntingtin
 CC interacting protein 1 is inhibited. The compound and the methods are
 CC useful in treating an animal having a disease or condition involving
 CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
 CC gene is located on chromosome 7q11.23. The present sequence is an
 CC antisense target region from the HIP1 cDNA.
 XX
 XX Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

CC useful in treating an animal having a disease or condition involving
 CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
 CC gene is located on chromosome 7q11.23. The present sequence is an
 CC antisense oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 813 CTGACGAGCGCTCTC 828
 DB 20 CTGACGAGCGCTCTC 5

RESULT 240
 ADN01806/c

ID ADN01806 standard; DNA; 20 BP.
 XX
 AC ADN01806;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human HIP1 antisense oligonucleotide ISIS251611.
 XX
 KW Human; antisense; ss; Huntington interacting protein 1; HIP1;
 KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages and all cytidines are 5
 FT -methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 XX
 FN US2004092465-A1.
 XX
 PD 13-MAY-2004.
 XX
 PF 11-NOV-2002; 2002US-00293864.
 XX
 PR 11-NOV-2002; 2002US-00293864.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dobie KW;
 XX
 WIPI; 2004-374983/35.
 XX
 DR New compound that modulates huntingtin interacting protein 1 expression,
 XX useful in treating an animal having a disease or condition involving
 XX dysregulation of cellular apoptosis.
 XX
 PS Example 15; SEQ ID NO 44; 85pp; English.
 XX
 CC The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
 CC nucleobases in length, is an antisense oligonucleotide, where the
 CC compound specifically hybridises with the nucleic acid molecule encoding
 CC huntingtin interacting protein 1 comprising a sequence appearing as
 CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
 CC Also included are inhibiting the expression of huntingtin interacting
 CC protein 1 in cells or tissues, screening for a modulator of huntingtin
 CC interacting protein 1, a diagnostic method for identifying a disease
 CC state, a kit or assay device comprising the compound and treating an
 CC animal having a disease or condition associated with huntingtin
 CC interacting protein 1 is inhibited. The compound and the methods are
 CC useful in treating an animal having a disease or condition involving
 CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
 CC gene is located on chromosome 7q11.23. The present sequence is an

CC protein 1 in cells or tissues, screening for a modulator of huntingtin
 CC interacting protein 1, a diagnostic method for identifying a disease
 CC state, a kit or assay device comprising the compound and treating an
 CC animal having a disease or condition associated with huntingtin
 CC interacting protein 1 compound so that expression of huntingtin
 CC interacting protein 1 is inhibited. The compound and the methods are
 CC useful in treating an animal having a disease or condition involving
 CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
 CC gene is located on chromosome 7q11.23. The present sequence is an
 CC antisense oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 GCTGACGAGCGCTCTC 827
 DB 16 GCTGACGAGCGCTCTC 1

RESULT 241
 ADN01883

ID ADN01883 standard; cDNA; 20 BP.
 XX
 AC ADN01883;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human HIP1 antisense target sequence ISIS168128.
 XX
 KW Human; antisense; ss; Huntington interacting protein 1; HIP1;
 KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
 XX
 OS Homo sapiens.
 XX
 FN US2004092465-A1.
 XX
 PD 13-MAY-2004.
 XX
 PF 11-NOV-2002; 2002US-00293864.
 XX
 PR 11-NOV-2002; 2002US-00293864.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dobie KW;
 XX
 WIPI; 2004-374983/35.
 XX
 DR New compound that modulates huntingtin interacting protein 1 expression,
 XX useful in treating an animal having a disease or condition involving
 XX dysregulation of cellular apoptosis.
 XX
 PS Example 15; SEQ ID NO 121; 85pp; English.
 XX
 CC The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
 CC nucleobases in length, is an antisense oligonucleotide, where the
 CC compound specifically hybridises with the nucleic acid molecule encoding
 CC huntingtin interacting protein 1 comprising a sequence appearing as
 CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
 CC Also included are inhibiting the expression of huntingtin interacting
 CC protein 1 in cells or tissues, screening for a modulator of huntingtin
 CC interacting protein 1, a diagnostic method for identifying a disease
 CC state, a kit or assay device comprising the compound and treating an
 CC animal having a disease or condition associated with huntingtin
 CC interacting protein 1 is inhibited. The compound and the methods are
 CC useful in treating an animal having a disease or condition involving
 CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
 CC gene is located on chromosome 7q11.23. The present sequence is an

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CC antisense target region from the HIP1 cDNA.
XX
SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 813 CTGAAGCAGGCTCTC 828
Db 1 CTGCAGCAGGCTCTC 16
RESULT 242
ADP78871
ID ADP78871 standard; DNA; 20 BP.
XX
AC ADP78871;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2670.
XX
KW GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..4
FT /*tag= a
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT modified_base 17..20
FT /*tag= b
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT
FT
XX WO2004035763-A2.
XX
XX 29-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US033332.
XX
XX 17-OCT-2002; 2002US-0419268P.
XX (PHAA) PHARMACIA CORP.
XX
XX Broschat KO, Crosby SD;
XX
XX WPI; 2004-348453/32.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
XX (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
XX ischemia/reperfusion injury.
XX
XX Claim 4; SEQ ID NO 2670; 175pp; English.
XX
XX The present invention relates to a compound which specifically hybridizes
XX with a nucleic acid molecule encoding GFAT, and inhibits the expression
XX of GFAT. Specifically claimed are antisense oligonucleotides capable of
XX modulating the expression of GFAT, and which comprise any of the 3063
XX sequences of 20 base pairs, given in the specification. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with GFAT, such as a disease or condition, e.g. diabetes, a
XX cardiovascular or neurologic disorder, ischemia/reperfusion injury.
XX They are also useful in research and diagnostics for modulating the
XX expression of GFAT. The present sequence represents a chimeric
XX phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
XX oligonucleotides inhibit human GFAT expression.

SQ Sequence 20 BP; 5 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 554 TAATATGCTGGGTTTT 569
Db 1 TAATAGCTGGGTTTT 16
RESULT 243
ADP78738
ID ADP78738 standard; DNA; 20 BP.
XX
AC ADP78738;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2537.
XX
KW GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..4
FT /*tag= a
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT modified_base 17..20
FT /*tag= b
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT
FT
XX WO2004035763-A2.
XX
XX 29-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US033332.
XX
XX 17-OCT-2002; 2002US-0419268P.
XX (PHAA) PHARMACIA CORP.
XX
XX Broschat KO, Crosby SD;
XX
XX WPI; 2004-348453/32.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
XX (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
XX ischemia/reperfusion injury.
XX
XX Claim 4; SEQ ID NO 2537; 175pp; English.
XX
XX The present invention relates to a compound which specifically hybridizes
XX with a nucleic acid molecule encoding GFAT, and inhibits the expression
XX of GFAT. Specifically claimed are antisense oligonucleotides capable of
XX modulating the expression of GFAT, and which comprise any of the 3063
XX sequences of 20 base pairs, given in the specification. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with GFAT, such as a disease or condition, e.g. diabetes, a
XX cardiovascular or neurologic disorder, ischemia/reperfusion injury.
XX They are also useful in research and diagnostics for modulating the
XX expression of GFAT. The present sequence represents a chimeric
XX phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
XX oligonucleotides inhibit human GFAT expression.

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 553 TTAATATGCTGGGTTT 568
 Db 5 TTAATAGCTGGGTTT 20

RESULT 244
 ADQ14074
 ID ADQ14074 standard; DNA; 20 BP.
 XX
 AC ADQ14074;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE CAPN3/DYSF PCR primer, SEQ ID 471.
 XX
 KW Human; SCAIP; CAPN3; DYSF; calpain; calcium-activated neutral protease;
 KW limb-girdle muscular dystrophy type 2A; LGMD2A; dysferlin;
 KW limb-girdle muscular dystrophy type 2B; LGMD2B; PCR; primer; ss;
 KW Single Condition Amplification/ Internal Primer.
 XX
 OS Homo sapiens.
 XX
 FN WO2004058985-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 17-DEC-2003; 2003WO-US040278.
 XX
 PR 17-DEC-2002; 2002US-0433774P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 FI Flanigan KM, Weiss RB, Dunn DM, Von Niederhausern A;
 XX
 DR WPI; 2004-525893/50.
 XX
 PT Characterizing a nucleic acid region, useful for detecting genetic
 PT mutations in any large multi-exon gene e.g., those indicating
 PT dystrophinopathy, comprises using a Single Condition
 PT Amplification/Internal Primer (SCAIP) sequencing method.
 XX
 PS Example 9; Page 45; 174pp; English.
 XX
 CC The present invention relates to a Single Condition Amplification/
 CC Internal Primer (SCAIP) sequencing method for direct sequence analysis of
 CC large multi-exon genes from genomic DNA samples and identifying mutations
 CC in multi-exon genes e.g. the dystrophin gene, CAPN3 gene and DYSF gene.
 CC Mutations in the dystrophin gene result in both Duchenne Muscular
 CC Dystrophy (DMD) and Becker Muscular Dystrophy (BMD). Mutations in the
 CC CAPN3 gene, encoding calpain (calcium-activated neutral protease) result
 CC in limb-girdle muscular dystrophy type 2A (LGMD2A) and mutations in the
 CC DYSF gene, encoding dysferlin, result in limb-girdle muscular dystrophy
 CC type 2B (LGMD2B). The method comprises bringing into contact in each of
 CC the reaction chambers an amplicon from a different one of the
 CC amplification reactions and one or more internal sequencing primers
 CC corresponding to the amplicon and analysing the sequences of the
 CC amplicons. The method allows for the rapid, accurate, and economical
 CC analysis of any large multi-exon gene. The method is useful in detecting
 CC genetic mutations in any large multi-exon gene. It is also useful for the
 CC identification and analysis of specific individual genomic mutations
 CC including deletions, point mutations, or its combinations, gene complexes
 CC with multiple exons/introns spanning large genomic regions. The present
 CC sequence is a PCR primer, used in the method of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 449 AGCTGGGAGCAGTGGT 464
 Db 1 AGCTGGGAGCAGTGGT 16

RESULT 245
 ADQ91206/C
 ID ADQ91206 standard; DNA; 20 BP.
 XX
 AC ADQ91206;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE PCR primer used to amplify murine TRPM calcium ion channel DNA Seq 13.
 XX
 KW murine; mouse; transient receptor potential melastatin; TRPM; primer; ss;
 KW pregnenolone sulphate; memory; learning ability; antidepressant;
 KW calcium permeable nonselective cation channel; dementia; nootropic;
 KW neuroprotective; PCR.
 XX
 OS Mus sp.
 XX
 FN WO2004065598-A1.
 XX
 PD 05-AUG-2004.
 XX
 PF 16-JAN-2004; 2004WO-JP000333.
 XX
 PR 17-JAN-2003; 2003JP-00009884.
 XX
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 FI Sano Y, Inamura K, Mochizuki S;
 XX
 DR WPI; 2004-571687/55.
 XX

New polypeptide with calcium ion channel transmissive activity, activated by pregnenolone sulfate, useful for screening memory improving agent, learning ability improving agent and/or anti-dementia agent.

Example 9; SEQ ID NO 13; 114pp; Japanese.

This invention relates to a protein that exhibits calcium ion channel transmissive activity and is activated by pregnenolone sulphate. Specifically, it refers to a novel screening method for identifying a substance that is useful as a memory improving agent, a learning ability improving agent and/or an antidepressant agent. The present invention describes this screening tool as one that involves contacting a test substance with cells expressing the calcium permeable nonselective cation channel and analysing the channel activity to select only those substances, for example pregnenolone sulphate, which can activate the channel. As such, it provides a means to develop pharmaceutical compositions comprising these substances that can be used to treat dementia, as well as improving memory and learning functions. Accordingly, they act as calcium channel agonists and exhibit nootropic and neuroprotective activities. This oligonucleotide sequence is a PCR primer given in an exemplification of the invention.

Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 699 ATGTAGTCACGGTCT 714
 Db 20 ATGAAGTCACGGTCT 5

RESULT 246
 AAT30234
 ID AAT30234 standard; DNA; 19 BP.

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XX AC AAT30234;
XX DT 12-NOV-1996 (first entry)
XX Target nucleic acid for probe with attached intercalating agent.
DE Probe; intercalating agent; flouochrome; hybridisation; assay;
XX detection; thiazole orange; oxazole yellow; flouorescent; fluorescence;
KW ss.
KW Synthetic.
OS EP714986-A1.
XX BP714986-A1.
XX 05-JUN-1996.
XX 01-DEC-1995; 95EP-00308660.
XX 01-DEC-1994; 94JP-00298665.
XX 21-JUL-1995; 95JP-00185599.
XX (TOYJ ) TOSOH CORP.
XX Ishiguro T, Otsuka M, Inoue T, Yawata H, Sugiura Y;
XX WPI; 1996-261625/27.
XX Oligo:nucleotide probes with intercalating fluoro:chrome label - only
PT fluoresces when bound to target sequences, removes need to separate un-
PT hybridised probes.
XX Example 4; Page 10; 32pp; English.
XX Oligonucleotide probes labelled with an intercalating fluorochrome, the
CC characteristics of which change when the probe is hybridised to the
CC target sequence, can be used to detect target nucleic acid in a
CC convenient single step method. The new probes allow homogeneous assays to
CC be performed without the need to separate unhybridised probe. If the
CC probe is added before PCR amplification of target DNA, the PCR time
CC profile can be monitored by measuring the fluorescent intensity of the
CC reaction mixture. The fluorochrome is preferably thiazole orange or
CC oxazole yellow. The method avoids the problem of nonspecific
CC intercalation associated with the use of free fluorochromes
XX Sequence 19 BP; 0 A; 11 C; 0 G; 8 T; 0 U; 0 Other;
XX Query Match 1.3%; Score 14.2; DB 1; Length 19;
XX Best Local Similarity 84.2%; Pred. No. 1.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX RESULT 247
XX AAV10771/c
XX ID AAV10771 standard; DNA; 19 BP.
XX AC AAV10771;
XX DT 21-JUL-1998 (first entry)
XX Human breast cancer gene CH13-2a12-1 primer pch14-sp6-3fb.
XX Breast cancer; malignant transformation; diagnostic; therapeutic;
XX screening; primer; ss.
XX Synthetic.
XX OS Homo sapiens.
XX PN WO9738085-A2.

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XX PD 16-OCT-1997.
XX 09-APR-1997; 97WO-US005930.
XX 10-APR-1996; 96US-0015167P.
XX 05-JUN-1996; 96WO-US009286.
XX 06-JUN-1996; 96US-0019202P.
XX 11-JUL-1996; 96US-00678280.
XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
XX Smith H, Chen L;
XX WPI; 1997-512705/47.
XX Breast cancer genes - used to develop products to design or screen
XX diagnostic reagents or therapeutic compounds.
XX Disclosure; Fig 18; 118pp; English.
XX AAV10748-V10777 are primers used in a method to identify the novel human
XX breast cancer gene CH13-2a12-1 by differential display. The identified
XX genes or fragments of these genes can be used for identifying genes and
XX gene products that are intimately related to malignant transformation or
XX maintenance of the malignant properties of cancer cells. It can also be
XX used to design or screen diagnostic reagents or therapeutic compounds.
XX Kits are included within the scope of the invention
XX Sequence 19 BP; 7 A; 4 C; 1 G; 7 T; 0 U; 0 Other;
XX Query Match 1.3%; Score 14.2; DB 1; Length 19;
XX Best Local Similarity 84.2%; Pred. No. 1.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1009 GTTTCAGAGCATCATCAT 1027
XX Db 19 GTTTGAAAAGCATGATTAT 1
XX RESULT 248
XX AAV46190
XX ID AAA46190 standard; DNA; 19 BP.
XX AC AAA46190;
XX 04-SEP-2000 (first entry)
XX PCR primer used to amplify a fragment of the human HFE gene.
XX Hereditary hemochromatosis gene; HFE gene; iron overload;
XX hereditary atransferrinemia; hypotransferrinemia; aceruloplasminemia;
XX polymetabolic syndrome; chronic liver disease; hematological disease;
XX delayed cutaneous porphyria; hematochromatosis; PCR primer; ss.
XX Homo sapiens.
XX WO200026403-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-FR002656.
XX 29-OCT-1998; 98FR-00013607.
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX (INRM ) INST NAT SANTE & RECH MEDICAL.
XX Rosmorduc O, Hermelin B, Poupon R, Clauser E;
XX WPI; 2000-387228/33.
XX Assessing risk of severe iron overload, e.g. in subjects with hereditary
PT

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PT hemochromatosis, by measuring a profile of the various HFE gene
 XX transcripts.

PS Claim 4; Page 11; 38pp; French.

CC PCR primers AAA46189-90 were used to amplify a fragment of the human
 CC hereditary hemochromatosis (HFE) gene. The primers were used in the
 CC method of the invention. The specification describes a method for
 CC evaluating the risk of developing severe iron overload, particularly in a
 CC predisposed subject. The method comprises determining the profile of the
 CC different transcripts of the HFE gene in a biological sample. The method
 CC is used to determine risk of iron overload, of inherited or acquired
 CC origin, e.g. in cases of hereditary or juvenile hemochromatosis,
 CC hereditary atransferrinemia, hypotransferrinemia, aceruloplasminemia,
 CC polymetabolic syndrome, chronic liver disease, delayed cutaneous
 CC porphyria or hematological disease

XX Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 238 CTATGACTCAGATGCAACC 256

Db 1 CTCTGACTCAGCTGCAGCC 19

RESULT 249

ABT23695

ID ABT23695 standard; DNA; 19 BP.

XX AC

ABT23695;

XX 22-MAY-2003 (first entry)

XX Stabilising reagent method related oligo SEQ ID No 147.

XX Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
 KW specific amplification; pathogenic microorganism; chimeric;
 KW genetic engineering; clinical medicine; ss.

XX Unidentified.

XX WO2002101042-A1.

XX 19-DEC-2002.

XX 12-JUN-2002; 2002WO-JP005832.

XX 12-JUN-2001; 2001JP-00177737.

XX 20-AUG-2001; 2001JP-00249689.

XX (TAKI) TAKARA BIO INC.

XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;

XX Enoki T, Asada K, Kato I;

XX WPI; 2003-148805/14.

XX Method for stabilizing and storing reaction reagents for specific
 PT amplification and detection of nucleic acids particularly in e.g.
 PT identifying pathogenic microorganisms or viruses in sample.

XX Example 15; Page 168; 177pp; Japanese.

XX The invention relates to a novel stabilising reaction reagent for use in
 CC the amplification and/or detection of a target nucleic acid comprising:
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
 CC defined period of time to form a reaction product during the
 CC amplification of such target nucleic acid. The method is useful for
 CC stabilising and long-term storage of reaction reagents for highly

CC sensitive and specific amplification and detection of nucleic acids
 CC particularly in identifying pathogenic microorganisms or viruses in a
 CC sample using chimeric oligonucleotide primers, which is useful in genetic
 CC engineering and clinical medicine. This polynucleotide sequence
 CC represents an oligo relating to the novel stabilising reaction reagent
 CC method of the invention

XX Sequence 19 BP; 6 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1064 CCACTGGCTAAACCACTTA 1082

Db 1 CCAGAGGCTGAACCACTTA 19

RESULT 250

ADI82218

ID ADI82218 standard; DNA; 19 BP.

XX AC

ADI82218;

XX 22-APR-2004 (first entry)

XX RTQ PCR primer #2 for Human LEFTB.

XX Human; ss; PCR; embryonic stem cell; pluripotent stem cell;

XX abnormal cell growth; malignancy; differentiation; primer; RTQ-PCR;

XX realtime quantitative PCR.

XX Homo sapiens.

XX OS

XX US2003224411-A1.

XX 04-DEC-2003.

XX 13-MAR-2003; 2003US-00388578.

XX 13-MAR-2003; 2003US-00388578.

XX (STAN/) STANTON L W.

XX (BRAN/) BRANDENBERGER R.

XX (GOLD/) GOLD J D.

XX (IRVI/) IRVING J M.

XX (MAND/) MANDALAM R.

XX (MOKM/) MOK M.

XX (SHEL/) SHELTON D.

XX Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;

XX Mok M, Shelton D;

XX WPI; 2004-119701/12.

XX Assessing culture of undifferentiated primate pluripotent stem cells by
 PT detecting expression of markers e.g., Zic family member 3, other than
 PT human telomerase reverse transcriptase/octamer binding transcription
 PT factor.

XX Example 4; SEQ ID NO 48; 106pp; English.

XX The invention relates to assessing a culture of undifferentiated primate
 CC pluripotent stem cells (pPS, e.g. embryonic stem cells), involving
 CC detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as
 CC given in specification, other than human telomerase reverse transcriptase
 CC (hTERT) or octamer binding transcription factor (Oct3/4, or a marker
 CC (MR2) such as crypto or podocalyxin-like protein and hTERT and/or Oct3/4
 CC or second marker chosen from (MR2). Also included are maintaining (M2)
 CC pPS cells in a pluripotent state (involves causing them to express one of
 CC the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypothetical
 CC protein FUJ20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsall2,
 CC KRAB-zinc finger protein SZF1-1 or zinc finger protein of cerebellum

CC ZIC2, or any other marker (MR4) chosen from PHD protein Jade-1 (Jade-1),
 CC kruppel-like zinc finger protein (ZNF300), etc., as given in the
 CC specification), causing pps cells to differentiate into a particular
 CC tissue type by causing them to express one of the markers chosen from
 CC (MR3) or (MR4) (or markers chosen from GATA binding protein 3 (GATA3),
 CC core promoter element binding protein (COPBP), etc., as given in the
 CC specification), maintaining pps cells in a pluripotent state (involves
 CC culturing pps cells or their progeny in the presence of a normally
 CC secreted protein that is encoded by a gene that down-regulated upon
 CC differentiation of human embryonic stem (hES) cells, chosen from
 CC Fibrillin 3 gene, LEFT B gene, ZIC3 gene, EPHA1 gene, etc., as given in
 CC the specification), causing pps cells to differentiate (involves
 CC culturing pps cells or their progeny in the presence of a normally
 CC secreted protein that is encoded by a gene that up-regulated upon
 CC differentiation of hES cells, chosen from p311 protein gene, Tax
 CC interaction protein 1 gene, KIAA0853 protein gene, keratin 19 (KRT 19)
 CC gene, etc., as given in the specification), causing an encoding sequence
 CC to be preferentially expressed in undifferentiated pps cells, causing an
 CC encoding sequence to be preferentially expressed in differentiated cells,
 CC sorting (M4) differentiated cells from less differentiated cells
 CC (involves separating cells expressing a surface marker chosen from any
 CC one of MR1 from cells not expressing the marker), causing pps cells to
 CC proliferate without differentiation, identifying genes that are up or
 CC down regulated during differentiation of pps cells, and a kit (I) for
 CC assessing a culture of pps cells by M1. The method (M1) is useful for
 CC assessing the growth characteristics of a cell population. The cell
 CC population has been obtained by culturing cells from human blastocyst or
 CC from a human patient suspected of having a clinical condition related to
 CC abnormal cell growth. The method further involves determining whether the
 CC cell population is pluripotent from the marker expression and assessing
 CC whether the patient has a malignancy from the marker expression. The
 CC present sequence is an RTQ-PCR primer. (realtime quantitative PCR) used to
 CC assay the expression of a human mRNA in a pps population.

XX SQ Sequence 19 BP; 6 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 827 TCATGACCCAGGAGCCG 845
 Db 1 TCATGACCCAGGAGCCG 19

RESULT 251
 ADQ27747
 ID ADQ27747 standard; DNA; 19 BP.
 XX AC ADQ27747;
 XX DT 26-AUG-2004 (first entry)
 XX DE RNA interference target sequence #655.
 XX KW ss; detection; RNA interference; siRNA; gene silencing; gene expression;
 XX KW cytotoxicity.
 XX OS Homo sapiens.
 XX PN WO2004048566-A1.
 XX PD 10-JUN-2004.
 XX PF 21-NOV-2003; 2003WO-JP014893.
 XX PR 22-NOV-2002; 2002JP-00340053.

XX (NATO/) NATORI Y.
 PA (SAIG/) SAIGO K.
 PA (TEIK/) TEI K.
 PA (NAIT/) NAITO Y.

XX PI Saigo K, Tei K, Naito Y;
 XX DR WPI; 2004-487423/46.
 XX PT Detecting sequence of RNA interference useful for synthesizing siRNA, by
 XX detecting regions in sequence fulfilling specific criteria such as base
 XX at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
 XX guanine or cytosine.
 XX PS Disclosure; SEQ ID NO 669; 325pp; Japanese.
 XX CC The invention relates to a method of detecting the base sequence for RNA
 XX interference by detecting the regions in the DNA sequence fulfilling the
 XX following requirements such as: (i) the base at 3' terminal is adenine,
 XX thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine;
 XX (iii) the seven base sequence at 3' terminal is rich in adenine, thymine
 XX and uracil, and; (iv) there are bases in a such a number that it causes
 XX RNA interference without showing cytotoxicity. The method is used for
 XX designing and synthesizing siRNA causing RNA interference. This sequence
 XX corresponds to an RNA interference target sequence of the invention.

XX SQ Sequence 19 BP; 5 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 709 GTTCTCTCCGAAATATA 727
 Db 1 GTTCTCTCCGAAATATA 19

RESULT 252
 ADQ61744/c
 ID ADQ61744 standard; RNA; 19 BP.

XX AC ADQ61744;
 XX DT 09-SEP-2004 (first entry)
 XX DE Anti-NR2E1 siRNA related DNA sequence SEQ ID NO:1446.
 XX KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
 XX KW RNA interference.
 XX OS Synthetic.
 XX PN WO2004045543-A2.
 XX PD 03-JUN-2004.
 XX PF 14-NOV-2003; 2003WO-US036787.
 XX PR 14-NOV-2002; 2002US-0426137P.
 XX PR 10-SEP-2003; 2003US-0502050P.

XX PA (DHAR-) DHARMACON INC.
 XX PI Anastasia K, Angela R, Devin L, William M, Stephen S;
 XX DR WPI; 2004-420527/39.

XX Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
 XX by selecting a target gene and measuring the functionality of the
 XX nucleotide sequences that are complementary to a stretch of nucleotides
 XX of the target sequence.

XX Example 12; SEQ ID NO 1446; 199pp; English.

XX The invention relates to a novel method for selecting siRNA (short
 XX interfering RNA) comprising selecting an siRNA molecule of 19-25
 XX nucleoside bases by selecting a target gene and measuring the

CC functionality of sequences of 19-25 nucleotides in length that are
 CC substantially complementary to a stretch of nucleotides of the target
 CC sequence, where the functionality is dependent upon non-target specific
 CC criteria. Also claimed are methods for gene-silencing, developing an
 CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
 CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
 CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
 CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
 CC sequence consisting of GGGAGAUGAUGAAGUA; GAAAGUACUCCAUUAAG;
 CC GUACGACACCGGAGAAU; AGAUGAUGAAGUACAU; UGAAGACUCUCAGUUU;
 CC CAUCGCGCUCUUUGA; UGCGGCGCUCUUUGAUU; GAGAUGAUGAAGUAC;
 CC GGAGAUGAUGAAGUAC; and GAAGACUCUCAGUUU. The siRNA molecule
 CC comprises a sense strand and an anti-sense strand. The siRNA molecule
 CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
 CC pairs. The kit comprises at least two siRNA, comprising a first optimised
 CC siRNA and a second optimised siRNA. The method is useful in selecting
 CC siRNA for generating a gene silencing reagent. The present sequence is
 CC used in the exemplification of the invention. The sequence is shown in
 CC the specification as DNA, but described as siRNA.

XX Sequence 19 BP; 6 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 723 ATATATTACGAGTCCTTG 741

||||| ||| ||||| |||||
 Db 19 ATATCTGAAGCAGTCCTTG 1

RESULT 253

ADR70528
 ID ADR70528 standard; DNA; 19 BP.

XX AC ADR70528;

XX DT 02-DEC-2004 (first entry)

XX DE Reverse RTQ primer for human LEFTB.

XX Human; ss; PCR; telomerase reverse transcriptase; TERT; POU domain;
 KW class 5 transcription factor; POU5F1; Oct3; Oct4;
 KW teratocarcinoma-derived growth factor; Cripto; podocalyxin-like; PODXL;
 KW gastrin-releasing peptide receptor; GRPR; human embryonic stem cell; hES;
 KW primate pluripotent stem cell; cancer; gene expression; cell separation;
 KW differentiation; primer; RTQ PCR; real time quantitative PCR.

XX OS Homo sapiens.

XX PN US2004180347-A1.

XX PD 16-SEP-2004.

XX PF 13-MAR-2003; 2003US-00389431.

XX PR 13-MAR-2003; 2003US-00389431.

PA (STAN/) STANTON L W.

PA (BRAN/) BRANDENBERGER R.

PA (GOLD/) GOLD J D.

PA (IRVI/) IRVING J M.

PA (MAND/) MANDALAM R.

PA (MOKW/) MOK M.

XX Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;

PI Mok M;

XX WPI; 2004-675599/66.

XX Assessing culture of undifferentiated human embryonic stem cells or their
 PT progeny, by detecting Cripto, gastrin-releasing peptide (GRP) receptor
 PT and podocalyxin-like protein markers, and either hTERT and/or Oct3/4, or

PT GRP receptor.

XX Disclosure; SEQ ID NO 48; 57bp; English.

XX The invention relates to assessing a culture of undifferentiated human
 CC embryonic stem (hES) cells (undifferentiated primate pluripotent stem
 CC cells) or their progeny, involves detecting or measuring a marker such as
 CC Cripto (teratocarcinoma-derived growth factor), gastrin-releasing peptide
 CC (GRP) receptor and podocalyxin-like protein, and either hTERT (telomerase
 CC reverse transcriptase) and/or Oct3/4 (also known as POU domain, class 5,
 CC transcription factor 1(POU5F1)), or GRP receptor. The method involves
 CC detecting or measuring at least two markers, and detecting or measuring
 CC hTERT and/or Oct3/4. The expression of the marker(s) is detected or
 CC measured at mRNA level by PCR amplification. The expression of the
 CC marker(s) is detected or measured at the protein level by antibody assay.
 CC The method involves quantifying the proportion of undifferentiated hES
 CC cells or differentiated cells in the culture from the marker expression.
 CC The level of the marker is determined to be at least 100-fold higher than
 CC the level of the marker in BJ fibroblasts or is determined to be no less
 CC than 100-fold lower than the level of the marker in hES cells, cultured
 CC on an extracellular matrix in medium conditioned with mouse embryonic
 CC fibroblasts and containing 4 ng/ml basic fibroblast growth factor. The
 CC method further involves modifying the culture conditions so as to cause
 CC the hES cells to increase expression of the marker detected or measured
 CC in the culture. The method is useful for assessing a culture of
 CC undifferentiated hES cells or their progeny. The marker used in the above
 CC method is useful for characterising pluripotent stem cells and their
 CC differentiated progeny, for clinical diagnosis of cancer, for assessing
 CC and manipulating culture conditions, regulating gene expression, cell
 CC separation and purification, and to influence differentiation. The
 CC present sequence is a real time quantitative PCR primer used to assay
 CC mRNA expression in undifferentiated stem cells.

XX Sequence 19 BP; 6 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 827 TCATGACCCAGGAGGCG 845

||||| ||||| ||||| |||||
 Db 1 TCATAGCCAGGAGGCG 19

RESULT 254

ADR75949/c

ID ADR75949 standard; DNA; 19 BP.

XX AC ADR75949;

XX DT 16-DEC-2004 (first entry)

XX DE Human apolipoprotein B (ApoB) oligonucleotide seqid 434.

XX antilipemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cytosolic; anticonvulsant; nootropic; muscular; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dialipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apob; ss.

XX OS Homo sapiens.

XX PN WO2004080406-A2.

XX PD 23-SEP-2004.

XX PF 08-MAR-2004; 2004WO-US007070.

XX PR 07-MAR-2003; 2003US-0452682P.

CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
 CC can be used to control ApoB gene expression.

XX Sequence 19 BP; 2 A; 4 C; 3 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1014 AGAAGCATCATCATGAGA 1032
 DB 19 AGAAGCATCATCAAGGAAA 1

RESULT 256
 ADR76227/C
 ID ADR76227 standard; DNA; 19 BP.
 XX
 AC ADR76227;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human apolipoprotein B (ApoB) oligonucleotide seqid 712.
 XX
 KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cytosstatic; anticonvulsant; nootropic; muscular; anti-HIV;
 KW RNA interference; RNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apob; ss.

XX Homo sapiens.
 XX WO2004080406-A2.
 XX
 XX 23-SEP-2004.
 XX
 XX 08-MAR-2004; 2004WO-US007070.
 XX
 XX 07-MAR-2003; 2003US-0452682P.
 XX 12-MAR-2003; 2003US-0454265P.
 XX 13-MAR-2003; 2003US-0454962P.
 XX 14-MAR-2003; 2003US-0455050P.
 XX 17-APR-2003; 2003US-0462894P.
 XX 25-APR-2003; 2003US-0463772P.
 XX 25-APR-2003; 2003US-0465665P.
 XX 09-MAY-2003; 2003US-0469612P.
 XX 08-AUG-2003; 2003US-0493986P.
 XX 11-AUG-2003; 2003US-0494597P.
 XX 26-SEP-2003; 2003US-0506341P.
 XX 09-OCT-2003; 2003US-0510246P.
 XX 10-OCT-2003; 2003US-0510318P.
 XX 07-NOV-2003; 2003US-0518453P.
 XX
 XX (ALNY-) ALNYLAM PHARM.

XX Manoharan M, Bumcrot D;
 XX WPI; 2004-677362/66.
 XX
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 XX disease, diabetes, cancer or neurological disease, comprises sense
 XX sequence and antisense sequence which has specific modifications.
 XX
 XX Example 5; SEQ ID NO 712; 378pp; English.

CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
 CC can be used to control ApoB gene expression.

XX Sequence 19 BP; 10 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 552 TTTAATATGCTGGCTTTT 570
 DB 19 TTGAATATGCTGAGTTTT 1

RESULT 257
 ADR78845/C
 ID ADR78845 standard; DNA; 19 BP.
 XX
 XX ADR78845;
 XX
 XX 16-DEC-2004 (first entry)
 XX
 XX Human apolipoprotein B (ApoB) oligonucleotide seqid 3330.
 XX
 XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 XX cytosstatic; anticonvulsant; nootropic; muscular; anti-HIV;
 XX RNA interference; RNA; antisense technology; lipid metabolism;
 XX cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 XX coronary artery disease; CAD; coronary heart disease; CHD;
 XX atherosclerosis; hepatic glucose production;
 XX glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 XX colon cancer; lung cancer; neurological disease; Huntington disease;
 XX spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apob; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO2004080406-A2.
 XX
 XX 23-SEP-2004.
 XX
 XX 08-MAR-2004; 2004WO-US007070.
 XX
 XX 07-MAR-2003; 2003US-0452682P.
 XX 12-MAR-2003; 2003US-0454265P.
 XX 13-MAR-2003; 2003US-0454962P.
 XX 14-MAR-2003; 2003US-0455050P.
 XX 17-APR-2003; 2003US-0462894P.
 XX 25-APR-2003; 2003US-0463772P.
 XX 25-APR-2003; 2003US-0465665P.
 XX 09-MAY-2003; 2003US-0469612P.
 XX 08-AUG-2003; 2003US-0493986P.
 XX 11-AUG-2003; 2003US-0494597P.
 XX 26-SEP-2003; 2003US-0506341P.
 XX 09-OCT-2003; 2003US-0510246P.
 XX 10-OCT-2003; 2003US-0510318P.
 XX 07-NOV-2003; 2003US-0518453P.
 XX
 XX (ALNY-) ALNYLAM PHARM.

XX CTV primer 5'.

DE TSWV; tomato spotted-wilt virus; BYMV; bean yellow mosaic virus; CLRV;

XX cherry leaf roll virus; CMV; cucumber mosaic virus; CTV;

KW citrus tristeza virus; GFLV; grapevine fanleaf virus; PLRV;

KW potato leaf roll virus; PMNV; pepper mild mottling virus; PSTV;

KW potato spindle tuber viroid; lycopersicum esculentum; detection; virus;

KW immunisation; amplification; tobamovirus; potyvirus; closterovirus;

KW luteovirus; nepovirus; identification; ss.

XX Synthetic.

OS

XX EP574345-A2.

PN

XX 15-DEC-1993.

PD

XX 10-JUN-1993; 93EP-00500079.

PP

XX 12-JUN-1992; 92ES-00001232.

PR

XX (NAIN-) INST NACIONAL INVESTIGACION & TECNOLOGIA.

XX

XX Bardosa Nolasco N, De Blas Beorlegui C, Borja Tome MJ;

PI

XX Pons Ascaso F, Torres Pascual V;

PI

XX WPI; 1993-396985/50.

DR

XX

XX Detection and identification of viral and sub-viral pathogens, partic. in

PT

PT plants - by immobilisation with antibodies and spectrophotometric

PT

XX quantitation or electrophoretic identification.

XX

PS Example 2; Page 6; 13pp; English.

XX

XX The primers (AA053267-86) are used to amplify the genomes of various

CC

CC viral plant pathogens or satellite viruses. The pathogen is then

CC

CC immobilised using antibodies against proteins in the virus coating or

CC

CC against double-chain RNAs in the case of viral pathogens. Detection of

CC

CC the pathogen is carried out by electrophoretic identification of the

CC

CC amplification products. (Updated on 25-MAR-2003 to correct PN field.)

CC

CC (Updated on 25-MAR-2003 to correct PI field.)

CC

XX

XX Sequence 20 BP; 11 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 857 TCCTTGTGTTGTCAT 875

Db 19 TCCTTGTGTTGTCAT 1

RESULT 260

AAQ97957/C

ID AAQ97957 standard; DNA; 20 BP.

AC

XX AAQ97957;

XX

XX 25-MAR-2003 (revised)

DT

XX 18-OCT-1995 (first entry)

XX

XX PNA oligomer targetting coding region of PKC-epsilon.

DE

XX

XX Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;

KW

KW cell proliferation; cell differentiation; isozyme; antisense;

KW

XX triple helix; cancer; psoriasis; inflammation.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

PH

FT misc_feature 1..20

FT

FT /*tag= a

FT /note= "at least one (and preferably all) of the backbone

FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine

FT peptide residues, the nucleobase being attached

FT covalently to the acetyl group and the peptide linkage

FT being formed by condensation of the glycine carboxy group

FT of one residue with the amino group of the 2-aminoethyl

XX moiety in the next residue"

PN WO9503833-A1.

XX

XX 09-FEB-1995.

PD

XX 28-JUL-1994; 94WO-US008465.

PF

XX 29-JUL-1993; 93US-00099098.

XX

XX (ISIS-) ISIS PHARM INC.

PA

XX Dean NM;

PI

XX WPI; 1995-082040/11.

DR

XX

XX New peptide nucleic acid oligomers specific for protein kinase C

PT

PT isozyme(s) - useful as anti:sense molecules for treating PKC mediated

PT

XX disease, e.g. cancer, psoriasis and inflammation.

XX

XX Claim 38; Page 274; 287pp; English.

XX

XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist

CC

CC of naturally occurring nucleobases covalently bound to a polyamide

CC

CC backbone and (b) hybridise to the translation initiation AUG region,

CC

CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region

CC

CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target RNA

CC

CC and single stranded DNA (ssDNA) to produce antisense-type gene regulation

CC

CC moieties. They inhibit expression of PKC-alpha and its isoforms

CC

CC (including beta, gamma, delta, epsilon, zeta and eta) and so are useful

CC

CC for treating and diagnosing cell proliferation and differentiation

CC

CC processes such as neoplastic, hyperproliferative and inflammatory

CC

CC diseases. PNA oligomers have high affinity for complementary single

CC

CC stranded DNA. They are also able to form triple helices in which a first

CC

CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the

CC

CC resulting double helix or with the first PNA strand. The PNAs possess no

CC

CC significant charge and are water soluble, which facilitates cellular

CC

CC uptake. Further, since they contain amides of non-biological amino acids,

CC

CC they are biostable and resistant to enzymatic degradation by proteases.

CC

CC The present sequence targets the coding region of PKC-epsilon. (Updated

CC

CC on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTAGCT 452

Db 19 AGAGGAGAGGATTTGGCT 1

RESULT 261

AAQ84260/C

ID AAQ84260 standard; DNA; 20 BP.

AC

XX AAQ84260;

XX

XX 25-MAR-2003 (revised)

DT

XX 21-SEP-1995 (first entry)

XX

XX PKC-epsilon coding region antisense oligo, ISIS #7941.

DE

XX

XX Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon; zeta;

KW

KW modulation; expression; isozyme; hybridise; 5' UTR; human;

KW

KW 3' untranslated region; translation initiation site; detection;

KW phosphorothioate linkage; 2'-O-methyl modification;
 KW 2'-O-propyl modification; ss.
 XX Synthetic.
 XX WO9502069-A1.
 PN 19-JAN-1995.
 XX
 XX
 XX 08-JUL-1994; 94WO-US007770.
 XX
 XX 09-JUL-1993; 93US-00089996.
 PR 22-FEB-1994; 94US-00199779.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Bennett CF, Boggs RT, Dean NM;
 XX WPI; 1995-066911/09.
 DR Oligo:nucleotide(s) hybridisable with Protein Kinase C mRNA or gene -
 XX also novel PKC-alpha 3'-UTR sequence, useful for diagnosis and treatment
 PT of hyperproliferative disorders.
 XX Example 16; Page 37; 125pp; English.
 XX
 XX The sequences given in AAQ84252-64 are oligos which are antisense to the
 CC protein kinase C-epsilon (PKC-epsilon) cDNA. These antisense molecules
 CC may be used in modulating the expression of this particular isozyme of
 CC PKC. These oligonucleotides have a %inhibition of PKC of <40%. The
 CC oligonucleotides of the invention preferably hybridise with the 5'- or 3'-
 CC -untranslated regions of the PKC gene, or the translation initiation
 CC site, or the coding region. These oligos may be used in the detection of
 CC the human PKC genes and for treatment of animals with conditions
 CC associated with PKC, esp. hyperproliferative diseases such as psoriasis,
 CC colorectal cancer, lung cancer, breast or skin cancer. These oligos may
 CC contain at least one phosphorothioate linkage and/or at least one of the
 CC nucleotides comprises a modification on the 2' position of the sugar,
 CC esp. a 2'-O-methyl or a 2'-O-propyl modification. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 434 AGAGGAGGATGATTTAGCT 452
 DB 19 AGAGAGAGGAGGATTTGGCT 1
 RESULT 262
 AA001278
 ID AA001278 standard; DNA; 20 BP.
 AC AA001278;
 XX 23-MAR-1998 (first entry)
 DT Guanylate cyclase 2D PCR primer for universal mammalian STS's.
 DE PCR primer; polymerase chain reaction; amplification; UM-STS;
 KW universal mammalian sequence tagged site; genomic map; clone; ss.
 KW Synthetic.
 OS WO9731012-A1.
 PN 28-AUG-1997.
 PD 18-FEB-1997; 97WO-US002403.
 XX

PR 22-FEB-1996; 96US-0012061P.
 XX (UNMI) UNIV MICHIGAN.
 PA (UNMS) UNIV MICHIGAN STATE.
 XX Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
 PI WPI; 1997-435083/40.
 XX
 DR New oligonucleotide primers amplifying gene regions conserved among
 XX mammals - useful for developing genomic maps, isolating clones and making
 PT cross-species comparisons.
 XX Claim 1; Page 11; 26pp; English.
 XX
 XX The present sequence represents a specifically claimed oligonucleotide
 CC PCR primer. The oligonucleotide can be used for polymerase chain reaction
 CC (PCR) amplification of DNA, specifically regions of specific genes that
 CC are conserved among mammalian species, i.e. pairs of oligonucleotides
 CC from the present specification represent universal mammalian sequence-
 CC tagged site (UM-STS) primers. The primers are used to develop genomic
 CC maps, to isolate clones from libraries, to make cross-species comparisons
 CC and to develop additional genetic markers. UM-STS allow genomic
 CC comparisons to be made between more species
 XX
 XX Sequence 20 BP; 2 A; 1 C; 9 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 783 TTGGGGATGCTCTTGAGCA 801
 DB 2 TTGGGGATGCTCTTGTTGA 20
 RESULT 263
 AA022647/c
 ID AA022647 standard; DNA; 20 BP.
 XX AC AA022647;
 XX 27-MAY-1999 (first entry)
 DT Human protein kinase C antisense oligonucleotide #86.
 DE Protein kinase C; PKC; human; antisense; primer; inhibitor; treatment;
 KW hyperproliferative condition; cancer; colorectal; breast; bladder; lung;
 KW brain; glioblastoma multiforme; skin; psoriasis; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX US5885970-A.
 PN 23-MAR-1999.
 PD 07-JUN-1995; 95US-00488177.
 PF 16-MAR-1992; 92US-00852852.
 XX 09-JUL-1993; 93US-00089996.
 XX (ISIS-) ISIS PHARM INC.
 PA Dean N, Bennett CF;
 PI WPI; 1999-228583/19.
 DR New human protein kinase C antisense oligonucleotides - useful for
 XX treating PKC-related hyperproliferative conditions e.g. cancer and
 PT psoriasis.
 XX Example 16; Col 21; 55pp; English.
 PS

XX This invention describes antisense oligonucleotides that specifically
CC bind to human protein kinase C (PKC) mRNA. These oligonucleotides can be
CC used to inhibit PKC mRNA and therefore be used to treat PKC-related
CC hyperproliferative conditions, e.g. cancer, especially colorectal cancer,
CC breast cancer, bladder cancer, lung cancer, or brain cancer (preferably
CC glioblastoma multiforme). The products of the invention may also be used
CC to treat skin cancer and psoriasis
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTTAGCT 452
Db 19 AGAGAGAGGAGATTGGCT 1

RESULT 264
AAAX76903/c
ID AAX76903 standard; DNA; 20 BP.
XX
AC AAX76903;
XX
DT 17-OCT-2003 (revised)
DT 05-AUG-1999 (first entry)
XX
XX H2-1 Pag1 gene direct repeat sequence.
XX
DE H2-1 pag1 promoter; persistence-associated gene 1; insect cell;
KW constitutive expression promoter; direct repeat; ss.
KW
XX Heliothis zea virus 1.
OS
XX US5911982-A.
PN
XX 15-JUN-1999.
XX
XX 18-APR-1996; 96US-00634350.
XX
PR 06-OCT-1995; 95US-0004894P.
PR 11-OCT-1995; 95US-0005128P.
XX
XX (NASC-) NAT SCI COUNCIL.
PA
XX Chao Y;
PI
XX WPI; 1999-357167/30.
XX
XX H2-1 virus persistence-associated gene promoter.
PT
XX Example 1; Fig 3c; 56pp; English.
PS
CC This sequence represents a direct repeat from the H2-1 persistence-
CC associated gene 1 (H2-1 pag1). The invention relates to the H2-1 pag1
CC promoter. The pag1 gene promoter is useful in insect cells for driving
CC constitutive expression of e.g. genes encoding foreign proteins. The
CC promoter of the pag1 gene is constitutively expressed and stronger than
CC that of the polyhedrin gene in insect cells, enabling it to express
CC foreign genes more strongly e.g. lacZ and luciferase, in addition to
CC which it can be expressed more prominently as a short promoter. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 20 BP; 13 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 566 TTTTAAATACCTTTATAT 584
|| ||||| ||||| || ||

Db 19 TTGTTTAATACCTTTGTTT 1

RESULT 265
AAAX78609/c
ID AAX78609 standard; DNA; 20 BP.
XX
AC AAX78609;
XX
DT 03-SEP-1999 (first entry)
XX
XX Human PKC-epsilon oligonucleotide primer ISIS # 7941.
DE
XX PKC; human; PKC-alpha; primer; protein kinase C; expression modulator;
KW PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-eta; PKC-delta;
KW PKC-epsilon; PKC-zeta; anti-inflammatory; cytostatic;
KW antisense targeting; isozyme; growth control; hyperproliferative disease;
KW colon cancer; glioblastoma; bladder cancer; inflammatory condition;
KW psoriasis; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX US5922686-A.
PN
XX 13-JUL-1999.
XX
XX 14-JUN-1996; 96US-00664336.
XX
XX 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Dean N, Bennett CF;
PI
XX WPI; 1999-404471/34.
XX
XX Oligonucleotides targetted against nucleic acids encoding protein kinase
C.
XX
XX Example 16; Col 63-64; 56pp; English.
PS
CC This invention describes novel oligonucleotides (AAX78524-X78644) having
CC up to 50 nucleotides hybridisable with, and able to modulate the
CC expression of, a nucleic acid encoding protein kinase C and its isoforms
CC alpha, beta type I, beta type II, gamma, eta, delta, epsilon and zeta.
CC The oligonucleotides of the invention have anti-inflammatory and
CC cytostatic activity and are used for antisense targeting to modulate the
CC expression of PKC or of a particular PKC isozyme or set of isoforms in
CC cells or tissues. The products of the invention also hybridise with
CC nucleic acids involved in the modulation of PKC expression, which is
CC known to be involved growth control in hyperproliferative diseases e.g.
CC colon cancer, glioblastoma and bladder cancer as well as in inflammatory
CC conditions e.g. psoriasis. Due to their specificity the oligonucleotides
CC are able to overcome the problems of toxicity associated with previous
CC agents designed to modulate PKC expression
XX
XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTTAGCT 452
|| ||||| ||||| || ||
Db 19 AGAGAGAGGAGATTGGCT 1

RESULT 266
AAAX83735/c
ID AAX83735 standard; DNA; 20 BP.
XX

Fri Aug 19 11:00:00 2005

```

AC AAX83735;
XX
XX 27-AUG-1999 (first entry)
XX
XX Human protein kinase C antisense oligonucleotide SEQ ID NO:86.
XX
XX Human; protein kinase C; PKC; antisense oligonucleotide; diagnosis; ss;
XX hybridisation; cancer; psoriasis; hyperproliferative disease; tumour.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5916807-A.
XX
XX 29-JUN-1999.
XX
XX 07-JUN-1995; 95US-00481072.
XX
XX 16-MAR-1992; 92US-00852852.
XX 09-JUL-1993; 93US-00089996.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean N, Bennett CF;
XX
XX WPI; 1999-403817/34.
XX
XX New antisense oligonucleotides specific for human protein kinase C useful
XX for diagnosis and treatment of cancer and psoriasis.
XX
XX Example 16; Col 21; 54pp; English.
XX
XX The present invention describes a method of inhibiting the expression of
XX human protein kinase C (PKC) in cells. The method comprises contacting
XX the cells with an antisense oligonucleotide which has up to 50 nucleotide
XX units. AAX83633 to AAX83720 represent specifically claimed antisense
XX oligonucleotides for use in the method of the invention. The antisense
XX oligonucleotides modulate hybridize to messenger RNA from the PKC gene
XX which results in modulation of expression of the PKC gene. This means
XX they can be used for diagnosis, therapeutic or prophylactic treatment of
XX PKC associated diseases such as cancer and psoriasis, and as research
XX agents. Abnormal proliferative states in tissue from patients suspected
XX of having a hyperproliferative disease e.g. cancer, psoriasis can be
XX diagnosed. Tumours associated with PKC can be distinguished from tumours
XX which are not PKC associated to allow an efficacious treatment regime to
XX be used. The antisense oligonucleotides have specific activity so are
XX able to modulate PKC activity without producing side effects and with
XX greater effectiveness than observed from administration of current
XX agents. AAX83721 to AAX83753 represent other oligonucleotides used in
XX examples from the present invention
XX
XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTACCT 452
Db ||||| ||||| ||||| |||||
19 AGAGAAGAGGATTTTGGCT 1

RESULT 267
AAX92824
ID AAX92824 standard; DNA; 20 BP.
XX
XX AAX92824;
XX
XX 13-SEP-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

```

```

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
XX Chlamydophila pneumoniae.
XX
XX WO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
XX 04-NOV-1998; 98US-0107078P.
XX
XX (GEST ) GENSET.
XX
XX Griffiths R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX
XX Page 1542; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX
XX Sequence 20 BP; 8 A; 7 C; 4 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 AGAATCTGAAGCCCACTC 958
Db ||||| ||||| ||||| |||||
1 AGAATCGGAAGCCCACTC 19

RESULT 268
AAX94795
ID AAX94795 standard; DNA; 20 BP.
XX
XX AAX94795;
XX
XX 13-SEP-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
XX Chlamydophila pneumoniae.
XX
XX WO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
XX 04-NOV-1998; 98US-0107078P.
XX

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XX (GBST ) GENSET.
XX Griffais R;
XX WPI; 1999-357842/30.
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1697; Disclosure; 1912pp; English.
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX Sequence 20 BP; 4 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 771 GAAACCTTTTCTTGGGA 789
DB 1 GAGACCTTTTCTTGGGA 19
RESULT 269
AAX95833
ID AAX95833 standard; DNA; 20 BP.
XX
AC AAX95833;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
OS Chlamydophila pneumoniae.
XX
XX WO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
XX
XX 04-NOV-1998; 98US-0107078P.
XX
XX (GBST ) GENSET.
XX
XX Griffais R;
OS Chlamydophila pneumoniae.
XX
XX WO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
XX
XX 04-NOV-1998; 98US-0107078P.
XX
XX (GBST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1779; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX Sequence 20 BP; 4 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 771 GAAACCTTTTCTTGGGA 789
DB 1 GAGACCTTTTCTTGGGA 19
RESULT 270
AAX97255
ID AAX97255 standard; DNA; 20 BP.
XX
AC AAX97255;
XX
DT 13-SEP-1999 (first entry)
XX
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
OS Chlamydophila pneumoniae.
XX
XX WO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
XX
XX 04-NOV-1998; 98US-0107078P.
XX
XX (GBST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1890; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 291 CTACTGGAATGTGTGTTTC 309
DB 2 CTTCTGGAGTCGTGTTTC 20

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pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae

Sequence 20 BP; 1 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAATGTGTGTTTC 309
DB 2 CTTCTGGAGTCGTGTTTC 20

RESULT 270
AAX97255
ID AAX97255 standard; DNA; 20 BP.
XX
AC AAX97255;
XX
DT 13-SEP-1999 (first entry)
XX
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
OS Chlamydophila pneumoniae.
XX
XX WO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
XX
XX 04-NOV-1998; 98US-0107078P.
XX
XX (GBST) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1890; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae

Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Y      460 GTGGTAGCACTTTTATTCTG 478
        |||||
b      2 GTGGTAGCACTATAACCTG 20

RESULT 271
AX95840
D AAX95840 standard; DNA; 20 BP.
X
X AAX95840;
X
X T 13-SEP-1999 (first entry)
E PCR primer used to amplify an ORF of Chlamydia pneumoniae.
X Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
W sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
X neutralising epitope; PCR primer; ss.
X Synthetic.
S Chlamydophila pneumoniae.
S WO927105-A2.
X N X
X O3-JUN-1999.
X 20-NOV-1998; 98WO-IB001890.
X F
X 21-NOV-1997; 97FR-00014673.
R R 04-NOV-1998; 98US-0107078P.
X
X (GEST ) GENSET.
A Griffais R;
X WPI; 1999-357842/30.
X Genome sequence of Chlamydia pneumoniae.
X Page 1779; Disclosure; 1912pp; English.
XX AAX91991-K97517 represent PCR primers used to amplify open reading frames
and other nucleic acid sequences from the genome of Chlamydia pneumoniae
(see AAX91990). C. pneumoniae causes respiratory disease such as
pneumonia and bronchitis and is thought to be a contributing factor in
heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
nodosum or pharyngitis. The polypeptides encoded by the open reading
frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
nucleotide sequences can also be used as immunogenic compositions,
especially where the vector directs the expression of a neutralising
epitope of C. pneumoniae
XX Sequence 20 BP; 1 A; 5 C; 5 G; 9 T; 0 U; 0 Other;
Query March 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0
DY 291 CTACTCGGAATGTGTGTTTC 309
DB 2 CTTCTGGAGTGCTGTGTTTC 20

RESULT 272
AAAX19212/c
IID AAAX19212 standard; DNA; 20 BP.
XX AAX19212;
XX (revised)
DT 20-MAR-2003
MK 1993 (first entry)
```


KW phosphorothioate; hybridisation; isozyme; target; inflammation;
 XX hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX US959096-A.
 PN 28-SEP-1999.
 XX 07-JUN-1995; 95US-00481066.
 XX 16-MAR-1992; 92US-00852852.
 PR 09-JUL-1993; 93US-00089996.
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Dean N;
 XX WPI; 1999-561076/47.
 DR Antisense oligonucleotides useful for treatment of hyperproliferative and
 XX inflammatory conditions including psoriasis, tumors and cancer.
 XX Example 16; Col 23; 56pp; English.
 XX The present invention describes antisense oligonucleotides up to 50
 CC nucleotides in length which specifically bind mRNA encoding human protein
 CC kinase C (PKC). AA27266 to AA27386 represent human PKC antisense
 CC oligonucleotides used in the exemplification of the present invention.
 CC The antisense oligonucleotides are useful for the treatment of diseases
 CC associated with PKC expression, such as hyperproliferative and
 CC inflammatory conditions including psoriasis, tumours and cancer
 CC (glioblastoma, bladder, breast, colon and lung cancer)
 XX
 XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 434 AGAGGAGATGATTTAGCT 452
 DB 19 AGAGAAGAGGATTTGGCT 1
 RESULT 274
 AAZ75053/c
 ID AAZ75053 standard; DNA; 20 BP.
 XX AC AAZ75053;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human biallelic marker downstream amplification primer SEQ ID NO:9409.
 XX
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX WO9954500-A2.
 PN 28-OCT-1999.
 XX 21-APR-1999; 99WO-IB000822.
 XX 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX

PA (GEST) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX
 XX Claim 8; Page 2236; 2745pp; English.
 XX AA265654 to AA269578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA26579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 427 ATTTGGAAGAGGAGATGAT 445
 DB 19 AGTTGGAGGGGAGATGAT 1
 RESULT 275
 AAA64912/c
 ID AAA64912 standard; DNA; 20 BP.
 XX AC AAA64912;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Antisense oligonucleotide #102333 to X-linked inhibitor of apoptosis.
 XX
 KW X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; 2'-methoxyethyl;
 KW antisense; antiinflammatory; cytostatic; tumour; MOE; phosphorothioate;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /note= "Optionally the internucleotide linkages are
 FT phosphorothioate"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Optionally the nucleotides are 2'-methoxyethyl"
 FT modified_base 3
 FT /*tag= d
 FT /mod_base= m5c
 FT /note= "Optional"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "Optionally the nucleotides are 2'-methoxyethyl"
 XX
 PN US6087173-A.

XX 11-JUL-2000.
PD 09-SEP-1999; 99US-00392580.
XX 09-SEP-1999; 99US-00392580.
PR (ISIS-) ISIS PHARM INC.
XX Bennett CF, Cowser LM, Ackermann EJ;
PI WPI; 2000-498201/44.
XX Antisense compound useful for research reagents, diagnostics, prophylaxis
XX and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
PT
XX
XX Claim 3; Col 40; 33pp; English.
XX The present sequence is an antisense oligonucleotide designed to inhibit
CC expression of the human X-linked inhibitor of apoptosis. This sequence is
CC targeted to the start codon region of the gene. The oligonucleotides may
CC be modified to consist of 10 nucleotides flanked on both sides by 5
CC nucleotide wings. The wings are composed of 2'-methoxyethyl (2'-MOE)
CC nucleotides. Cytidine residues in the 2'-MOE wings are 5-methylcytidines.
CC Throughout the modified oligonucleotides, the internucleoside linkages
CC are phosphorothioate. The modified oligonucleotides are more effective
CC inhibitors than unmodified oligonucleotides. The oligonucleotides may be
CC used to inhibit X-linked inhibitor of apoptosis expression in cells and
CC tissues in vitro. The oligonucleotides are also useful for treating
CC animals or humans, prone to a disease associated with X-linked inhibitor
CC of apoptosis. The oligonucleotides may also be used prophylactically to
CC prevent infection, inflammation or tumour formation
XX
XX Sequence 20 BP; 6 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 426 TATTTCGAGAGAGATGA 444
|||||
DB 20 TATTTCGAGAGAGATGA 2
RESULT 276
AAF62444/C
ID AAF62444 standard; DNA; 20 BP.
XX
XX AAF62444;
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX A thaliana VRN1 gene PCR primer S49.
XX
XX VRN1; vernalisation; flowering; crop; PCR primer; ss.
XX Arabidopsis thaliana.
XX
XX WO200121822-A1.
XX
XX 29-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-GB003525.
XX
XX 17-SEP-1999; 99GB-00022071.
XX
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX
XX Dean C, Levy Y;
PI
XX WPI; 2001-273467/28.
XX

PT Novel VRN1 polynucleotide sequence encoding a polypeptide which alters
PT vernalization response of plant in which VRN1 nucleic acid is expressed,
XX useful for influencing and assessing vernalization phenotype of plants.
XX Claim 10; Page 76; 91pp; English.
XX The present invention provides the protein and coding sequences of
CC Arabidopsis thaliana VRN1. This protein is capable of altering the
CC vernalisation responses of a plant. Also provided are a number of PCR
CC primers used to isolate the sequences. The sequences are useful in the
CC production of crop plants, where they are able to control the timing of
CC flowering, the duration of vernalisation required, the optimum
CC temperature, or even eliminate the need for vernalisation completely. The
CC present sequence is a PCR primer used to isolate the VRN1 coding sequence
XX
XX Sequence 20 BP; 5 A; 10 C; 1 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 448 TAGCTGGGAGCAGTGGTAG 466
|||||
DB 19 TAGGTGGGAACTGTGGTAG 1
RESULT 277
AAF23509
ID AAF23509 standard; DNA; 20 BP.
XX
XX AAF23509;
XX
XX 22-MAR-2001 (first entry)
DT
XX
XX Primer cadF-RIC.
XX
XX Fibronectin binding protein; CadF; vaccine; diagnostic assay; ss.
XX
XX Campylobacter coli.
XX Campylobacter jejuni.
XX
XX US6156546-A.
XX
XX 05-DEC-2000.
XX
XX 15-MAY-1998; 98US-00080025.
XX
XX 16-MAY-1997; 97US-0046763P.
XX
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
XX Garvis SG, Konkel MB;
XX
XX WPI; 2001-079546/09.
XX
XX Novel isolated polynucleotide useful for producing fibronectin binding
PT proteins which are useful in production of vaccine, in diagnostic assays
PT and for prophylactic and therapeutic purposes.
XX
XX Example 2; Col 28; 29pp; English.
XX
XX The present invention relates to a Campylobacter jejuni or Campylobacter
CC coli fibronectin binding protein (CadF). A recombinant expression vector
CC with cadF is useful in an assay for determining the presence of C.jejuni
CC or C.coli in a test sample or for determining whether a test isolate of
CC Campylobacter is a strain of C.coli. cadF is useful in the construction
CC of DNA probes for identifying and quantifying the level of expression of
CC CadF in a cell. The gene can also be used in a vaccine
XX
XX Sequence 20 BP; 1 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 676 TTATGTTACTGTTGGCT 694
||| ||||| ||||| |||||
Db 2 TTTCTTACTGTTGGCT 20

RESULT 278
AAC92586/c
ID AAC92586 standard; DNA; 20 BP.
XX
AC AAC92586;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:36.
XX
DE Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
KW ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
KW cell growth; transcriptional repression; replication;
KW signal transduction; chromatin decondensation; Ag-NOR family;
KW nucleolin antibody; systemic connective tissue disease; SLE;
KW systemic lupus erythematosus;
KW scleroderma-like chronic graft versus host disease;
KW expression inhibition; tumour formation; cancer; inflammation;
KW immune disorder; phosphorothioate; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
XX
XX US6165786-A.
XX
XX 26-DEC-2000.
XX
XX 03-NOV-1999; 99US-00433699.
XX
XX 03-NOV-1999; 99US-00433699.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowseert LM;
XX
XX WPI; 2001-079948/09.
XX
XX Novel antisense compound targeted to human nucleolin which specifically
PT hybridizes with and inhibits the expression of human nucleolin, useful
PT for modulating the expression of nucleolin in cells.
XX
XX Example 15; Col 41-42; 41pp; English.
XX
XX Sequences AAC92560-C92639 represent antisense oligonucleotides targeted
CC to the human nucleolin gene, which inhibit its expression. The antisense
CC oligonucleotides were designed to target different regions of the human
CC nucleolin mRNA, and were analyzed for their effect on nucleolin mRNA
CC levels by quantitative real-time PCR. Nucleolin (also known as P92 or
CC C23) is the most abundant nucleolar phosphoprotein in actively growing
CC cells. Nucleolin primarily participates in ribosome biogenesis and
CC transport of ribosomal components, being able to transiently bind to pre-
CC ribosomes in the nucleolus via a ribonucleoprotein consensus sequence.
CC However, it has also been shown to be involved in cytokinesis,
CC nucleogenesis, cell proliferation and growth, transcriptional repression,
CC replication, signal transduction, and chromatin decondensation. Nucleolin
CC is a member of the Ag-NOR (active ribosomal gene located in the nucleolar
CC organiser region) family of proteins which are markers of active
CC ribosomal genes, and whose expression is associated with the prediction
CC of tumour growth rate. The presence of antibodies against nucleolin are
CC associated with systemic connective tissue diseases such as systemic
CC lupus erythematosus (SLE) and scleroderma-like chronic graft versus host
CC disease. The oligonucleotides of the invention are useful for diagnosis,
CC prevention and treatment of conditions associated with nucleolin
CC expression, such as tumour formation, immune disorders and inflammation
XX
XX Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 800 GAGGCAGATACGCTGAAG 818
||||| ||||| ||||| |||||
Db 19 GAGGAAGATGACTCTGAAG 1

RESULT 279
AAI65644/c
ID AAI65644 standard; DNA; 20 BP.
XX
AC AAI65644;
XX
DT 03-JAN-2002 (first entry)
XX
DE Primer for microsatellite marker D16S408, used to localise IBD1.
XX
KW Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox;
KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;
KW inflammatory disease; immune disease; cryptogenetic inflammation;
KW hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX FR2806739-A1.
XX
XX 28-SEP-2001.
XX
XX 27-MAR-2000; 2000FR-00003832.
XX
XX 27-MAR-2000; 2000FR-00003832.
XX
XX (DAUS-) FOND DAUSSET-CERPH JEAN.
XX
XX Hugot JP, Thomas G, Zouali M, Lesage S, Chamailard M;
XX WPI; 2001-608364/70.
XX
XX New human nucleic acids associated with intestinal inflammatory disease,
PT useful for diagnosis, prognosis and control of these diseases, also
PT related proteins.
XX
XX Example 1; Page 84; 97pp; French.
XX
XX PCR primers AAI65595-AAI65646 were used to amplify polymorphic
CC microsatellite markers, for localisation of a human gene encoding
CC inflammatory bowel disease 1 (IBD1) polypeptide, which is associated with
CC intestinal inflammatory disease. The specification also describes a
CC polypeptide which is in proximity to IBD1, and is designated IBD1prox.
CC The IBD1 gene is probably involved in regulation of apoptosis and
CC activation of NF-kappa B. The IBD1 and IBD1prox polynucleotides are is
CC useful as source of probes and primers, as source of (anti)sense
CC oligonucleotides, for recombinant production of polypeptides, and in
CC screening for interactive compounds. The polypeptides are used to raise
CC specific antibodies which useful for diagnostic detection or purification
CC of IBD1 and IBD1prox, to screen for specific binding agents, potential
CC therapeutic agents. The IBD1 and IBD1prox polynucleotides and
CC polypeptides are useful for treatment and prevention of inflammatory
CC and/or immune diseases or cancer, where associated with mutations in
CC genes corresponding to IBD1 and IBD1prox, especially cryptogenetic
CC inflammation of the intestines (hemorrhagic rectocolitis, Crohn's disease
CC and Blau syndrome)
XX
XX Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 776 CTTTGGCTGGGATGTC 794
||| ||||| ||||| |||||

PA (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Dean NM, Cook PD, Hoke G;
 PI WPI; 2002-215022/27.
 XX
 DR New antisense oligonucleotide having nucleoside units which specifically
 PT binds mRNA encoding human protein kinase C isoform, useful for treating
 PT hyperproliferative and inflammatory diseases e.g. psoriasis, tumor and
 PT cancer.
 XX
 PS Example 16; Col 47-48; 77pp; English.
 XX
 CC The invention comprises antisense oligonucleotides designed to bind mRNA
 CC encoding a human protein kinase C (PKC) isoform (i.e. PKC-alpha, PKC-beta
 CC type I, PKC-beta type II, PKC-gamma, PKC-delta, PKC-epsilon, PKC-zeta,
 CC and PKC-eta). The antisense oligonucleotides of the invention are useful
 CC for modulating the expression of the PKC isoforms. The antisense
 CC oligonucleotides are useful for treating hyperproliferative conditions
 CC (e.g. tumour, glioblastoma, bladder cancer, breast cancer, colon cancer
 CC and lung cancer), and inflammatory conditions (e.g. psoriasis). The
 CC antisense oligonucleotides of the invention are also useful for detection
 CC and diagnosis of PKC expression. The present sequence represents a human
 CC PKC antisense oligonucleotide of the invention. NOTE: The present
 CC sequence contains a phosphorothioate backbone
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 434 AGAGGAGATGATTTTAGCT 452
 DB 19 AGAGGAGAGGATTTGGCT 1
 RESULT 283
 AAL45924/c
 ID AAL45924 standard; DNA; 20 BP.
 XX
 AC AAL45924;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Murine dystrophin-specific antisense oligonucleotide mAON#6.
 XX
 KW Antisense oligonucleotide; exon skipping; exon inclusion signal;
 KW disease treatment; splice-modulation; gene therapy; dystrophin;
 KW haemostatic; antithyroid; muscular; mouse; ss.
 XX
 OS Mus sp.
 XX
 PN EP1191097-A1.
 XX
 PD 27-MAR-2002.
 XX
 PF 21-SEP-2000; 2000EP-00203283.
 XX
 PR 21-SEP-2000; 2000EP-00203283.
 XX
 PA (UYLE-) UNIV LEIDS MEDISCH CENT.
 XX
 PI Van Ommen GB, Van Deutekom JCT, Den Dunnen JT, Dauwerse JG;
 PI Datoon NA;
 XX
 DR WPI; 2002-354071/39.
 XX
 CC Decreasing the production of an aberrant protein in a cell, for treatment
 PT of inherited diseases such as Duchenne Muscular Dystrophy or Hemophilia,
 PT comprises a splice modulation therapy of exons.
 XX
 PS Example 1; Page 6; 18pp; English.

XX The present invention relates to a method of decreasing the production of
 CC an aberrant protein in a cell containing pre-mRNA of exons coding for the
 CC protein, involving providing the cell with an agent capable of
 CC specifically inhibiting an exon inclusion signal of one of the exons, and
 CC allowing translation of mRNA produced from splicing of pre-mRNA. The new
 CC method decreases the production of an aberrant protein in a cell by using
 CC a process known as exon-skipping. The process is carried out by providing
 CC an agent such as a nucleic acid to inhibit the exon inclusion signal. The
 CC nucleic acid agent can therefore be used as a preparation of a medicament
 CC for treatment of inherited diseases such as haemophilia A, clotting
 CC factor VIII deficiency, some forms of congenital hypothyroidism, Duchenne
 CC Muscular Dystrophy, and Becker Muscular Dystrophy. The present sequence
 CC is an antisense oligonucleotide directed at the murine dystrophin pre-
 CC mRNA
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 793 GCTTGGAGGAGCAGATTAAC 811
 DB 19 GCTGGAAGAGCAGATTAAC 1
 RESULT 284
 ABL45469/c
 ID ABL45469 standard; DNA; 20 BP.
 XX
 AC ABL45469;
 XX
 DT 11-APR-2002 (first entry)
 XX
 DE Human chromosome 21q22.1 PCR primer SEQ ID NO:2513.
 XX
 KW Human; chromosome 1p36-35; chromosome 21q22.1; Genetic analysis; genome;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2001321190-A.
 XX
 PD 20-NOV-2001.
 XX
 PF 12-MAR-2001; 2001JP-00068285.
 XX
 PR 10-MAR-2000; 2000JP-00066716.
 XX
 PA (RIKA) RIKAGAKU KENKYUSHO.
 PA (GENO-) GENOTEX YG.
 XX
 DR WPI; 2002-144136/19.
 XX
 PT Arraying genome clones.
 XX
 PS Claim 6; Page 54; 528pp; Japanese.
 XX
 CC The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals

QY 149 TTAGGAGTATTATGCGTTT 167
 Db 1 TTCGAAGTTTATGCGTTT 19

RESULT 287
 ABQ62452/c
 ID ABQ62452 standard; DNA; 20 BP.
 XX AC ABQ62452;
 XX DT 16-AUG-2002 (first entry)
 XX DE Mouse syntaxin 4 interacting protein antisense oligonucleotide 39.
 XX KW Mouse; antisense gene therapy; Syntaxin 4 interacting protein; ss;
 KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
 KW inflammation; tumour formation; phosphorothioate backbone;
 KW 2'-O-methoxyethyl wing.
 XX OS Mus musculus.
 XX PN WO200224864-A2.
 XX PD 28-MAR-2002.
 XX PF 19-SEP-2001; 2001WO-US029251.
 XX PR 22-SEP-2000; 2000US-00668313.
 XX FA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Wyatt JR;
 XX WPI; 2002-404952/43.
 XX PT Novel antisense compound that hybridizes and inhibits nucleic acid
 PT molecule encoding Syntaxin 4 interacting protein, useful for treating
 PT diabetes, obesity and skeletal muscle disorder.
 XX PS Claim 3; Page 88; 154pp; English.
 XX CC The invention comprises antisense oligonucleotides designed to inhibit
 CC expression of Syntaxin 4 interacting protein. The antisense
 CC oligonucleotides of the invention are useful for inhibiting the
 CC expression of Syntaxin 4 interacting protein in cells or tissues. The
 CC antisense oligonucleotides are also useful for treating an animal having
 CC a disease or condition associated with Syntaxin 4 interacting protein
 CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
 CC oligonucleotides can also be used to prevent or delay infection,
 CC inflammation and tumour formation. The present DNA sequence represents a
 CC mouse Syntaxin 4 interacting protein antisense oligonucleotide. NOTE: The
 CC present sequence contains a phosphorothioate backbone and 2'-O-
 CC methoxyethyl wings
 XX SQ Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 932 AGAATGCAGAACTCTGAAG 950
 Db 19 AGAATCCAGAACTGTGAAG 1

RESULT 288
 ABK23082/c
 ID ABK23082 standard; DNA; 20 BP.
 XX AC ABK23082;
 XX DT 09-APR-2002 (first entry)

QY 382 AAAAGTGTGCCCCACAC 900
 Db 19 AATATTGTGCCCCACAC 1

RESULT 289
 ABS68905
 ID ABS68905 standard; DNA; 20 BP.
 XX AC ABS68905;
 XX DT 20-NOV-2002 (first entry)
 XX DE Human RecQ protein-like 4 (RECQL4) DNA antisense oligonucleotide #48.
 XX

Human Zmax1 cDNA reverse PCR primer #122.
 Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
 lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
 osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
 neurovascular condition; wound healing; gene therapy; PCR primer; probe;
 bone development disorder; antiarteriosclerotic; cardiovascular;
 osteopathic; cerebroprotective.
 OS Homo sapiens.
 XX WO200192891-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016946.
 XX PR 26-MAY-2000; 2000US-00578900.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
 XX Carulli JP, Little RD, Recker RR, Johnson ML;
 WPI; 2002-097784/13.
 Identifying molecules involved in lipid regulation, useful for
 diagnosing, treating or preventing e.g., arteriosclerosis, comprises
 identifying a molecule that binds to high bone mass gene or its
 corresponding wild type gene.
 PS Disclosure; Page 39; 409pp; English.
 CC The invention relates to a method for identifying a molecule involved in
 CC lipid regulation comprising identifying a molecule that binds to or
 CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
 CC gene, Zmax1. Compounds identified by the method are useful for treating,
 CC diagnosing, preventing or screening for normal and abnormal lipid-
 CC associated conditions, including arteriosclerosis, cardiovascular
 CC disease, stroke, and osteoporosis. The compounds may also be used in the
 CC treatment or prevention of diabetic atherosclerosis, neurovascular
 CC conditions caused by plaque build-up, poor circulation due to plaque
 CC build-up and associated poor wound healing. The methods may be used in
 CC gene therapy, pharmaceutical development, and diagnostic assays for bone
 CC development disorders. Molecules identified by comparison of Zmax1 and
 CC HBM systems can be used as surrogate markers in pharmaceutical
 CC development, in diagnosis of human or animal bone disease, and in the
 CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
 CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
 CC and adapters of the invention
 XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

KW Human; RecQ protein-like 4; RECQL4; ss; chromosome 8q24; infection;
KW inflammation; tumour formation; cancer; cytostatic; antiinflammatory;
KW antimicrobial; antisense therapy; antisense oligonucleotide.
XX
OS Homo sapiens.
XX
PN US6436706-B1.
XX
XX 20-AUG-2002.
PD
XX
XX 23-FEB-2001; 2001US-00792594.
PF
XX
XX 23-FEB-2001; 2001US-00792594.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Ward DT, Watt AT;
PI
XX WPI; 2002-689941/74.
DR
XX New antisense compounds targeted to nucleic acids encoding RecQ protein-
PT like 4, useful for modulating expression of the nucleic acid and treating
PT diseases associated with expression of the nucleic acid in humans.
XX
XX Claim 14; Col 45; 45pp; English.
PS
XX The invention relates to a compound targeted to specific nucleobases of
CC RecQ protein-like 4 (RECQL4) and which hybridises and inhibits the
CC expression of RECQL4. The compound is useful for inhibiting the
CC expression of RECQL4 in cells or tissues and for treating an animal,
CC particularly a human suspected of having or being prone to a disease or
CC condition associated with expression of RECQL4. The compound is useful
CC for diagnostics, therapeutics and as a research reagent, e.g.
CC prophylactically to prevent or delay infection, inflammation or tumour
CC formation. This sequence represents an antisense oligonucleotide used in
CC inhibition of human RECQL4 expression
XX
SQ Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GGCGAGGCTGCCGCGGCCG 28
Db 1 GGCGAGGCTGCCGCTCAG 19

RESULT 290
AAD41640
ID AAD41640 standard; DNA; 20 BP.
AC
XX AAD41640;
XX
XX 30-OCT-2002 (first entry)
DT
XX Human interleukin-12 p35 subunit DNA amplifying forward PCR primer.
DE
XX Human; interleukin-12; IL-12 p35 subunit; therapeutic; infection; tumour;
KW inflammation; antisense therapy; antisense; prophylactic; PCR; primer;
KW ss.
XX
XX Homo sapiens.
OS
XX US6399379-B1.
PN
XX 04-JUN-2002.
PD
XX
XX 07-MAY-2001; 2001US-00851520.
PF
XX 07-MAY-2001; 2001US-00851520.
PR
XX (ISIS-) ISIS PHARM INC.
PA

XX Baker BF, Freier SM;
PI WPI; 2002-535980/57.
DR
XX Novel antisense compounds targeted to nucleic acids encoding interleukin-
PT 12 p35 subunit, useful for modulating interleukin-12 p35 subunit
PT expression and treating diseases associated with expression of the
PT subunit in humans.
XX
XX Example 13; Col 53; 44pp; English.
PS
XX The present invention relates to novel antisense oligonucleotides which
CC specifically hybridise with specific regions of nucleic acids encoding
CC interleukin-12 (IL-12) p35 subunit and inhibit the expression of human IL
CC -12 p35 subunit. Sequences of the invention are useful for inhibiting the
CC expression of human IL-12 p35 subunit in human cells or tissues and for
CC treating animals, particularly humans suspected of having or being prone
CC to diseases or conditions associated with expression of IL-12 p35
CC subunit. They are useful for diagnostics, therapeutics and as research
CC reagent, e.g. prophylactically to prevent or delay infection, tumour
CC formation or inflammation. Sequences of the invention are useful for
CC antisense therapy. The present DNA sequence is a PCR primer which is used
CC for amplifying human IL-12 p35 subunit DNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 822 GCCTCTCATGACCCAGGAA 840
Db 1 GCCACTCCAGACCCAGGAA 19

RESULT 291
ADE31838/c
ID ADE31838 standard; DNA; 20 BP.
XX
AC ADE31838;
XX
XX 29-JAN-2004 (first entry)
DT
XX Solid surface assembly oligonucleotide Lib1-D.
DE
XX Lipopeptide synthetase; multifunctional enzyme; lipid module;
KW peptide module; DNA library; lipopeptide synthesis; antimicrobial;
KW solid surface; immobilisation; ss.
XX
OS Synthetic.
XX
XX WO200132845-A2.
PN
XX 10-MAY-2001.
PD
XX 06-NOV-2000; 2000WO-EP011237.
PF
XX 05-NOV-1999; 99EP-00203674.
PR
XX (BIOM-) BIOMADE BV.
PA
XX Leenhouts CJ, Noback MA, Van Den Burg L, Hamoen LW, Duitman EH;
PI Kuipers OP;
XX
XX WPI; 2002-239393/29.
DR
XX Preparing lipopeptide synthetases, useful for producing new combinations
PT of lipid molecules and amino acid modules, comprises modifying the lipid
PT moiety and optionally a peptide moiety of one or more known (lipo)peptide
PT synthetase.
XX

CC amplify the regions of the vex2 and pep27 genes which contain the single
CC nucleotide polymorphisms (SNPs). The genes are located within the
CC vex/pep27/vncR/s operon encoding the major pneumococcal autolytic enzyme,
CC LytA. The operon encodes for a signal peptide, Pep27, that is transported
CC out of the cell via the vex dedicated transporter. Once it reaches a
CC critical density in the supernatant, it signals through the two-component
CC regulatory system, Vncs and VncR, which subsequently induces activation
CC of LytA. Mutations in any one of the operon genes prevents proper
CC signaling, resulting in a lack of LytA activation and antibiotic
CC tolerance. The method is useful for determining whether a bacteria is
CC likely to be tolerant to an antibiotic, preferably a beta-lactam such as
CC penicillin and vancomycin and, therefore, for determining whether a
CC subject suffering from a bacterial infection can be effectively treated
CC with those antibiotics. The method is rapid and correctly predicts
CC whether a subject can be successfully treated with a particular
CC antibiotic. Unsuccessful treatment of the subject with conventional
CC antibiotics can be avoided so that alternative therapies can be
CC administered without delay. The sequence presented is the reverse PCR
CC primer which was used to amplify the S. pneumoniae vncS SNP containing
CC gene fragment

XX Sequence 20 BP; 4 A; 5 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 ATTTGATTTCTTAGAATC 507
||||| ||||| ||||| |||||
DB 1 ATTTGATTTCTTCTTAATC 19

RESULT 294
ACC45665/C
ID ACC45665 standard; DNA; 20 BP.

XX ACC45665;

XX 02-JUN-2003 (first entry)

DE Human HBM STS marker reverse primer #122.

XX Human; high bone mass; HBM; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.

XX Homo sapiens.

XX WO200292764-A2.

XX 21-NOV-2002.

XX 13-MAY-2002; 2002WO-US014876.

XX 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.

XX Babij P, Bex FJ, Yaworsky PJ, Bodine PV;

XX WPI; 2003-129278/12.

XX New transgenic animals (e.g. mice), useful as models for studying bone

PT density modulation, developing drugs for treating or preventing bone

PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by

PT reduced bone density.

PS Disclosure; Page 56; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development, is
CC or characterized by reduced bone density or mass. The present sequence, is
CC used in the exemplification of the invention

XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
||| ||||| ||||| |||||
DB 19 AATATTGTGGCCACACAC 1

RESULT 295

ABZ80435

ID ABZ80435 standard; DNA; 20 BP.

XX ABZ80435;

XX 28-MAY-2003 (first entry)

XX Human protein PPI3671 PCR primer #2.

XX Human; cancer; cancer suppression; cancer inhibitor; PCR primer; ss.

XX Homo sapiens.

XX CN1368509-A.

XX 11-SEP-2002.

XX 08-FEB-2001; 2001CN-00105310.

XX 08-FEB-2001; 2001CN-00105310.

XX (SHAN-) SHANGHAI INST ONCOLOGY.

XX Gu J;

XX WPI; 2003-112778/11.

XX Human protein that suppresses cancer cell growth and its coding sequence.

XX Example 2; Page 10 (Disclosure); 36pp; Chinese.

XX ABZ80408 to ABZ80418 encode the human proteins ABP96551 to ABP96561 which
CC have cancer inhibiting functions. Also described is a method for
CC preparing the proteins using recombination techniques. The human proteins
CC from the present invention, and nucleotide sequences encoding them, can
CC be used for treating diseases such as cancer. The present sequence
CC represents a PCR primer for a human cancer inhibiting function related
CC protein from the present invention

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 819 CAGGCTCTCATGACCCAG 837
 ||||| ||||| ||||| |||||
 Db 1 CAGGCTCTCTTGACGCAG 19

RESULT 296
 ACH11218/c
 ID ACH11218 standard; DNA; 20 BP.
 XX
 AC ACH11218;
 XX
 DT 08-OCT-2003 (first entry)
 XX
 DE Human protein kinase C-epsilon targeted oligonucleotide ISIS#7941.
 XX
 KW Human; ss; antisense; PKC; protein kinase C; hyperproliferation; tumour;
 KW inflammation; psoriasis; cancer; non-small cell lung cancer; lung cancer;
 KW non-Hodgkin's lymphoma; glioblastoma; bladder cancer; colon cancer;
 KW breast cancer; ovarian cancer; pancreatic cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6537973-B1.
 XX
 PD 25-MAR-2003.
 XX
 PF 18-DEC-2001; 2001US-00025139.
 XX
 PR 16-MAR-1992; 92US-00852852.
 PR 09-JUL-1993; 93US-00089996.
 PR 07-JUN-1995; 95US-00478178.
 PR 31-MAR-1997; 97US-00829637.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dean NM, Holmlund JT, Dorr FA;
 XX
 DR WPI; 2003-531084/50.
 XX
 PT New pharmaceutical composition, useful for treating cancer, e.g., non-
 PT small cell lung cancer or non-Hodgkin's lymphoma.
 XX
 PS Example 16; Col 22; 56pp; English.
 XX
 CC The invention relates to a new pharmaceutical composition comprising: (a)
 CC an oligonucleotide sequence having up to 50 base pairs (bp); and (b)
 CC carboplatin and paclitaxel, cisplatin and gemcitabine, 5-fluorouracil and
 CC leucovorin, or docetaxel. The pharmaceutical composition is useful for
 CC treating diseases associated with protein kinase C such as
 CC hyperproliferative and inflammatory conditions e.g. psoriasis, tumours
 CC and cancer e.g. non-small cell lung cancer, non-Hodgkin's lymphoma,
 CC glioblastoma, bladder cancer, lung cancer, colon cancer, breast cancer,
 CC ovarian cancer and pancreatic cancer. The present sequence represents an
 CC antisense oligonucleotide targeted against protein kinase C
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
 ||||| ||||| ||||| |||||
 Db 19 AGAGGAGAGATTTTGCT 1

RESULT 297

ACA62693/c
 ID ACA62693 standard; DNA; 20 BP.
 XX
 AC ACA62693;
 XX
 DT 20-AUG-2003 (first entry)
 XX
 DE RIZ(A)8 tract primer RIZA8-F.
 XX
 KW RIZ1; microsatellite instability; tumour; apoptosis; ss; PCR; primer;
 KW retinoblastoma protein interacting zinc finger gene; colorectal tumour;
 KW endometrial tumour; hereditary nonpolyposis colon carcinoma; MSI;
 KW gastric tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032606-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 17-DEC-2001; 2001US-00024450.
 XX
 PR 19-DEC-2000; 2000US-0256582P.
 XX
 PA (HUAN/) HUANG S.
 PA (CHAD/) CHADWICK R B.
 XX
 PI Huang S, Chadwick RB;
 XX
 DR WPI; 2003-492075/46.
 XX
 PT Inhibiting growth of microsatellite instability-positive tumor, by
 PT introducing a nucleic acid molecule encoding a retinoblastoma protein-
 PT interacting zinc finger gene-1 polypeptide into the tumor.
 XX
 PS Example 2; Page 7; 41pp; English.
 XX
 CC The invention relates to a method of inhibiting growth of a
 CC microsatellite instability (MSI)-positive tumor, which involves
 CC introducing into the tumor a nucleic acid molecule encoding a
 CC retinoblastoma protein-interacting zinc finger gene (RIZ)-1 polypeptide
 CC and expressing the polypeptide in the tumor in an effective amount to
 CC inhibit growth of the tumor. The method is useful for inhibiting growth
 CC of a microsatellite instability (MSI)-positive tumor. The tumor
 CC contains cells having an abnormal number of adenine nucleotides in a
 CC RIZ poly(A) tract. The MSI-positive tumor is colorectal tumour, gastric
 CC tumour, endometrial tumour or hereditary nonpolyposis colon carcinoma.
 CC Also disclosed is a method for determining MSI status of the tumor. Both
 CC methods are useful for detecting and treating MSI(+) tumours and for
 CC inducing apoptotic cell killing both in vitro and in vivo. The present
 CC sequence represents the RIZ(A)8 tract primer RIZA8-F
 XX
 SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 966 AGGACATTTTCATGATC 984
 ||||| ||||| ||||| |||||
 Db 19 ACGACATTTTCTGAGCTC 1

RESULT 298
 ABT44202/c
 ID ABT44202 standard; DNA; 20 BP.
 XX
 AC ABT44202;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Chimeric antisense oligonucleotide ISIS 199198 to inhibit human NOD1.
 XX

Fri Aug 19 11:00:00 2005

KW Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss;
KW caspase associated recruitment domain 4; programmed cell death; cancer;
KW apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4;
KW amyotrophic lateral sclerosis; retinitis pigmentosa; autoimmune disorder;
KW viral infection; human; chimeric.
XX
OS Chimeric - Homo sapiens.
XX
XX WO2003050246-A2.
XX
XX 19-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038606.
XX
XX 05-DEC-2001; 2001US-00006883.
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KW, Roach MP;
PI WPI; 2003-577293/54.
XX
XX New compound, comprising a sequence targeted to a nucleic acid encoding
PT nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing
PT a composition for treating hyperproliferative disease, e.g., cancer.
XX
XX Example 15; Page 76; 138pp; English.
XX
XX This invention relates to novel chimeric antisense oligonucleotides that
CC specifically hybridize to and inhibit the expression of the nucleotide
CC binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4
CC (caspase associated recruitment domain 4) is a domain that is involved in
CC the elimination of cells via programmed cell death and in the host
CC defence against pathogens, i.e. it works to regulate apoptosis. Apoptosis
CC is a naturally occurring process, however, if it becomes overstimulated
CC it can lead to cell loss and neurodegenerative conditions including
CC Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), retinitis
CC pigmentosa and blood cell disorders. Conversely, insufficient apoptosis
CC can contribute to the development of cancer, autoimmune disorders and
CC viral infections. The present invention describes antisense
CC oligonucleotides that can modulate NOD1 expression (and variants
CC thereof), such that these compounds, via gene therapy, can be used to
CC treat various human diseases caused by aberrant apoptosis. This
CC oligonucleotide sequence is the chimeric antisense oligo used to inhibit
CC expression of human NOD1, the aim of the invention. Note that it has two
CC terminal five nucleotide 2'-methoxyethyl (2'-MOE) wings separated by a
CC ten deoxynucleotide gap. The oligonucleotide backbone is phosphorothioate
CC throughout
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1096 TTACTGCTCATTTGTTTA 1114
Db 19 TTGCCCGCTCATTTGTTAA 1

RESULT 299
ADB98363/C
ID ADB98363 standard; DNA; 20 BP.
XX
XX ADB98363;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Sequence tagged site #244 used to prepare Zmax1 (LRP5) gene region map.
DE
XX Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
KW
XX

OS Homo sapiens.
XX
XX WO200292000-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US014877.
XX
XX 11-MAY-2001; 2001US-0290071P.
XX
XX 17-MAY-2001; 2001US-0291311P.
XX
XX 01-FEB-2002; 2002US-0353058P.
XX
XX 04-MAR-2002; 2002US-0361293P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX (AMHP) WYETH.
PA
XX Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
PI WPI; 2003-129214/12.
XX
XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
XX Example 2; Page 62; 629pp; English.
XX
XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)
CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
CC region.
XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
Db 19 AATATTGTGGCCACACAC 1

RESULT 300
ADD20426
ID ADD20426 standard; DNA; 20 BP.
XX
XX ADD20426;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Oreochromis niloticus microsatellite primer SEQ ID NO:1061.
XX
XX single nucleotide polymorphism; SNP; fish; Salmo salar;
KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW detection; primer; ss.
XX
XX Synthetic.
OS
XX Oreochromis niloticus.
XX
XX WO2003060160-A2.
PN
XX
XX 24-JUL-2003.
PD
XX
XX 17-JAN-2003; 2003WO-IB000112.
PF
XX
XX 18-JAN-2002; 2002US-0349950P.
PR

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PR 16-AUG-2002; 2002US-0404200P.
PA (GENO-) GENOMAR ASA.
PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX WPI; 2003-627388/59.
DR Novel isolated nucleic acid molecule comprising single nucleotide
PT polymorphism associated with fish, useful for forming PCR primers which
PT are used for detecting single nucleotide polymorphisms in fish nucleic
PT acids.
XX Claim 18; SEQ ID NO 1061; 233pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) comprising a
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC (i), or its complement under highly stringent hybridisation conditions.
CC Also described: (1) an isolated oligonucleotide (II) comprising at least
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites, or their complement; (2)
CC a primer pair (III) suitable for use in PCR, comprising two (II) capable
CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC origin of fish sample comprising providing a parent genotype database
CC comprising a collection of candidate parent genotypes, where each of the
CC candidate parent genotype represents a distinct origin, and comparing a
CC sample genotype to the parent genotype database, where a match between
CC the sample genotype and one of the candidate parent genotype identifies
CC to the origin of the sample. (M1) is useful for determining the origin of
CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC detecting nucleic acid molecule comprising SNP in a sample, which
CC involves contacting the sample containing nucleic acids with one or more
CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC useful for detecting nucleic acid molecule comprising a polymorphic
CC sequence in a sample, comprising contacting the sample containing nucleic
CC acids with one or more (II) which is derived from O. niloticus
CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC sites or seabass polymorphic sites, and identifying a nucleic acid that
CC hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC comprising a microsatellite sequence in sample. The present sequence is
CC used in the exemplification of the present invention.
XX
XX Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 782 CTGGGGATGCTGGAG 800
Db 2 CTGGGTTGAGCTGGAG 20
| | | | | | | | | |
RESULT 301
ADD90778
ID ADD90778 standard; DNA; 20 BP.
XX
XX ADD90778;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX S. pneumoniae vncS gene PCR primer #2.
DE
XX ss; PCR; primer; antibiotic; antibiotic tolerance; bacterial resistance;
KW beta-lactam; penicillin; vancomycin; vncS.
XX

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OS Streptococcus pneumoniae.
XX US2003175796-A1.
XX
XX 18-SEP-2003.
XX
XX 02-MAY-2003; 2003US-00428617.
XX
XX 13-NOV-2001; 2001US-00054225.
XX
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX Atkinson RM, Tuomanen EI;
PI
XX WPI; 2003-852128/79.
DR
XX
XX Determining whether a bacteria is likely to be tolerant to beta-lactam,
PT penicillin or vancomycin by determining the genotype of the vex2 and
PT pep27 genes.
XX
XX Claim 16; SEQ ID NO 12; 11pp; English.
XX
XX The invention relates to a method of determining whether a bacteria is
CC likely to be tolerant to antibiotics. The methods are used for
CC determining bacterial resistance to beta-lactam, penicillin and/or
CC vancomycin. The present sequence represents the S. pneumoniae vncS PCR
CC primer.
XX
XX Sequence 20 BP; 4 A; 5 C; 1 G; 10 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 489 ATTGAATTTCTTAGAATC 507
Db 1 ATTGAATTTCTTAGAATC 19
| | | | | | | | | |
RESULT 302
ACH00690/C
ID ACH00690 standard; DNA; 20 BP.
XX
XX ACH00690;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Mammalian inverted nipple associated microsatellite PCR primer #144.
DE
XX
XX Inverted nipple; microsatellite; PCR; primer; ss; pig.
XX
XX Mammalia.
OS
XX
XX WO2003066891-A2.
PN
XX
XX 14-AUG-2003.
PD
XX
XX 03-FEB-2003; 2003WO-EP001045.
PF
XX
XX 05-FEB-2002; 2002EP-00002632.
PR
XX
XX (FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE.
PA
XX
XX Hardge T, Schellander K, Wimmers K;
PI
XX WPI; 2003-671539/63.
DR
XX
XX Determining predisposition to inverted nipples useful e.g. for selecting
PT breeding animals comprises detecting specific microsatellite markers.
XX
XX Disclosure; Page 24; 63pp; German.
XX
XX The present invention relates to the use of a nucleic acid to determine
CC

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CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 191 TTCCACGCCATCTCCCCA 209
 |||||
 Db 1 TTGGAGGCCATCTCCCCA 19

RESULT 305

ABZ88740/C
 ID ABZ88740 standard; DNA; 20 BP.

XX AC ABZ88740;

DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX FA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 3982; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 540 TTTACTATGAATTTAATA 558
 |||||
 Db 20 TTCACATGACATTAATA 2

RESULT 306

ABQ84375/C

ID ABQ84375 standard; DNA; 20 BP.

XX AC ABQ84375;

DT 20-FEB-2003 (first entry)

XX DE DPP10 PCR primer #6.

XX KW DPP10; dipeptidyl peptidase; prolololigopeptidase; enzyme; asthma;
 KW antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;
 KW antirheumatic; vaccine; gene therapy; inflammatory disease;
 KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
 KW chromosome 2q14; PCR primer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200286113-A2.

XX PD 31-OCT-2002.

XX PF 24-APR-2002; 2002WO-GB001887.

XX PR 24-APR-2001; 2001GB-00010044.

XX PR 24-APR-2001; 2001GB-00010046.

XX PR 12-OCT-2001; 2001GB-00024575.

XX PR 12-OCT-2001; 2001GB-00024594.

XX PA (ISIS-) ISIS INNOVATIONS LTD.

XX PI Cookson WOCM, Moffat MF, Allen M, Lench N;

XX DR WPI; 2003-093132/08.

XX PT New nucleic acid sequence comprising DPP10 mRNA, useful for the
 PT manufacture of a medicament for regulating DPP10 protein expression or
 PT for preventing or treating inflammatory disease e.g., inflammatory bowel
 PT disease.

XX PS Claim 43; Page 313; 321pp; English.

XX CC The present invention describes a new isolated nucleic acid sequence (I)
 CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
 CC known as prolololigopeptidase). (I) has antiinflammatory, antiasthmatic,
 CC antipsoriatic, antiarthritic and antirheumatic activities, and can be
 CC used in vaccines and gene therapy. A composition comprising (I) can be
 CC used for the manufacture of a medicament for regulating DPP10 expression
 CC or for preventing or treating inflammatory disease e.g., inflammatory
 CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
 CC also be used in an assay for detecting or measuring DPP10 in a sample. A

CC host cell comprising (I) can be used for producing recombinant DPP10 gene
 CC products, or in drug screening systems to identify agents for diagnosis
 CC or treatment of individuals having or susceptible to inflammatory
 CC disease. Human DPP10 is located on chromosome 2, more specifically
 CC chromosome 2q14. ABQ84234 to ABQ84612 and ABP55629 represent
 CC sequences used in the exemplification of the present invention

SQ Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 472 TATTCTGATTACAGTGCAT 490
 Db 19 TGTCTGTTACATGCAT 1

RESULT 307
 ABZ77118
 ID ABZ77118 standard; DNA; 20 BP.

XX AC ABZ77118;

XX DT 07-MAY-2003 (first entry)

XX DE Human stearyl-CoA desaturase phosphorothioate oligonucleotide SEQ:73.
 KW Human; stearyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
 KW 2'-MOE; cardiovascular; antiarteriosclerotic; antilipemic; cytostatic;
 KW antinflammatory; antisense therapy; antisense oligonucleotide; tumour;
 KW abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
 KW atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.

OS Homo sapiens.
 OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"

XX WO2003012031-A2.

XX 13-FEB-2003.

XX 16-JUL-2002; 2002WO-US022676.

XX 30-JUL-2001; 2001US-00918187.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ;

XX WPI; 2003-248160/24.

XX New antisense oligonucleotides targeted to nucleic acids encoding human
 PT stearyl-CoA desaturase, useful for treating diseases associated with the
 PT desaturase, e.g. atherosclerosis, and in diagnostic and research
 PT applications.

XX Claim 3; Page 95; 117pp; English.

XX The present invention describes a compound (I) that is 8-50 nucleobases

CC in length targeted to a nucleic acid molecule encoding human stearyl-CoA
 CC desaturase, and which specifically hybridises with and inhibits the
 CC expression of human stearyl-CoA desaturase, or which specifically
 CC hybridises with at least an 8-nucleobase portion of an active site on a
 CC nucleic acid molecule encoding human stearyl-CoA desaturase. Human
 CC stearyl-CoA desaturase is mapped to chromosome 10. (I) has antilipemic,
 CC cardiovascular, antiarteriosclerotic, cytostatic and antinflammatory
 CC activities, and can be used in antisense therapy. The antisense compounds
 CC (I) can be used for modulating the expression of human stearyl-CoA
 CC desaturase and for treating diseases or conditions associated with
 CC expression of human stearyl-CoA desaturase, e.g. abnormal lipid or
 CC cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
 CC antisense compounds (I) can also be used for diagnostics, therapeutics
 CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
 CC tumour formation, as research reagents and kits, and in distinguishing
 CC between functions of various members of a biological pathway. The present
 CC sequence represents a human stearyl-CoA desaturase inhibiting chimeric
 CC phosphorothioate antisense oligonucleotide, which is given in an example
 CC from the present invention

SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 814 TGAAGCAGGCCTCTCATGA 832

Db 2 TCAGCAGGCATCTCATGA 20

RESULT 308

ABV99953

ID ABV99953 standard; DNA; 20 BP.

XX AC ABV99953;

XX DT 06-MAR-2003 (first entry)

XX DE Coriolus versicolor cytochrome P450 PCR primer SEQ ID 6.

XX KW Cytochrome P450; antidote; PCR; primer; ss.

XX OS Coriolus versicolor.

XX PN JP2002253248-A.

XX PD 10-SEP-2002.

XX PF 28-FEB-2001; 2001JP-00055452.

XX PR 28-FEB-2001; 2001JP-00055452.

XX (WARI/) WARIISHI H.

XX PA (KUBI) KUBOTA CORP.

XX WPI; 2003-096531/09.

XX A new polypeptide with cytochrome P450 activity useful for producing
 PT antidotes.

XX Example 1; Page 8; 16pp; Japanese.

XX The present invention relates to a novel cytochrome P450 (see ABP70653).
 CC (I) is useful for producing antidotes. Also disclosed are a recombinant
 CC vector containing the coding sequence for (I); a transformant transformed
 CC by the recombinant vector; and a method for preparing cytochrome P450,
 CC comprising culturing the transformant and recovering cytochrome P450 from
 CC the culture. The present sequence is a PCR primer, which was used in an
 CC example from the invention

XX Sequence 20 BP; 5 A; 10 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 952 CCCACTCTGGAGCCAGGAC 970
 ||||| ||||| ||||| |||||
 DB 2 CCCACCGAGCCAGGAC 20

RESULT 309
 ADM83692
 ID ADM83692 standard; DNA; 20 BP.
 XX AC ADM83692;
 XX DT 03-JUN-2004 (first entry)
 XX DE Serine protease-like protease NES-1 primer #3.
 XX KW cellular proliferative disorder; breast cancer; methylation;
 KW predisposition; methylation specific PCR; PCR; primer; CpG island; ss;
 KW human; serine protease-like protease; NES-1.
 XX OS Homo sapiens.
 XX US2003138783-A1.
 XX PD 24-JUL-2003.
 XX PF 28-JAN-2002; 2002US-00059579.
 XX PR 26-JAN-2001; 2001US-00771357.
 XX PA (SUKU/) SUKUMAR S.
 XX PA (EVRO/) EVRON E.
 XX PA (DOOL/) DOOLEY W C.
 XX PA (SACC/) SACCCHI N.
 XX PA (DAVI/) DAVIDSON N.
 XX PA (FACK/) FACKLER M J.

Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
 WPI; 2003-851722/79.
 Diagnosing a cellular proliferative disorder of breast tissue in a
 subject comprises determining the state of methylation of one or more
 nucleic acid isolated from the subject.
 Claim 13; SEQ ID NO 79; 59pp; English.
 The invention describes a method of diagnosing a cellular proliferative
 disorder of breast tissue in a subject comprising determining the state
 of methylation of one or more nucleic acid isolated from the subject,
 where the state of methylation of one or more nucleic acids is compared
 with the state of methylation of one or more nucleic acids from a subject
 not having the cellular proliferative disorder of breast tissue. Also
 described are: a method for determining a predisposition to a cellular
 proliferative disorder of breast tissue in a subject; a method of
 diagnosing a cellular proliferative disorder of breast tissue in a
 subject; and a kit for the detecting a cellular proliferative disorder of
 breast tissue in a subject. The method is useful for diagnosing a
 cellular proliferative disorder of breast tissue in a subject. This
 sequence represents a methylation specific primer used in the analysis of
 the methylation state of the serine protease-like protease NES-1 gene CpG
 islands in normal mammary epithelium, breast cancer cell lines and in
 primary mammary tumours.
 Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGCGGTTT 167
 ||||| ||||| ||||| |||||
 DB 1 TTCGAAGTTTATGCGGTTT 19

RESULT 310
 ADM83766
 ID ADM83766 standard; DNA; 20 BP.
 XX AC ADM83766;
 XX DT 03-JUN-2004 (first entry)
 XX DE Serine protease-like protease NES-1 primer #14.
 XX KW cellular proliferative disorder; breast cancer; methylation;
 KW predisposition; methylation specific PCR; PCR; primer; CpG island; ss;
 KW human; serine protease-like protease; NES-1.
 XX OS Homo sapiens.
 XX US2003138783-A1.
 XX PD 24-JUL-2003.
 XX PF 28-JAN-2002; 2002US-00059579.
 XX PR 26-JAN-2001; 2001US-00771357.
 XX PA (SUKU/) SUKUMAR S.
 XX PA (EVRO/) EVRON E.
 XX PA (DOOL/) DOOLEY W C.
 XX PA (SACC/) SACCCHI N.
 XX PA (DAVI/) DAVIDSON N.
 XX PA (FACK/) FACKLER M J.

Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
 WPI; 2003-851722/79.
 Diagnosing a cellular proliferative disorder of breast tissue in a
 subject comprises determining the state of methylation of one or more
 nucleic acid isolated from the subject.
 Disclosure; SEQ ID NO 158; 59pp; English.
 The invention describes a method of diagnosing a cellular proliferative
 disorder of breast tissue in a subject comprising determining the state
 of methylation of one or more nucleic acid isolated from the subject,
 where the state of methylation of one or more nucleic acids is compared
 with the state of methylation of one or more nucleic acids from a subject
 not having the cellular proliferative disorder of breast tissue. Also
 described are: a method for determining a predisposition to a cellular
 proliferative disorder of breast tissue in a subject; a method of
 diagnosing a cellular proliferative disorder of breast tissue in a
 subject; and a kit for the detecting a cellular proliferative disorder of
 breast tissue in a subject. The method is useful for diagnosing a
 cellular proliferative disorder of breast tissue in a subject. This
 sequence represents a methylation specific primer used in the analysis of
 the methylation state of the serine protease-like protease NES-1 gene CpG
 islands in normal mammary epithelium, breast cancer cell lines and in
 primary mammary tumours.
 Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGCGGTTT 167
 ||||| ||||| ||||| |||||
 DB 1 TTCGAAGTTTATGCGGTTT 19

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RESULT 311
ID ABD27535 standard; DNA; 20 BP.
XX
AC ABD27535;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA486238-derived oligonucleotide SEQ ID 6547.
XX
OS Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6547; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC of the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

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CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 429 TTGCAAGAGGAGATGATT 447
DB 20 TTGCAAGAGGAGATGACTT 2
RESULT 312
ID ABD24970 standard; DNA; 20 BP.
XX
AC ABD24970;
XX
DT 29-JUL-2004 (first entry)
XX
DE A1138216-derived oligonucleotide SEQ ID 3982.
XX
OS Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 3982; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC of the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

```

CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 XX Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 540 TTTACTATGAATTTAATA 558
 |||||
 Db 20 TTCACATGACATTTAATA 2

RESULT 313
 ABD32349
 ID ABD32349 standard; DNA; 20 BP.
 XX
 AC ABD32349;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human PDE4C-derived oligonucleotide SEQ ID 14560.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 PA (EPFIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandraaagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-093058/08.
 XX
 PT Pharmacetical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 14560; 763pp; English.
 XX
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 XX Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 1.3%; Score 14.2; DB 1;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 191 TTCCACGCCCATCTCCCCCA 209
 |||||
 Db 1 TTGGAGGCCATCTCCCCCA 19

RESULT 314
 ADH47993/C
 ID ADH47993 standard; DNA; 20 BP.
 XX
 AC ADH47993;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Protein kinase C epsilon antisense oligonucleotide seq id 86.
 XX
 KW cytostatic; protein-kinase-inhibitor-C-alpha; gene therapy; carboplatin;
 KW paclitaxel; docetaxel; cisplatin; gemcitabine; 5-fluorouracil;
 KW leucovorin; protein kinase C alpha inhibitor; PKC-alpha inhibitor;
 KW cancer; non-small cell lung cancer; non-Hodgkin's lymphoma;
 KW antisense technology; ss; PKC-epsilon.
 XX
 OS Synthetic.
 XX
 PN US2003148989-A1.
 XX
 PD 07-AUG-2003.
 XX
 PR 21-JAN-2003; 2003US-00348485.
 XX
 PR 16-MAR-1992; 92US-00852852.
 PR 09-JUL-1993; 93US-00089996.
 PR 07-JUN-1995; 95US-00478178.
 PR 31-MAR-1997; 97US-00829637.
 PR 18-DEC-2001; 2001US-00025139.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dean NM, Holmlund JT, Dorr FA;
 XX WPI; 2004-106519/11.
 DR

PT New pharmaceutical compositions comprising oligonucleotide in combination
PT with e.g. arboptatin or cisplatin, useful for inhibiting protein kinase C
PT expression, particularly for treating cancer, e.g. non-Hodgkin's
PT lymphoma.

XX Example 16; SEQ ID NO 86; 52pp; English.

CC The invention describes new pharmaceutical compositions comprising an
CC oligonucleotide up to 50 nucleotide units in length of a sequence having
CC 20 bp (dnal), in combination with any of the following: carboplatin and
CC paclitaxel; docetaxel; cisplatin and gemcitabine; or 5-fluorouracil and
CC leucovorin. Also described are: a method of inhibiting protein kinase C
CC (PKC)-alpha expression in human cells by contacting the cells with any of
CC the pharmaceutical compositions; and methods of treating a condition
CC associated with expression of human PKC-alpha by administering to an
CC animal, or its cells, tissues or bodily fluid any of the pharmaceutical
CC compositions. The compositions are useful for inhibiting PKC-alpha
CC expression in human cells. The compositions are useful for treating a
CC condition associated with the expression of human PKC-alpha, particularly
CC cancer. In particular, the compositions are useful for treating non-small
CC cell lung cancer or non-Hodgkin's lymphoma in a human. This sequence
CC represents a human protein kinase C antisense oligonucleotide.

XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTAGCT 452
|||||
Db 19 AGAGGAGAGGATTTGGCT 1

RESULT 315

ADH58845
ID ADH58845 standard; DNA; 20 BP.

XX AC ADH58845;

XX 25-MAR-2004 (first entry)

XX Human CDC-like kinase 1 antisense oligonucleotide #127.

XX antisense oligonucleotide; CDC-like kinase 1; cancer;
KW autoimmune disorder; infection; inflammation; tumour formation; human;
KW ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone.

XX OS Homo sapiens.

XX PN US2003219895-A1.

XX 27-NOV-2003.

XX 22-MAY-2002; 2002US-00154708.

XX 22-MAY-2002; 2002US-00154708.

XX (ISIS-) ISIS PHARM INC.

XX Watt AT;

XX WPI; 2004-051714/05.

XX New antisense oligonucleotides targeted to nucleic acid molecules
PT encoding CDC-like kinase 1, useful for treating diseases or conditions
PT associated with expression of CDC-like kinase 1, e.g. cancers or
PT autoimmune disorders.

XX Example 15; SEQ ID NO 140; 64pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
CC CDC-like kinase 1. The antisense oligonucleotides of the invention are

CC useful for modulating the expression of CDC-like kinase 1, and for
CC treating diseases or conditions associated with expression of CDC-like
CC kinase 1 (e.g. cancers and autoimmune disorders). The antisense
CC oligonucleotides may also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents an
CC antisense oligonucleotide of the invention that is targeted to human CDC-
CC like kinase 1. NOTE: The present sequence is a 2'-O-methoxyethyl gapmer
CC with a phosphorothioate backbone.

XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 220 CATTGCCAAGAAGATCACC 238

Db 2 CGTTTCCAGAAGATCACC 20

RESULT 316

ADH58791/C

ID ADH58791 standard; DNA; 20 BP.

XX AC ADH58791;

XX 25-MAR-2004 (first entry)

XX Human CDC-like kinase 1 antisense oligonucleotide #73.

XX antisense oligonucleotide; CDC-like kinase 1; cancer;
KW autoimmune disorder; infection; inflammation; tumour formation; human;
KW ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone.

XX OS Homo sapiens.

XX PN US2003219895-A1.

XX 27-NOV-2003.

XX 22-MAY-2002; 2002US-00154708.

XX 22-MAY-2002; 2002US-00154708.

XX (ISIS-) ISIS PHARM INC.

XX Watt AT;

XX WPI; 2004-051714/05.

XX New antisense oligonucleotides targeted to nucleic acid molecules
PT encoding CDC-like kinase 1, useful for treating diseases or conditions
PT associated with expression of CDC-like kinase 1, e.g. cancers or
PT autoimmune disorders.

XX Claim 1; SEQ ID NO 86; 64pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
CC CDC-like kinase 1. The antisense oligonucleotides of the invention are
CC useful for modulating the expression of CDC-like kinase 1, and for
CC treating diseases or conditions associated with expression of CDC-like
CC kinase 1 (e.g. cancers and autoimmune disorders). The antisense
CC oligonucleotides may also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents an
CC antisense oligonucleotide of the invention that is targeted to human CDC-
CC like kinase 1. NOTE: The present sequence is a 2'-O-methoxyethyl gapmer
CC with a phosphorothioate backbone.

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

PF 02-JUL-2002; 2002US-00190366.
 XX
 PR 02-JUL-2002; 2002US-00190366.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dean NM, Freier SM, Dobie KW;
 XX
 WIPI; 2004-081743/08.
 XX
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding HMG-CoA reductase, useful for treating
 PT atherosclerosis, or a disease involving cholesterol metabolism or
 PT angiogenesis.
 XX
 PS Example 16; SEQ ID NO 308; 110pp; English.
 XX
 XX The invention relates to novel compounds of 8-80 nucleobases in length
 CC targeted to, and which specifically hybridises with, a nucleic acid
 CC molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
 CC reductase, and inhibits the expression of HMG-CoA reductase. The novel
 CC compounds have cardiant, antiarteriosclerotic, and antilipemic
 CC activities. The compound can be used to treat disorders by antisense gene
 CC therapy. The compounds, compositions and methods are useful for treating
 CC a disease or condition associated with HMG-CoA reductase, such as a
 CC cardiovascular disorder e.g. atherosclerosis, or a disease or condition
 CC involving cholesterol metabolism. They are also useful in research and
 CC diagnostics for modulating the expression of HMG-CoA reductase. This
 CC polynucleotide sequence represents an antisense oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 95 GCATTATCTCTCAGTGGG 113
 DB 2 GCATTATCTTCAGAGGG 20
 ADI44833
 RESULT 325
 ID ADI44833 standard; DNA; 20 BP.
 AC ADI44833;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human cystic fibrosis CFTR 1-related PCR primer SeqID333.
 XX
 KW genetic marker;
 KW human cystic fibrosis transmembrane conductance regulator; CFTR;
 KW PCR assay; cystic fibrosis; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003235834-A1.
 XX
 PD 25-DEC-2003.
 XX
 PF 19-NOV-2002; 2002US-00300683.
 XX
 PR 12-NOV-1999; 99US-0165301P.
 PR 03-NOV-2000; 2000WO-US030493.
 PR 08-MAY-2001; 2001US-00851501.
 PR 19-NOV-2001; 2001US-0333531P.
 PR 08-MAY-2002; 2002US-00142722.
 XX
 XX (DUNL/) DUNLOP C L M.
 PA (WEIS/) WEISEL J M.
 XX

PI Dunlop CLM, Weisel JM;
 XX
 DR WPI; 2004-070574/07.
 XX
 PT Identifying the presence or absence of a genetic marker in the human
 PT cystic fibrosis transmembrane conductance regulator gene of a subject by
 PT contacting the DNA and primer set and separating the extension product.
 XX
 XX Claim 1; SEQ ID NO 333; 154pp; English.
 PS
 XX This invention relates to a novel method of identifying the presence or
 CC absence of a genetic marker in the human cystic fibrosis transmembrane
 CC conductance regulator (CFTR) gene of a subject using a PCR assay. The
 CC method comprises providing a DNA sample from the subject, providing at
 CC least one primer set given in the specification, contacting the DNA and
 CC the primer set, generating an extension product from the at least one
 CC primer set that comprises a region of DNA that includes the location of
 CC the genetic marker, separating the extension product on the basis of
 CC melting behaviour and identifying the presence or absence of the genetic
 CC marker in the subject by analysing the melting behaviour of the extension
 CC product. The present sequence is that of a PCR primer which was used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 2 G; 10 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 670 CTCGAATATCTTACTTGT 688
 DB 1 CTCATACTTGTACTTGT 19
 RESULT 326
 ADJ61611/c
 ID ADJ61611 standard; DNA; 20 BP.
 XX
 AC ADJ61611;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Oligonucleotide associated to ILSR-X61176 #303.
 XX
 KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
 KW airway inflammation; allergy; asthma; impeded respiration;
 KW cystic fibrosis; acute respiratory distress syndrome;
 KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011613-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 25-JUL-2003; 2003WO-US023509.
 XX
 PR 29-JUL-2002; 2002US-0399076P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 WIPI; 2004-203534/19.
 XX
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codons and introns of respiratory disease-relevant genes e.g.,
 PT CCRI, RANTES, MCP4, useful for prophylaxis or treating respiratory
 PT disease e.g., asthma.
 XX
 PS Claim 2; SEQ ID NO 2467; 85pp; English.

XX The present invention relates to an oligonucleotide anti-sense to e.g.,
 CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
 CC end of nucleic acid target comprising gene(s) chosen from e.g.
 CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
 CC oligonucleotide and optionally surfactant operatively linked to the
 CC oligonucleotide. The method is useful for preventing or treating a
 CC respiratory or lung disease, which involves administering to the airways
 CC of a subject an effective amount of an inhibitor. The oligonucleotide is
 CC useful for production of a medicament for the prevention and/or treatment
 CC of a respiratory or lung disease. The respiratory or lung disease is
 CC chosen from airway inflammation, allergy(ies), asthma, impeded
 CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
 CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
 CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
 CC obstruction. The present sequence represents an oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 676 TTAAGTTACTGTTGGCT 694
 Db 20 TAAAGTTACTGTTGGCT 2
 RESULT 327
 ADJ61203
 ID ADJ61203 standard; DNA; 20 BP.
 XX
 AC ADJ61203;
 XX
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Oligonucleotide associated to PDB4C #269.
 XX
 KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
 KW airway inflammation; allergy; asthma; impeded respiration;
 KW cystic fibrosis; acute respiratory distress syndrome;
 KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011613-A2.
 XX
 PD 05-FEB-2004.
 XX
 XX 25-JUL-2003; 2003WO-US023509.
 XX
 PF 29-JUL-2002; 2002US-0399076P.
 XX
 PR (EPIG-) EPIGENESIS PHARM INC.
 XX
 PA Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI; 2004-203534/19.
 XX
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codons and introns of respiratory disease-relevant genes e.g.,
 PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
 PT disease e.g., asthma.
 XX
 PS Claim 2; SEQ ID NO 2059; 85pp; English.
 XX
 CC The present invention relates to an oligonucleotide anti-sense to e.g.,
 CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
 CC end of nucleic acid target comprising gene(s) chosen from e.g.
 CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the

CC oligonucleotide and optionally surfactant operatively linked to the
 CC oligonucleotide. The method is useful for preventing or treating a
 CC respiratory or lung disease, which involves administering to the airways
 CC of a subject an effective amount of an inhibitor. The oligonucleotide is
 CC useful for production of a medicament for the prevention and/or treatment
 CC of a respiratory or lung disease. The respiratory or lung disease is
 CC chosen from airway inflammation, allergy(ies), asthma, impeded
 CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
 CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
 CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
 CC obstruction. The present sequence represents an oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 191 TTCCACGCCATCTCCCCCA 209
 Db 1 TTGGAGGCCATCTCCCCCA 19
 RESULT 328
 ADJ19254
 ID ADJ19254 standard; DNA; 20 BP.
 XX
 AC ADJ19254;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Antisense 2-MOE gapmer oligo targeted to human Itgb5 - SEQ ID 69.
 XX
 KW integrin beta 5; Itgb5; cytostatic; antiinflammatory; antimicrobial;
 KW antisense; gene therapy; hyperproliferative; cancer; inflammation;
 KW infection; 2-MOE wing; 2'-methoxyethyl gapmer; ss; human;
 KW phosphorothioate backbone.
 XX
 OS Homo sapiens.
 XX
 PN US2004005707-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00188470.
 XX
 PR 02-JUL-2002; 2002US-00188470.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Cooper S, Dobie KW;
 XX
 DR WPI; 2004-081731/08.
 XX
 XX New antisense compounds targeted to nucleic acid molecules encoding
 PT integrin beta 5, useful for treating diseases associated with expression
 PT of integrin beta 5, e.g. hyperproliferative disorder, infection or
 PT inflammation.
 XX
 PS Example 15; SEQ ID NO 69; 105pp; English.
 XX
 CC The invention relates to a novel compound 8-80 nucleobases in length
 CC targeted to a nucleic acid molecule encoding integrin beta 5 (Itgb5). The
 CC compound specifically hybridises with the nucleic acid molecule encoding
 CC integrin beta 5, thus inhibiting the expression of integrin beta 5. The
 CC compound of the invention demonstrates cytostatic, antiinflammatory and
 CC antimicrobial activities and may be useful for inhibiting the expression
 CC of integrin beta 5, via antisense gene therapy and thus for treating
 CC diseases associated with expression of integrin beta 5, including
 CC hyperproliferative disorders such as cancer, inflammation or infection.
 CC The current sequence is that of an antisense 2-MOE (2'-methoxyethyl)
 CC gapmer oligo targeted to human Itgb5 of the invention. The

CC oligonucleotide has central "gap" region flanked on both sides by 2-MOE
 CC "wings". the backbone linkages are phosphorothioate and all cytidine
 CC residues are 5-methylcytidines.
 CC
 SQ Sequence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1029 GAGAGTAACATCACACC 1047
 ||||| ||||| ||||| |||||
 Db 1 GAGAGGAACATCATGTC 19
 RESULT 329
 ADJ18790
 ID ADJ18790 standard; DNA; 20 BP.
 XX
 AC ADJ18790;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Antisense DNA oligo used to modulate human LRH1 expression SeqID 3340.
 XX
 KW human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
 KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
 KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
 KW gall stone; triglyceridaemia; obesity; hepatitis;
 KW hepatocellular carcinoma; aromatase; cytostatic; antilipaeamic;
 KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;
 KW antiinflammatory; virucidal.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /label= OTHER= phosphorothioate backbone
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
 FT cytidine nucleobases are 5-methylcytidine."
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
 FT cytidine nucleobases are 5-methylcytidine."
 XX
 PN WO2004003201-A2.
 XX
 XX 08-JAN-2004.
 XX
 XX 01-JUL-2003; 2003WO-US020865.
 XX
 XX 01-JUL-2002; 2002US-0392813P.
 PR
 XX (PHAA) PHARMACIA CORP.
 XX
 XX Kane CD;
 XX
 XX WFI; 2004-083058/08.
 DR
 XX New antisense oligonucleotides targeted to a nucleic acid encoding liver
 XX related homologue-1 (LRH1), useful for treating breast cancer,
 PT dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
 PT
 XX Example 15; SEQ ID NO 3340; 909pp; English.
 PS
 XX This invention relates to novel antisense compounds useful for modulating
 CC

CC the expression of liver related homologue-1 (LRH1) and splice variants
 CC thereof. Specifically, it refers to compositions 8-30 nucleobases in
 CC length that target a portion of an active site on the nucleic acid
 CC molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan
 CC nuclear receptor protein that functions as a tissue specific
 CC transcription factor. The present invention describes antisense
 CC oligonucleotides that comprise at least one modified internucleoside
 CC linkage, a phosphorothioate linkage; at least one modified sugar moiety,
 CC a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-
 CC methylcytidine. These antisense compounds are useful for treating or
 CC diagnosing a disease associated with LRH1, such as breast cancer,
 CC dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high
 CC LDL (low density lipoprotein), hypercholesterolaemia, gall stones,
 CC triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic
 CC hepatitis, as well as hepatocellular carcinoma or a condition associated
 CC with aromatase activity. Accordingly, these compositions exhibit
 CC cytostatic, antilipaeamic, antiarteriosclerotic, anorectic, hepatotropic,
 CC litholytic, antiinflammatory and virucidal activities. This
 CC oligonucleotide sequence is an antisense DNA oligo used to modulate the
 CC expression of the human LRH1 protein of the invention.
 XX
 SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 433 AAGAGGAGATGATTTTAGC 451
 ||||| ||||| ||||| |||||
 Db 2 AATAGGCCATGATTTTAGC 20
 RESULT 330
 ADJ18263
 ID ADJ18263 standard; DNA; 20 BP.
 XX
 AC ADJ18263;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Antisense DNA oligo used to modulate human LRH1 expression SeqID 2813.
 XX
 KW human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
 KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
 KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
 KW gall stone; triglyceridaemia; obesity; hepatitis;
 KW hepatocellular carcinoma; aromatase; cytostatic; antilipaeamic;
 KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;
 KW antiinflammatory; virucidal.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /label= OTHER= phosphorothioate backbone
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
 FT cytidine nucleobases are 5-methylcytidine."
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
 FT cytidine nucleobases are 5-methylcytidine."
 XX
 PN WO2004003201-A2.
 XX
 XX 08-JAN-2004.
 XX

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PF 01-JUL-2003; 2003WO-US020865.
XX
PR 01-JUL-2002; 2002US-0392813P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Kane CD;
XX
DR WPI; 2004-083058/08.
XX
XX New antisense oligonucleotides targeted to a nucleic acid encoding liver
PT related homologue-1 (LRH1), useful for treating breast cancer.
PT dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
XX
PS Example 15; SEQ ID NO 2813; 909pp; English.
XX
XX This invention relates to novel antisense compounds useful for modulating
CC the expression of liver related homologue-1 (LRH1) and splice variants
CC thereof. Specifically, it refers to compositions 8-30 nucleobases in
CC length that target a portion of an active site on the nucleic acid
CC molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan
CC nuclear receptor protein that functions as a tissue specific
CC transcription factor. The present invention describes antisense
CC oligonucleotides that comprise at least one modified internucleoside
CC linkage, a phosphorothioate linkage; at least one modified sugar moiety,
CC a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-
CC methylcytidine. These antisense compounds are useful for treating or
CC diagnosing a disease associated with LRH1, such as breast cancer,
CC dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high
CC LDL (low density lipoprotein), hypercholesterolaemia, gall stones,
CC triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic
CC hepatitis, as well as hepatocellular carcinoma or a condition associated
CC with aromatase activity. Accordingly, these compositions exhibit
CC cytostatic, antilipaeamic, antiarteriosclerotic, anorectic, hepatotropic,
CC litholytic, antiinflammatory and virucidal activities. This
CC oligonucleotide sequence is an antisense DNA oligo used to modulate the
CC expression of the human LRH1 protein of the invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 433 AAGAGGAGATGATTTTAC 451
Db 1 AATAGGCCATGATTTTAC 19

RESULT 331
ADJ18084
ID ADJ18084 standard; DNA; 20 BP.
XX
AC ADJ18084;
XX
XX 20-MAY-2004 (first entry)
XX
XX Antisense DNA oligo used to modulate human LRH1 expression SeqID 2634.
XX
XX human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
KW gall stone; triglyceridaemia; obesity; hepatitis;
KW hepatocellular carcinoma; aromatase; cytostatic; antilipaeamic;
KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;
KW antiinflammatory; virucidal.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b

FT 01-JUL-2003; 2003WO-US020865.
FT /label= OTHER= phosphorothioate backbone
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT cytidine nucleobases are 5-methylcytidine."
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT cytidine nucleobases are 5-methylcytidine."
XX
PN WO2004003201-A2.
XX
PD 08-JAN-2004.
XX
XX 01-JUL-2003; 2003WO-US020865.
XX
XX 01-JUL-2002; 2002US-0392813P.
XX (PHAA ) PHARMACIA CORP.
XX
XX Kane CD;
XX
XX WPI; 2004-083058/08.
XX
XX New antisense oligonucleotides targeted to a nucleic acid encoding liver
XX related homologue-1 (LRH1), useful for treating breast cancer.
XX dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
XX
XX Example 15; SEQ ID NO 2634; 909pp; English.
XX
XX This invention relates to novel antisense compounds useful for modulating
XX the expression of liver related homologue-1 (LRH1) and splice variants
XX thereof. Specifically, it refers to compositions 8-30 nucleobases in
XX length that target a portion of an active site on the nucleic acid
XX molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan
XX nuclear receptor protein that functions as a tissue specific
XX transcription factor. The present invention describes antisense
XX oligonucleotides that comprise at least one modified internucleoside
XX linkage, a phosphorothioate linkage; at least one modified sugar moiety,
XX a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-
XX methylcytidine. These antisense compounds are useful for treating or
XX diagnosing a disease associated with LRH1, such as breast cancer,
XX dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high
XX LDL (low density lipoprotein), hypercholesterolaemia, gall stones,
XX triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic
XX hepatitis, as well as hepatocellular carcinoma or a condition associated
XX with aromatase activity. Accordingly, these compositions exhibit
XX cytostatic, antilipaeamic, antiarteriosclerotic, anorectic, hepatotropic,
XX litholytic, antiinflammatory and virucidal activities. This
XX oligonucleotide sequence is an antisense DNA oligo used to modulate the
XX expression of the human LRH1 protein of the invention.
XX
XX Sequence 20 BP; 5 A; 4 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 391 AGTCATTTCCCTTACATTT 409
Db 2 AGTCATTTCCCTTAAATTT 20

RESULT 332
ADJ17966
ID ADJ17966 standard; DNA; 20 BP.
XX
XX ADJ17966;
XX
XX 20-MAY-2004 (first entry)
XX

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XX DE Antisense DNA oligo used to modulate human LRH1 expression SeqID 2516.
XX KW human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
XX KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
XX KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
XX KW gall stone; triglyceridaemia; obesity; hepatitis;
XX KW hepatocellular carcinoma; aromatase; cytostatic; antilipaeamic;
XX KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;
XX KW antiinflammatory; virucidal.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /label= OTHER= phosphorothioate backbone
XX FT modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
XX FT cytidine nucleobases are 5-methylcytidine."
XX FT modified_base 16..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
XX FT cytidine nucleobases are 5-methylcytidine."
XX PN WO2004003201-A2.
XX XX
XX PD 08-JAN-2004.
XX PF 01-JUL-2003; 2003WO-US020865.
XX XX
XX PR 01-JUL-2002; 2002US-0392813P.
XX XX
XX PA (PHAA ) PHARMACIA CORP.
XX PI Kane CD;
XX PS WPI; 2004-083058/08.
XX XX
XX KW New antisense oligonucleotides targeted to a nucleic acid encoding liver
XX FT related homologue-1 (LRH1), useful for treating breast cancer,
XX FT dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
XX PS Example 15; SEQ ID NO 2516; 909pp; English.
XX XX
XX CC This invention relates to novel antisense compounds useful for modulating
XX CC the expression of liver related homologue-1 (LRH1) and splice variants
XX CC thereof. Specifically, it refers to compositions 8-30 nucleobases in
XX CC length that target a portion of an active site on the nucleic acid
XX CC molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan
XX CC nuclear receptor protein that functions as a tissue specific
XX CC transcription factor. The present invention describes antisense
XX CC oligonucleotides that comprise at least one modified internucleoside
XX CC linkage, a phosphorothioate linkage; at least one modified sugar moiety,
XX CC a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-
XX CC methylcytidine. These antisense compounds are useful for treating or
XX CC diagnosing a disease associated with LRH1, such as breast cancer,
XX CC dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high
XX CC LDL (low density lipoprotein), hypercholesterolaemia, gall stones,
XX CC triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic
XX CC hepatitis, as well as hepatocellular carcinoma or a condition associated
XX CC with aromatase activity. Accordingly, these compositions exhibit
XX CC cytostatic, antilipaeamic, antiarteriosclerotic, anorectic, hepatotropic,
XX CC litholytic, antiinflammatory and virucidal activities. This
XX CC oligonucleotide sequence is an antisense DNA oligo used to modulate the
XX CC expression of the human LRH1 protein of the invention.
XX XX
XX SQ Sequence 20 BP; 6 A; 4 C; 1 G; 9 T; 0 U; 0 Other;

```

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Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 391 AGTCATTTTCCTTACAAATT 409
   ||||| ||||| ||||| |||||
Db 1 AGTCATTTTCCTTAAATATT 19

RESULT 333
ADJ24119/c
ID ADJ24119 standard; DNA; 20 BP.
XX AC ADJ24119;
XX XX
XX DT 20-MAY-2004 (first entry)
XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2517.
XX KW Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
XX KW cardiovascular disorder; metabolic syndrome X; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "This oligonucleotide has a phosphorothioate
XX FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
XX FT and 3' ends, which are 4 nucleotides in length. Also all
XX FT cytidine residues are 5-methylcytidines"
XX PN WO2004009541-A2.
XX XX
XX PD 29-JAN-2004.
XX PF 18-JUL-2003; 2003WO-US022410.
XX PR 19-JUL-2002; 2002US-0397106P.
XX XX
XX PA (PHAA ) PHARMACIA CORP.
XX PI Bhat BG;
XX XX
XX DR WPI; 2004-132912/13.
XX XX
XX PT New antisense oligonucleotide for modulating endothelial lipase
XX PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX PS Claim 3; SEQ ID NO 2517; 1007pp; English.
XX CC The present invention relates to antisense oligonucleotides (ADJ21603-
XX CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX XX
XX SQ Sequence 20 BP; 12 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

```

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Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 315 TTGATTTCCTGTATTCT 333

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```

Db      19 TTGGCTTTCCCTATTTTCT 1
||||| ||||| || |||||
RESULT 334
ADJ24136
ID ADJ24136 standard; DNA; 20 BP.
AC
XX
ADJ24136;
DT 20-MAY-2004 (first entry)
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2534.
KW Antilipaeic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX
FN WO2004009541-A2.
XX
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Bhat BG;
XX
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 2534; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of EL. The antisense oligonucleotides
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 867 GTAGTCCATGCTATTAAAA 885
||||| ||||| |||||
Db 1 GTAGCCAATGCTATTACAA 19

RESULT 335
ADJ24120/c
ID ADJ24120 standard; DNA; 20 BP.
AC
XX
ADJ24120;
DT 20-MAY-2004 (first entry)
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2518.
KW Antilipaeic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX
FN WO2004009541-A2.
XX
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Bhat BG;
XX
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 2518; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of EL. The antisense oligonucleotides
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 12 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 315 TTGGATTTCCCTGTTATTTCT 333
||||| ||||| |||||
Db 20 TTGGCTTTCCCTATTTTCT 2

RESULT 336
ADK80500
ID ADK80500 standard; DNA; 20 BP.
AC
XX
ADK80500;
DT 20-MAY-2004 (first entry)
XX

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```

DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #7834.
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX Synthetic.
OS
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Robertds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 7834; 417pp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'WOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1062 TTCAGTGGCTAACCACT 1080
DB 2 TTCAGTACCTACCACT 20

RESULT 337
ADK80983
ID ADK80983 standard; DNA; 20 BP.
XX
XX ADK80983;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8317.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
OS
XX WO2004016754-A2.
XX
XX

```

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PD 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Robertds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 8317; 417pp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'WOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1062 TTCAGTGGCTAACCACT 1080
DB 1 TTCAGTACCTACCACT 19

RESULT 338
ADL97965/C
ID ADL97965 standard; DNA; 20 BP.
XX
XX ADL97965;
XX
XX 17-JUN-2004 (first entry)
XX
XX Mx2 probe, SEQ ID 4.
XX
XX Osteopathic; calvarial osteoblast differentiation;
KW osteoblast differentiation; calvarial osteoblast mineralization;
KW osteoblast mineralization; NELL-1; bone fracture repair; bone density;
XX Mx2; probe; ss.
XX
XX Synthetic.
XX
XX WO2004024893-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US029281.
XX
XX 13-SEP-2002; 2002US-0410846P.
XX
XX (UYCA-) UNIV CALIFORNIA LOS ANGELES.
XX
XX Kang T;
PI

```

XX DR WPI; 2004-329478/30.

XX PT Modulating calvarial osteoblast differentiation and mineralization.

XX PT useful for facilitating repair of bone fractures and/or to generally

XX PT increase bone density, comprises altering expression or activity of NELL-1.

XX PS

XX PS Example 2; Page 54; 85pp; English.

XX CC The present invention relates to a method for modulating calvarial

XX CC osteoblast differentiation and mineralization. The method comprises

XX CC altering expression or activity of NELL-1, where the increased expression

XX CC or activity of NELL-1 increases osteoblast differentiation or

XX CC mineralization and decreased expression or activity of NELL-1 decreases

XX CC osteoblast differentiation or mineralization. The methods and NELL-1 gene

XX CC are useful for facilitating repair of bone fractures and/or to generally

XX CC increase bone density. The present sequence is a PCR primer, used to

XX CC illustrate the invention.

XX SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 697 TCATGTACTACGGTGCTC 715

Db 19 TCGTGTATCCACGGTGCTC 1

RESULT 339

ADO46593

ID ADO46593 standard; DNA; 20 BP.

XX AC ADO46593;

XX DT 15-JUL-2004 (first entry)

XX DE Human oligonucleotide #1959.

XX KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;

XX KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;

XX KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;

XX KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;

XX KW asthma; lung allergy; inflammation; inflammatory disease;

XX KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;

XX KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;

XX KW acute respiratory distress syndrome; pulmonary hypertension;

XX KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX OS Homo sapiens.

XX PN US2004049022-A1.

XX PD 11-MAR-2004.

XX PF 25-JUL-2003; 2003US-00627930.

XX PR 23-APR-2002; 2002WO-US013135.

XX PR 23-APR-2002; 2002WO-US013143.

XX PA (NYCE// NYCE J W.

XX PA (SAND// SANDRASAGRA A.

XX PA (TANG// TANG L.

XX PA (AGUI// AGUILAR D.

XX PA (MILL// MILLER S.

XX PA (SHAH// SHAHABUDDIN S.

XX PA (LUHH// LU H.

XX PA (CONG// CONG H.

XX NYce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;

PI Shahabuddin S, Lu H, Cong H;

XX WPI; 2004-293804/27.

XX Novel single or multiple target oligonucleotide anti-sense to e.g.

XX PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,

XX PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.

XX PT asthma.

XX PS

XX PS Claim 2; SEQ ID NO 2059; 174pp; English.

XX CC The invention relates to oligonucleotides anti-sense to an initiation

XX CC codon, coding region, 5' or 3' intron-exon junction, intron or region

XX CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target

XX CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)

XX CC -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,

XX CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention

XX CC also relates to a method of screening a candidate compound that binds to

XX CC one or more nucleic acid target(s) or expressed product(s), for the

XX CC prevention and/or treatment of a respiratory or lung disease. The

XX CC oligonucleotides are useful for reducing or inhibiting expression of a

XX CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,

XX CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,

XX CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are

XX CC useful for preventing or treating a respiratory or lung disease. The

XX CC respiratory or lung disease is associated with hyper-responsiveness to

XX CC and/or increased levels of, adenosine and/or levels of adenosine A

XX CC receptor(s), and/or asthma and/or lung allergies associated with

XX CC inflammation or an inflammatory disease. The respiratory or lung disease

XX CC is chosen from airway inflammation, allergy, asthma, impeded respiration,

XX CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),

XX CC allergic rhinitis, acute respiratory distress syndrome, pulmonary

XX CC hypertension, lung inflammation, bronchitis, airway obstruction or

XX CC bronchoconstriction. This sequence represents an oligonucleotide of the

XX CC invention.

XX SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 191 TTCACGCCATCTCCCCCA 209

Db 1 TTGAGGCCATCTCCCCCA 19

RESULT 340

ADO47001/c

ID ADO47001 standard; DNA; 20 BP.

XX AC ADO47001;

XX DT 15-JUL-2004 (first entry)

XX DE Human oligonucleotide #2367.

XX KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;

XX KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;

XX KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;

XX KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;

XX KW asthma; lung allergy; inflammation; inflammatory disease;

XX KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;

XX KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;

XX KW acute respiratory distress syndrome; pulmonary hypertension;

XX KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX OS Homo sapiens.

XX PN US2004049022-A1.

XX PD 11-MAR-2004.

XX PF 25-JUL-2003; 2003US-00627930.

```

XX 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
XX (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-293804/27.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
XX
XX Claim 2; SEQ ID NO 2467; 174pp; English.
XX
XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX
XX Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 676 TTAAGTTACTGTTGGCT 694
DB 20 TAAAGTTACTGTTGGCT 2
RESULT 341
ADP12146/C
ID ADP12146 standard; DNA; 20 BP.
XX
XX ADP12146;
AC
XX 12-AUG-2004 (first entry)
DT
XX
XX Taqman probe set 2 #4.
DE
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.

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XX Homo sapiens.
OS
XX WO2004042346-A2.
FN
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 58; SEQ ID NO 2155; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC probe for a 50 mer oligonucleotide marker for diagnosis and monitoring of
CC allograft rejection and other disorders.
XX
XX Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 363 CCTGGCGCCTTGTTGGC 381
DB 20 CCTGGCGCATTGTGCTGGC 2
RESULT 342
ADP68640/C
ID ADP68640 standard; DNA; 20 BP.
XX
XX ADP68640;
AC
XX 09-SEP-2004 (first entry)
DT
XX
XX Human PPAR-alpha antisense oligonucleotide seqid 76.
DE
XX
XX cytostatic; gene therapy; PPAR-alpha;
KW peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator;
KW PPAR-alpha associated disorder; hyperproliferative disorder; human;
KW antisense oligonucleotide; antisense technology; ss.
XX
XX Homo sapiens.
OS
XX US2004115637-A1.
PN
XX 17-JUN-2004.
XX
XX

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PF 11-DEC-2002; 2002US-00317500.
XX
PR 11-DEC-2002; 2002US-00317500.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX McKay R, Dobie KW;
XX
XX WPI; 2004-449378/42.
XX
XX New oligonucleotide compound that inhibits expression of PPAR-alpha,
XX useful for preparing a composition for treating hyperproliferative
XX disorders, e.g. cancer.
XX
XX Example 15; SEQ ID NO 76; 121pp; English.
XX
XX The invention describes a compound, having a sequence comprising 8-80 bp
XX targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-
XX activated receptor-alpha), that specifically hybridizes with the nucleic
XX acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits
XX expression of PPAR-alpha. Also described are: a method of inhibiting the
XX expression of PPAR-alpha in cells or tissues; a method of screening for a
XX modulator of PPAR-alpha; a diagnostic method for identifying a disease
XX state; a kit or assay device comprising the compound; and a method of
XX treating an animal having a disease or condition associated with PPAR-
XX alpha. The oligonucleotide compound is useful for preparing a composition
XX for treating hyperproliferative disorder e.g. cancer. This sequence
XX represents a human peroxisome proliferator-activated receptor-alpha (PPAR
XX -alpha) antisense oligonucleotide.
XX
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14.2; DB 1; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 1.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 266 TGTCGGGAACGGCATATT 284
XX ||| ||| ||| ||| ||| |||
XX 20 TGTAGGTAAACGGCATATT 2
XX
XX RESULT 343
XX ADR27036
XX ID ADR27036 standard; DNA; 20 BP.
XX
XX AC ADR27036;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human single nucleotide polymorphism detection primer #126.
XX
XX ss; primer; single nucleotide polymorphism; SNP; diagnosis;
XX disease association; linkage analysis; autoimmune disease;
XX rheumatoid arthritis; diabetes; multiple sclerosis;
XX systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
XX thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
XX glomerulonephritis; Graves' disease; myocarditis; Sjogren disease;
XX primary systemic vasculitis; genotyping; gene therapy; PCR primer.
XX
XX Homo sapiens.
XX
XX WO2004067779-A2.
XX
XX 12-AUG-2004.
XX
XX 30-JAN-2004; 2004WO-US002652.
XX
XX 30-JAN-2003; 2003US-0443566P.
XX
XX 18-MAR-2003; 2003US-0455444P.
XX
XX 25-APR-2003; 2003US-0465241P.
XX
XX 15-AUG-2003; 2003US-0495115P.
XX
XX 13-NOV-2003; 2003US-0519270P.
XX
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Begovich AB, Carlton VE, Schrodi SJ, Alexander HC;
XX
XX WPI; 2004-594223/57.
XX
XX New single nucleotide polymorphisms (SNPs) associated with rheumatoid
XX arthritis (RA), useful in identification of individuals at risk of
XX developing RA or other autoimmune disease, and in development of
XX therapeutic agents.
XX
XX Claim 21; SEQ ID NO 49708; 141pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising at
XX least 8 contiguous nucleotides where one of the nucleotides is a single
XX nucleotide polymorphism (SNP) selected from any one of the nucleotide
XX sequences of SEQ ID NOS:1-669 and 1339-49592, or their complements. The
XX SNPs are useful as targets for the design of diagnostic reagents and the
XX development of therapeutic agents, as well as for disease association and
XX linkage analysis. In particular, the SNPs are useful for identifying an
XX individual who is at an increased or decreased risk for developing an
XX autoimmune disease such as rheumatoid arthritis, type 1 diabetes,
XX multiple sclerosis, systemic lupus erythematosus, inflammatory bowel
XX diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia,
XX asthma, vitiligo, glomerulonephritis, Graves' disease, myocarditis,
XX Sjogren disease, or primary systemic vasculitis. Methods associated with
XX the SNPs are useful for early detection of the disease, for providing
XX clinically important information for the prevention and/or treatment of
XX the autoimmune diseases particularly rheumatoid arthritis, and for
XX screening and selecting therapeutic agents. The SNPs are useful for human
XX identification applications. The genes containing the SNPs are useful for
XX treating the diseases defined above. The nucleic acid molecules are
XX useful as hybridization probes for genotyping SNPs in messenger RNA,
XX cDNA, genomic DNA, and genomic clones. The nucleic acid molecules are
XX useful for constructing host cells expressing a part or all of the
XX nucleic acid molecules and variant peptides, for constructing transgenic
XX animals, for assaying or screening drugs that modulate nucleic acid
XX expression, or for gene therapy in patients whose cells have aberrant
XX gene expression. This sequence corresponds to a PCR primer which
XX hybridises to the nucleic acids of the invention to amplify the SNP
XX containing region. (Note: SEQ ID NOS 1-49592 are claimed and stated as
XX being provided in the specification, however these sequences are not
XX provided in the printed specification).
XX
XX Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14.2; DB 1; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 1.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1046 CCCAATCTCTTATCTTTC 1064
XX ||| ||| ||| ||| ||| |||
XX 1 CCCAATCTCTTATCTTTC 19
XX
XX RESULT 344
XX ADR17228/c
XX ID ADR17228 standard; DNA; 20 BP.
XX
XX AC ADR17228;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human chromosome 11 Zmax1 region reverse mapping primer #122.
XX
XX Human; high bone mass; Zmax1; ss; primer; HBM; osteoporosis; osteopathic;
XX LDL receptor; bone development; metabolic bone disease; PCR.
XX
XX Homo sapiens.
XX
XX US6780609-B1.
XX
XX 24-AUG-2004.
XX

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XX 05-APR-2000; 2000US-00543771.
 XX 13-JAN-1998; 98US-0071449P.
 PR 23-OCT-1998; 98US-0105511P.
 PR 13-JAN-1999; 99US-00229319.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX Carulli JP, Little RD, Recker RR, Johnson ML;
 XX WPI; 2004-623529/60.
 XX New high bone mass gene of chromosome 1.1013.3, encoding protein useful
 PT for treating, diagnosing, preventing, or screening for normal and
 PT abnormal conditions of bone, including metabolic bone diseases, e.g.
 PT osteoporosis.
 XX Disclosure; SEQ ID NO 310; 284pp; English.
 XX The invention relates to an isolated amino acid protein sequence selected
 CC from an amino acid sequence appearing as ADR16922 or an amino acid
 CC sequence comprising or consisting of the extracellular domain of
 CC ADR16922(amino acids 23-1385). ADR16922 is encoded by the HBM (high bone
 CC mass) allele of the human Zmax1 gene and has sequence similarity to LDL
 CC receptors. Also disclosed are nucleic acids, proteins, cloning vectors,
 CC expression vectors, transformed hosts, methods of developing
 CC pharmaceutical compositions, methods of identifying molecules involved in
 CC bone development, and methods of diagnosing and treating diseases
 CC involved in bone development. Specifically disclosed is the Zmax1 gene
 CC and the high bone mass (HBM) allele on chromosome 11q13.3 encoding
 CC ADR16922. The protein is useful for treating, diagnosing, preventing, or
 CC screening for normal and abnormal conditions of bone, including metabolic
 CC bone diseases, e.g. osteoporosis. The present sequence is a PCR primer
 CC used in the mapping of the Zmax1/HBM gene.
 XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 882 AAAAGTGTGGCCACACAGAC 900
 DB 19 AATATTGTGGCCACACAC 1
 RESULT 345
 ADR67431
 ID ADK67431 standard; DNA; 20 BP.
 XX AC ADK67431;
 XX 18-NOV-2004 (first entry)
 XX PCR primer used to amplify human ABCG2 DNA - SEQ ID 61.
 XX drug absorption; ABCG2; ATP-binding cassette gene; human;
 XX chromosome 4q22; ss; PCR; primer.
 XX Homo sapiens.
 XX JP2004016042-A.
 XX 22-JAN-2004.
 XX 13-JUN-2002; 2002JP-00172759.
 XX 13-JUN-2002; 2002JP-00172759.
 XX (KOKU-) KOKURITSU IYAKUJIN SHOKUJIN EISEI KENKYU.
 PA (IYAK-) IYAKUJIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
 XX

DR WPI; 2004-113852/12.
 XX Novel ABCG2 polynucleotide having a mutation at a specific position,
 PT useful for gene diagnosis of abnormality of medicine absorption
 PT associated with ABCG2 protein.
 XX Example 1; SEQ ID NO 61; 53pp; Japanese.
 XX The invention relates to a novel polynucleotide having a mutation in the
 CC codon encoding a glutamine residue present at the 126 position of a 655
 CC amino acid sequence. The polynucleotide of the invention may be useful
 CC for the estimation or diagnosis of a condition which is associated with
 CC abnormal drug absorption and in which the ABCG2 (ATP-binding cassette
 CC gene) protein is associated. The current sequence is that of a PCR primer
 CC which was used to amplify the human ABCG2 DNA of the invention.
 XX Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 432 GAAGAGGAGTGTGATTTTAG 450
 DB 2 GCAGAGGAGAGAGGTTTAG 20
 RESULT 346
 ADR47879/c
 ID ADR47879 standard; DNA; 20 BP.
 XX AC ADR47879;
 XX 02-DEC-2004 (first entry)
 XX Human chromosome 11 Zmax1 region reverse mapping primer #122.
 XX Human; ss; PCR; high bone mass; Zmax1; HBM; bone modulation;
 KW bone development disorder; osteoporosis; chromosome 11; gene therapy;
 KW primer.
 XX Homo sapiens.
 OS US2004176582-A1.
 PN 09-SEP-2004.
 XX 10-DEC-2003; 2003US-00731739.
 XX 13-JAN-1998; 98US-0071449P.
 PR 23-OCT-1998; 98US-0105511P.
 PR 13-JAN-1999; 99US-00229319.
 PR 05-APR-2000; 2000US-00544398.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (UYCR-) UNIV CREIGHTON.
 XX Carulli JP, Little RD, Recker RR, Johnson ML;
 XX WPI; 2004-661408/64.
 XX New nucleic acid sequence encoding high bone mass, useful in diagnosing,
 PT treating and/or preventing osteoporosis.
 XX Disclosure; SEQ ID NO 310; 303pp; English.
 XX The invention relates to an isolated nucleic acid sequence encoding a
 CC high bone mass protein (HBM). The gene exists in two alleles, Zmax1, the
 CC notional wild-type (the cDNA for which appears as ADR47570 encoding
 CC ADR47572) and the HBM allele (the cDNA for which appears as ADR47571
 CC encoding ADR47573). The two alleles differ by a single nucleotide
 CC polymorphism (G to T at position 582 of ADR47570) causing a Gly to Val
 CC change at position 171 of the protein. Also included are a replicative

CC cloning vector comprising HBM/Zmax1 (and a replicon operative in an
 CC isolated host cell), an expression vector comprising HBM/Zmax1 operably
 CC linked to a transcription regulatory region, an isolated host cell
 CC transformed with the vector(s), a method for testing a substance as a
 CC therapeutic agent for bone modulation in a host, a method of identifying
 CC a molecule involved in bone modulation, a method for identifying a
 CC (candidate) protein involved in bone modulation, a method of testing for
 CC HBM activity, a method of developing a pharmaceutical for the treatment
 CC of bone development disorders, a method for treating a bone development
 CC disorder in an animal, a method of altering bone development in a host, a
 CC method for diagnostic screening for a genetic predisposition to a bone
 CC development disorder, a diagnostic assay for bone development disorders,
 CC a method of expressing the HBM protein in bone tissue, a bacterial
 CC artificial chromosome comprising HBM/Zmax1 sequence (appearing as
 CC ADRA47574-ADRA47580), a method for amplifying a nucleotide polymorphism in
 CC the Zmax1 or HBM gene, a method for identifying a regulatory element of a
 CC HBM gene and an isolated nucleic acid segment of at least 15 contiguous
 CC nucleotides including a polymorphic site from HBM/Zmax1. The nucleic acid
 CC molecule and the encoded polypeptide, composition, and methods are useful
 CC in diagnosing, treating and preventing a bone development disorder, i.e.
 CC osteoporosis. The gene for HBM/Zmax1 is located on chromosome 11q13.3.
 CC The present sequence is a primer used in the mapping of the HBM/Zmax1
 CC gene.
 XX
 SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 882 AAAGTGTGGCCACAGAC 900
 |||||
 Db 19 AATATTGTGGCCACACAC 1

RESULT 347
 ADS31697
 ID ADS31697 standard; DNA; 20 BP.
 XX
 AC ADS31697;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Gene expression inhibition method erbB2 gene PCR primer #8.
 XX
 KW cytosatic; gene promoter methylation inducer; cell growth inhibitor;
 KW erbB2 gene expression inhibitor; DNA methylation inducer; daRNA; CpG;
 KW human; gene expression; erbB2; tumour; gene transcription; promoter;
 KW small interfering RNA; siRNA; gene silencing; ss; primer.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004076663-A1.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-JP002448.
 XX
 PR 27-FEB-2003; 2003US-0449860P.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Taira K, Kawasaki H;
 XX
 DR WPI; 2004-662014/64.
 XX
 PT Novel DNA methylation inducer containing double-stranded RNA targeting
 PT region having CpG on DNA in mammalian cell, useful in suppressing gene
 PT expression, and as cell growth inhibitor.
 XX
 PS Example 4; SEQ ID NO 58; 98pp; Japanese.
 XX

CC The invention relates to a DNA methylation inducer (I) containing double-
 CC stranded (ds) RNA that targets the region which contains CpG or CpNG (N is
 CC A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having
 CC DNA that codes daRNA that targets the region which contains CpG or CpNG
 CC on DNA in mammalian cell. (I) is useful in the DNA methylation process,
 CC which involves introducing (I) in a mammalian cell, where the mammalian
 CC cell is obtained from human. (I) is useful as gene expression inhibitor
 CC or cell growth inhibitor. A gene expression inhibitor (II) is useful for
 CC suppressing gene expression, where the gene is a disease related gene
 CC relevant to a disease, and the expression of the gene causes the disease.
 CC The gene is erbB2 and the disease is the tumour. (I) is useful for
 CC controlling various biological activities in a mammal by controlling the
 CC transcription level of the respective gene by methylating the respective
 CC DNA. (I) or (II) enables specific methylation of the CpG island-
 CC containing domain on a gene promoter of the target gene, where the
 CC methylation of a promoter suppresses the expression of the target gene.
 CC (I) induces sequence specific DNA methylation in a plant, and controls
 CC the expression of the specific gene at the transcription level. (I)
 CC enables DNA methylation in the promoter region of a gene, where the
 CC methylation changes the structure of the DNA, enabling suppression of the
 CC gene expression at the transcription level (DNA to mRNA). This sequence
 CC corresponds to an erbB2 gene PCR primer used in the method to silence
 CC gene expression in cells.
 XX
 SQ Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 840 AGCGCGGGTGGATCCCTC 858
 |||||
 Db 2 AGGCCTGGTGGTCCCTC 20

RESULT 348
 ADS31698/C
 ID ADS31698 standard; DNA; 20 BP.
 XX
 AC ADS31698;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Gene expression inhibition method erbB2 gene PCR primer #9.
 XX
 KW cytosatic; gene promoter methylation inducer; cell growth inhibitor;
 KW erbB2 gene expression inhibitor; DNA methylation inducer; daRNA; CpG;
 KW human; gene expression; erbB2; tumour; gene transcription; promoter;
 KW small interfering RNA; siRNA; gene silencing; ss; primer.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004076663-A1.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-JP002448.
 XX
 PR 27-FEB-2003; 2003US-0449860P.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Taira K, Kawasaki H;
 XX
 DR WPI; 2004-662014/64.
 XX
 PT Novel DNA methylation inducer containing double-stranded RNA targeting
 PT region having CpG on DNA in mammalian cell, useful in suppressing gene
 PT expression, and as cell growth inhibitor.
 XX
 PS Example 4; SEQ ID NO 59; 98pp; Japanese.
 XX

CC The invention relates to a DNA methylation inducer (I) containing double-stranded (ds)RNA that targets the region which contains CpG or CpNG (N is A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having DNA that codes dsRNA that targets the region which contains CpG or CpNG on DNA in mammalian cell. (I) is useful in the DNA methylation process, which involves introducing (I) in a mammalian cell, where the mammalian cell is obtained from human. (I) is useful as gene expression inhibitor or cell growth inhibitor. A gene expression inhibitor (II) is useful for suppressing gene expression, where the gene is a disease related gene relevant to a disease, and the expression of the gene causes the disease. The gene is erbB2 and the disease is the tumour. (I) is useful for controlling various biological activities in a mammal by controlling the transcription level of the respective gene by methylating the respective DNA. (I) or (II) enables specific methylation of the CpG island-containing domain on a gene promoter of the target gene, where the methylation of a promoter suppresses the expression of the target gene. (I) induces sequence specific DNA methylation in a plant, and controls the expression of the specific gene at the transcription level. (I) enables DNA methylation in the promoter region of a gene, where the methylation changes the structure of the DNA, enabling suppression of the gene expression at the transcription level (DNA to mRNA). This sequence corresponds to an erbB2 gene PCR primer used in the method to silence gene expression in cells.

XX Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 AGCGCGGGTGGATCCCTC 858
||||| ||||| |||||
Db 19 AGCGCTGGTGGTCCCTC 1

RESULT 349

ADR27673
ID ADR27673 standard; DNA; 14 BP.

AC ADR27673;

XX 04-NOV-2004 (first entry)

DT Leptin receptor related protein, OB-RGRP, RT-PCR primer #1.

DE Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW human; RT-PCR; primer; ss.

XX Homo sapiens.

XX FR2850971-A1.

XX 13-AUG-2004.

XX 10-FEB-2003; 2003FR-00001543.

XX 10-FEB-2003; 2003FR-00001543.

XX (AVET) AVENTIS PHARMA SA.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

XX New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g.

PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and

PT angiogenesis.

XX Disclosure; Page 23; 104pp; French.

XX The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPe) and their coding sequences comprising OB-RGRP or MYO47 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also related interfering RNA, are used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes; anorexia; disorders of sexual maturity; haematopoiesis; angiogenesis; thrombus formation; regulation of immunity and inflammation; fetal development and cancer. The present sequence is a RT-PCR primer used to illustrate the invention.

XX Sequence 14 BP; 3 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CCGTGGCAGGAAGC 39

||||| ||||| |||||
Db 1 CCGTGGCAGGAAGC 14

RESULT 350

AAT54666

ID AAT54666 standard; RNA; 15 BP.

AC AAT54666;

XX 25-MAR-2003 (revised)

DT 22-APR-1997 (first entry)

XX Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1148).

DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW Interleukin-5; downregulation; interleukin-5; IL-5; ICAM-1;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.

XX Mus musculus.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB0000156.

XX 23-FEB-1994; 94US-00201109.

XX 29-MAR-1994; 94US-00218934.

XX 04-APR-1994; 94US-00222795.

XX 07-APR-1994; 94US-00224483.

XX 15-APR-1994; 94US-00227958.

XX 15-APR-1994; 94US-00228041.

PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-002711280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Trak D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX Claim 2; Page 221; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
 CC of the mRNA that do not form secondary folding structures and that
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were
 CC identified by computer analysis. Ribozymes directed against these mRNA
 CC sequences were designed and synthesised with modifications that improve
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
 CC and thereby inhibit IL-5 expression, making them useful for treating
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
 CC and preventing the recruitment and activation of eosinophils. The
 CC ribozymes can also be used to treat eosinophilia (related to parasitic
 CC infection or with pulmonary infiltration) and L-tryptophan-associated
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX SQ Sequence 15 BP; 2 A; 2 C; 2 G; 0 T; 9 U; 0 Other;
 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1.8e+02;
 Matches 6; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 QY 123 TGACTTTTCTTATG 136
 :|||:::|:|:
 Db 1 UGACUUUUUUUAUG 14
 RESULT 351
 ID AA263871 standard; RNA; 15 BP.
 XX AA263871
 AC AA263871;
 XX 28-MAR-2000 (first entry)
 DT Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2483.
 DE Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW

KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX Hepatitis C virus.
 OS WO9955847-A2.
 PN 04-NOV-1999.
 XX 26-APR-1999; 99WO-US009027.
 XX 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 99US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 PI WPI; 2000-062023/05.
 XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 XX Claim 1; Page 73; 123pp; English.
 PS The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX SQ Sequence 15 BP; 4 A; 1 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 346 TGTGATCAAAATGGG 359
 :|||:|:|:|:
 Db 2 UGUGAUCAAAUUGG 15
 RESULT 352
 ABX00924
 ID ABX00924 standard; RNA; 15 BP.
 XX ABX00924;
 AC ABX00924;
 XX 23-DEC-2002 (first entry)
 DT Hepatitis C virus substrate #706 for HCV hammerhead ribozyme #706.
 DE Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; viroicide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX Hepatitis C virus.
 OS

```

PN  US2002082225-A1.
XX
PD  27-JUN-2002.
XX
XX  23-MAR-1999; 99US-00274553.
XX
XX  23-MAR-1999; 99US-00274553.
XX
XX  (BLAT/) BLATT L.
PA  (MCSW/) MCSWIGGEN J A.
PA  (ROBE/) ROBERTS B.
PA  (PAVC/) PAVCO P A.
PA  (MACE/) MACEJACK D.
XX
XX  Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
PI  WPI; 2002-617759/66.
XX
DR  WPI; 2002-617759/66.
XX
XX  New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT  replication and are useful to treat hepatitis C virus infections and
PT  cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX  Claim 1; Page 41; 80pp; English.
XX
XX  The present invention relates to enzymatic nucleic acids which
CC  specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC  enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC  (HP) motif where the binding arms comprise sequences complementary to one
CC  of the substrate sequences defined in the specification. The HCV
CC  ribozymes are useful for modulating the expression and/or replication of
CC  HCV. They can be used to treat cirrhosis, liver failure and/or
CC  hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC  a condition associated with HCV infection in conjunction with one or more
CC  other drug therapies, particularly type I interferon, especially
CC  interferon alpha, beta or gamma or consensus interferon. The present
CC  sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC  Some of the sequence data for this patent did not form part of the
CC  printed specification. The complete sequence data for this patent was
CC  obtained in electronic format directly from the USPTO web site at
CC  seqdata.uspto.gov/psipdsIDEntry.html
XX
XX  Sequence 15 BP; 4 A; 1 C; 5 G; 0 T; 5 U; 0 Other;
SQ
    Query Match      1.3%; Score 14; DB 1; Length 15;
    Best Local Similarity 71.4%; Pred. No. 1.8e+02;
    Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY  346 TGTGATCAAAATGGG 359
    :|:|:|:|:|:|:|
DB  2 UGUGAUCAAAUGGG 15

RESULT 353
ABT39781/C
ID  ABT39781 standard; DNA; 17 BP.
XX
XX  ABT39781;
AC
XX  12-JUN-2003 (first entry)
DT
XX
XX  Tumour suppression related human fukutin oligo SEQ ID No 5418.
DE
XX
XX  Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW  antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW  schizophrenia; protein chip; gene therapy; tumour suppression;
KW  human fukutin; ds.
XX
XX  Homo sapiens.
OS
XX
XX  WO2003025175-A2.
PN
XX  27-MAR-2003.
XX
XX

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PF  17-SEP-2002; 2002WO-IB004208.
XX
XX  17-SEP-2001; 2001FR-00011978.
XX
XX  (MOLE-) MOLECULAR ENGINES LAB.
PA
XX  Telerman A, Amson R, Tuijnder M;
PI  WPI; 2003-313353/30.
XX
XX  New isolated nucleic acid, useful for treating viral diseases associated
PT  with tumors and cell degeneration, also related polypeptides, antibodies
PT  and transfected cells.
XX
XX  Disclosure; Page 667; 720pp; French.
XX
XX  The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC  given in the specification, a sequence containing at least 15 consecutive
CC  nucleotides from the 17 mer sequence, a sequence with, after optimal
CC  alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC  hybridizes to them under highly stringent conditions, or the complement
CC  of any of them, or the corresponding RNA. The novel isolated nucleic
CC  acids of the invention are useful as probes and primers for detecting,
CC  identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC  component of a gene chip, in vitro as (anti)sense reagents, and for
CC  production of recombinant polypeptides. Any of the nucleic acids,
CC  polypeptides, vectors containing the nucleic acids, cells containing the
CC  vector or antibodies directed against the polypeptides are useful for
CC  preparation of pharmaceuticals for prevention and/or treatment of viral
CC  diseases that are characterised by development of tumours or cell
CC  degeneration, specifically cancer but also Alzheimer's disease and
CC  schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC  patient samples is useful for diagnosis and/or prognosis of these
CC  diseases. The polypeptides can also be used to generate antibodies, and
CC  both the polypeptide and antibodies are useful as components of protein
CC  chips. The nucleic acid sequences of the invention can be used in gene
CC  therapy. This polynucleotide sequence represents a tumour suppression
CC  related human fukutin oligonucleotide of the invention
XX
XX  Sequence 17 BP; 8 A; 3 C; 1 G; 5 T; 0 U; 0 Other;
SQ
    Query Match      1.3%; Score 14; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 1.9e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  971 ATTTTGATGAGATC 984
    |||||
DB  14 ATTTTGATGAGATC 1

RESULT 354
AAZ71197
ID  AAZ71197 standard; DNA; 18 BP.
XX
XX  AAZ71197;
AC
XX  10-SEP-2001 (first entry)
DT
XX
XX  Human biallelic marker upstream amplification primer SEQ ID NO:5553.
DE
XX
XX  Human genome; biallelic marker; high density disequilibrium map;
KW  genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW  haplotyping; hybridisation; identification; characterisation;
KW  amplification; single nucleotide polymorphism; SNP; PCR primer;
KW  diagnosis; ss.
XX
XX  Homo sapiens.
OS
XX
XX  WO9954500-A2.
PN
XX  28-OCT-1999.
XX
XX  21-APR-1999; 99WO-IB000822.
XX

```

```

XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 1415; 2745pp; English.
PS
XX AA265654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 200 ATCTCCCCCATCCC 213
Db 5 ATCTCCCCCATCCC 18
RESULT 355
AAZ69829/C
ID AAZ69829 standard; DNA; 20 BP.
AC AAZ69829;
XX
DT 10-SEP-2001 (first entry)
DE Human biallelic marker upstream amplification primer SEQ ID NO:4185.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 1430; 2745pp; English.
PS
XX AA265654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 200 ATCTCCCCCATCCC 213
Db 5 ATCTCCCCCATCCC 18
RESULT 356
AAZ71268
ID AAZ71268 standard; DNA; 20 BP.
XX
AC AAZ71268;
XX
DT 10-SEP-2001 (first entry)
DE Human biallelic marker upstream amplification primer SEQ ID NO:5624.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 1430; 2745pp; English.
PS
XX AA265654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 562 TGGGTTTTTTAATA 575
Db 19 TGGGTTTTTTAATA 6

```

CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTGTTATTCTTGCT 337
 |||||
 DB 4 CTGTTATTCTTGCT 17

RESULT 357
 AAD34452/c
 ID AAD34452 standard; DNA; 20 BP.

XX AAD34452;
 AC
 DT 16-JUL-2002 (first entry)
 XX
 DE Human TREK2 cDNA specific forward PCR primer.

XX Human; hTREK2 protein; cancer; diabetes; pulmonary disease; asthma;
 KW cardiovascular disease; inflammatory disease; psychiatric disorder;
 KW renal disease; neurodegenerative disease; neurological disorder;
 KW Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma;
 KW pain; PCR; primer; ss.

OS Homo sapiens.
 XX
 PN GB2365010-A.
 XX
 PD 13-FEB-2002.

XX 24-APR-2001; 2001GB-00010129.
 PF
 XX 25-APR-2000; 2000GB-00010060.
 PR
 PR 01-JUN-2000; 2000GB-00013370.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA

XX Chapman CG, Duckworth DM;
 PI
 XX WPI; 2002-332557/37.
 DR

XX Novel human TREK2 (HTREK2) polypeptide and polynucleotide encoding it,
 PT useful for identifying agonists and antagonists in the treatment of
 PT diseases associated with a HTREK2 imbalance, such as diabetes, cancers or
 PT asthma.

XX Example 1; Page 20; 29pp; English.

XX The invention relates to human HTREK2 polypeptides and nucleic acid
 CC molecules encoding such polypeptides. TREK2 polypeptides are useful in
 CC screening assays to identify compounds that may stimulate or inhibit
 CC their function or level of expression. Sequences of the invention are
 CC used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular
 CC diseases, inflammatory disease, renal disease, pain, psychiatric

CC disorders including depression and schizophrenia, neurodegenerative
 CC disease including Alzheimer's disease, stroke and head trauma and
 CC neurological disorders. They are also used as vaccines. The present
 CC sequence is human hTREK2 cDNA specific PCR primer
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 CTATTGGACTGACT 127
 |||||
 DB 19 CTATTGGACTGACT 6

RESULT 358
 ABN79739/c
 ID ABN79739 standard; DNA; 20 BP.

XX ABN79739;
 AC
 DT 29-JUL-2002 (first entry)
 XX
 DE Human Fas target oligonucleotide #54.

XX Human; immunosuppressive; antiinflammatory; hepatotropic; cytostatic;
 KW vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.

XX Homo sapiens.
 OS
 XX US2002004490-A1.
 PN
 PD 10-JAN-2002.

XX 09-MAR-2001; 2001US-00802669.
 PF
 XX 12-APR-1999; 99US-00290640.
 PR
 PR 18-SEP-2000; 2000US-00665615.

XX (DEAN/) DEAN N M.
 PA (MARC/) MARCUSSEON E G.
 PA (WYAT/) WYATT J.
 PA (ZHAN/) ZHANG H.

XX Dean NM, Marcusson EG, Wyatt J, Zhang H;
 PI
 XX WPI; 2002-204886/26.
 DR

XX Novel antisense compound targeted to nucleic acid encoding Fas, Fas
 PT ligand or Fas associated protein-1 is useful for inhibiting expression of
 PT Fas, Fas ligand, or Fas-1 in cells or tissues, and for treating
 PT hepatitis.

XX Example 18; Page 24; 84pp; English.

XX This invention relates to an antisense compound encoding Fas, Fas ligand,
 CC or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated
 CC signalling is thought to be immunosuppressive, antiinflammatory,
 CC hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were
 CC designed to target human Fas. Oligonucleotides were synthesised as
 CC chimeric oligonucleotides and are useful for treating an animal having an
 CC autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition
 CC associated with apoptosis, allograft rejection, or ischemia reperfusion
 CC injury. Optionally, the above mentioned conditions are prevented by
 CC contacting the allograft with the antisense oligonucleotide. The
 CC oligonucleotides are used in diagnostics, therapeutics, prophylaxis and
 CC as research reagents and in kits. The oligonucleotides are also useful
 CC for research purposes. The present nucleotide sequence is related to
 CC human Fas

XX Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
 DB 18 AGATGAGTTTATT 5

RESULT 359
 AAL42518/c
 ID AAL42518 standard; DNA; 20 BP.
 XX AC AAL42518;
 XX DT 28-JUN-2002 (first entry)
 XX DE Alpha-V integrin-specific inhibitory antisense nucleic acid 7.
 XX KW Antisense nucleic acid; ss; alpha-V integrin chain; antisense inhibition;
 KW cell adhesion modulation; platelet aggregation; immune function;
 KW tissue repair; cell proliferation; tumour invasion; cancer; gingivitis;
 KW chronic inflammatory disease; Chron's disease; rheumatoid arthritis;
 KW ocular neovascular disease; diabetic retinopathy; osteoporosis;
 KW excessive bone resorption; inflammatory skin disorder; psoriasis.
 XX OS Unidentified.
 XX PI EP1197553-A1.
 XX PN 17-APR-2002.
 XX PD 12-OCT-2000; 2000EP-00121394.
 XX PF 12-OCT-2000; 2000EP-00121394.
 XX PR 12-OCT-2000; 2000EP-00121394.
 XX PA (ATHR-) A3D GMBH ANTISENSE DESIGN & DRUG DEV.
 XX PI Kronenwett R, Graef T, Haas R, Nedbal W;
 XX DR WPI; 2002-364499/40.
 XX KW Antisense nucleic acid against alpha V integrin for use in pharmaceutical
 PT compositions for the specific inhibition of the expression of alpha
 PT integrins in mammalian cells useful.
 XX PS Claim 8; Page 3; 17pp; English.
 XX CC The invention comprises antisense nucleic acids that are capable of
 CC binding to the transcription product of the gene coding for the alpha-V
 CC integrin chain, thereby inhibiting the expression of alpha-V integrins in
 CC mammalian cells. The antisense nucleic acids of the invention are useful
 CC for the treatment of pathological disorders by the modulation of cell
 CC adhesion which affects platelet aggregation, immune functions, tissue
 CC repair, cell proliferation, tumour invasion, inflammation and inherited
 CC diseases. Disorders which can be treated include: cancer; restenosis
 CC after angioplasty; stenosis to vein bypass; chronic inflammatory diseases
 CC (e.g. Chron's disease and rheumatoid arthritis); ocular neovascular
 CC diseases (e.g. diabetic retinopathy); disorders associated with excessive
 CC bone resorption (e.g. osteoporosis); disorders of mammalian oral cavity
 CC (e.g. gingivitis); and inflammatory skin disorders (e.g. psoriasis). The
 CC present DNA sequence represents an antisense nucleic acid of the
 CC invention used to inhibit alpha-V integrin expression
 XX SQ Sequence 20 BP; 11 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 TTTTCCTTATT 430
 DB 17 TTTTCCTTATT 4

RESULT 360
 ACH00628
 ID ACH00628 standard; DNA; 20 BP.
 XX AC ACH00628;
 XX DT 12-FEB-2004 (first entry)
 XX DE Mammalian inverted nipple associated microsatellite PCR primer #82.
 XX KW Inverted nipple; microsatellite; PCR; primer; ss; pig.
 XX OS Mammalia.
 XX PN WO2003066891-A2.
 XX PD 14-AUG-2003.
 XX PF 03-FEB-2003; 2003WO-EP001045.
 XX PR 05-FEB-2002; 2002EP-00002632.
 XX PA (FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE.
 XX PI Hardge T, Schellander K, Wimmers K;
 XX PN WPI; 2003-671539/63.
 XX DR Determining predisposition to inverted nipples useful e.g. for selecting
 PT breeding animals comprises detecting specific microsatellite markers.
 XX PS Disclosure; Page 23; 63pp; German.
 XX CC The present invention relates to the use of a nucleic acid to determine
 CC the predisposition of appearance or inheritance of inverted nipples,
 CC where the nucleic acid is identical to the region of microsatellites
 CC S0200, SW2443, S0097, S0007, SW1301 or S0164 on chromosomes 6, 2, 4, 14,
 CC 1 and 3, respectively, in pigs, or homologous positions in the genomes of
 CC other mammals. The nucleic acids can be used to select pigs, breeding or
 CC farm animals that lack inverted nipples, particularly by genomic
 CC screening of many related mammals in a population. The present sequence
 CC is a PCR primer used in the exemplification of the invention to identify
 CC microsatellite markers associated with the inverted nipple phenotype
 XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 894 CACAGACCAGAGC 907
 DB 2 CACAGACCAGAGC 15

RESULT 361
 ADH77414
 ID ADH77414 standard; DNA; 20 BP.
 XX AC ADH77414;
 XX DT 22-APR-2004 (first entry)
 XX DE Human PTPN12 antisense oligonucleotide seq id 55.
 XX KW cytosolic; PTPN12 Inhibitor; PTPN12;
 KW protein tyrosine phosphatase, non-receptor type 12;
 KW hyperproliferative disorder; colon cancer; metabolic disorder;
 KW antisense technology; antisense oligonucleotide; human; ss.
 XX OS Homo sapiens.

```

XX Key Location/Qualifiers
PH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidine
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl (2'-MOE) nucleotides"
XX
XX US2003232434-A1.
XX
XX 18-DEC-2003.
XX
XX 17-JUN-2002; 2002US-00172911.
XX
XX 17-JUN-2002; 2002US-00172911.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowseert LM, Dobie KW;
XX
XX WPI; 2004-061282/06.
XX
XX New antisense oligonucleotides targeted to a nucleic acid encoding
XX protein tyrosine phosphatase, non-receptor type 12 (PTPN12) useful for
XX treating a disease associated with PTPN12, e.g. colon cancer.
XX
XX Example 15; SEQ ID NO 55; 117pp; English.
XX
XX The invention describes a compound 8-80 nucleobases in length targeted
XX to, and which specifically hybridizes with a nucleic acid molecule
XX encoding PTPN12 (protein tyrosine phosphatase, non-receptor type 12), and
XX inhibits the expression of PTPN12. The compound, composition and methods
XX are useful for treating a disease or condition associated with PTPN12,
XX such as a hyperproliferative disorder, e.g. colon cancer, or a metabolic
XX disorder. They are also useful in research and diagnostics for modulating
XX the expression of PTPN12. This sequence represents a human protein
XX tyrosine phosphatase, non-receptor type 12 (PTPN12) antisense
XX oligonucleotide.
XX
XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 345 CTGTGATCAATGG 358
XX |||||||
XX 1 CTGTGATCAATGG 14
XX
XX RESULT 362
XX ADL27795/C
XX ID ADL27795 standard; DNA; 20 BP.
XX
XX AC ADL27795;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human Fas cDNA, antisense oligonucleotide #75.
XX
XX Antisense therapy; human; Fas; Fas ligand; FasL; Apo-1L; CD95L;
XX Fas associated protein 1; Fap-1; signal transduction; autoimmune disease;
XX inflammatory disease; cancer; immunosuppressive; antiinflammatory;
XX cytostatic; phosphorothioate; ss.
XX

```

```

OS Homo sapiens.
XX Key Location/Qualifiers
PH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
XX
XX US6653133-B1.
XX
XX 25-NOV-2003.
XX
XX 18-SEP-2000; 2000US-00665615.
XX
XX 12-APR-1999; 99US-00290640.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean NM, Marcusson EG, Wyatt J;
XX
XX WPI; 2004-050524/05.
XX
XX New antisense oligonucleotides of 20-50 nucleobases, useful for treating
XX autoimmune or inflammatory diseases, and cancer.
XX
XX Example 18; SEQ ID NO 156; 76pp; English.
XX
XX The present invention relates to antisense compounds targeted to nucleic
XX acids encoding human Fas (also known as Apo-1 or CD95), Fas ligand (FasL,
XX also Apo-1L and CD95L), and Fas associated protein 1 (Fap-1). The
XX antisense compound comprises an antisense oligonucleotide that
XX specifically hybridizes with one of the said nucleic acids and inhibits
XX Fas, FasL or Fap-1 mediated signal transduction. The antisense
XX oligonucleotide is a chimeric oligonucleotide. The antisense
XX oligonucleotide comprises at least one modified internucleoside linkage,
XX preferably a phosphorothioate linkage. It also comprises at least one
XX modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
XX moiety. The antisense oligonucleotide further comprises at least one
XX modified nucleobase, preferably a 5-methylcytosine. The antisense
XX oligonucleotides are useful for the treatment of autoimmune or
XX inflammatory diseases, and cancers associated with overexpression of or
XX constitutive activation of Fas, FasL, or Fap-1. The present sequence
XX represents an antisense oligonucleotide used in the examples of the
XX present invention.
XX
XX Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 14; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 620 AGATGAGTTTATT 633
XX |||||||
XX 18 AGATGAGTTTATT 5
XX
XX RESULT 363
XX ADM53567/C
XX ID ADM53567 standard; DNA; 20 BP.
XX
XX AC ADM53567;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human Fas antisense oligonucleotide seqid 156.
XX
XX immunosuppressive; antiinflammatory; hepatotropic; virucide; cytostatic;
XX antisense technology; Fas; Fas ligand; Fap-1; Fas associated disorder;
XX Fap-1 associated disorder; ischaemia reperfusion injury; apoptosis;
XX allograft; autoimmune disease; inflammatory disease; hepatitis; cancer;
XX

```

KW lymphoma; human; antisense oligonucleotide; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= Phosphorothioate backbone. All cytidines
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 15..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
 XX
 PN US2004033979-A1.
 XX
 XX 19-FEB-2004.
 XX
 XX 14-JUL-2003; 2003US-00619220.
 XX
 XX 12-APR-1999; 99US-00290640.
 PR 18-SEP-2000; 2000US-0065615.
 PR 09-MAR-2001; 2001US-00802669.
 XX
 PA (DEAN/) DEAN N M.
 PA (MARC/) MARCUSSON E G.
 PA (WYAT/) WYATT J.
 PA (ZHAN/) ZHANG H.
 XX
 XX Dean NM, Marcussone EG, Wyatt J, Zhang H;
 XX WPI; 2004-180091/17.
 DR
 XX New antisense compound targeted to nucleic acid molecule encoding Fas or
 FT Fas-1, useful in diagnosing, treating or preventing autoimmune or
 FT inflammatory disease, cancer, apoptosis, allograft rejection or ischemia
 FT reperfusion injury.
 XX
 XX Example 18; SEQ ID NO 156; 83pp; English.
 PS
 XX The invention describes an antisense compound 8-30 or 8-50 nucleobases in
 XX length targeted to the 5'-untranslated region, translational start site,
 CC translational termination region or 3'-untranslated region of a nucleic
 CC acid molecule encoding Fas, Fas ligand or Fas-1. Also described are: a
 CC pharmaceutical composition comprising the anti-sense compound and a
 CC pharmaceutical carrier or diluent; a method of inhibiting the expression
 CC of Fas or Fas-1 in cells or tissues; treating an animal having a disease
 CC or condition associated with Fas or Fas-1; and preventing allograft
 CC rejection, ischemia reperfusion injury or apoptosis in an allograft
 CC recipient. The antisense compound and pharmaceutical composition is
 CC useful in diagnosing, treating or preventing autoimmune or inflammatory
 CC disease, e.g. hepatitis, cancer, e.g. cancer of the colon, liver, lung or
 CC a lymphoma, apoptosis, allograft rejection, e.g. cardiac, renal, hepatic
 CC or skin allograft and ischemia reperfusion injury. This sequence
 CC represents a human Fas antisense oligonucleotide.
 XX
 SQ Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 AGATGAGTTTATT 633
 Db 18 AGATGAGTTTATT 5
 RESULT 364

AAQ40912
 ID AAQ40912 standard; DNA; 17 BP.
 XX
 AC AAQ40912;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1993 (first entry)
 XX
 DE C-erb-B2 sense oligonucleotide.
 XX
 XX Double; triple; helix; duplex; triplex; major groove; SKBR3 cell; ss.
 KW
 XX Synthetic.
 OS
 XX WO9309813-A1.
 PN
 XX 27-MAY-1993.
 PD
 XX 10-NOV-1992; 92WO-GB002073.
 PF
 XX 12-NOV-1991; 91GB-00023947.
 PR
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA
 XX Epenetos AA;
 PI
 XX WPI; 1993-182253/22.
 DR
 XX Cpd. comprising anti-sense oligo:nucleotide and radioactive moiety - for
 FT treating viral infection, sepsis, leukaemia and tumours.
 FT
 XX Example 3; Page 26; 43pp; English.
 PS
 XX For the selective killing of SKBR3 cells the following radiolabelled c-
 CC erb-B2 oligonucleotides were used: (1) the antisense oligonucleotide
 CC given in AAQ40911, complementary to the non-transcribed sequence at the
 CC 5' end of the gene; (2) the sense oligonucleotide given in AAQ40912,
 CC complementary to the transcribed sequence at the 5' end of the gene; and
 CC (3) the random sequence given in AAQ40913, having the same base compsn.
 CC as the antisense oligonucleotide. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 360 GAGCTCGCGCCTTG 376
 Db 1 GAGCTCGCGCCTTG 17
 RESULT 365
 AAQ40911/C
 ID AAQ40911 standard; DNA; 17 BP.
 XX
 AC AAQ40911;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1993 (first entry)
 XX
 XX C-erb-B2 antisense oligonucleotide.
 DE
 XX Double; triple; helix; duplex; triplex; major groove; SKBR3 cell; ss.
 KW
 XX Synthetic.
 OS
 XX WO9309813-A1.
 PN
 XX 27-MAY-1993.
 PD
 XX 10-NOV-1992; 92WO-GB002073.
 PF

XX 12-NOV-1991; 91GB-00023947.
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA Epenetos AA;
 PI WPI; 1993-182253/22.
 DR Cpd. comprising anti-sense oligo:nucleotide and radioactive moiety - for
 XX treating viral infection, sepsis, leukaemia and tumours.
 PT Example 3; Page 26; 43pp; English.
 PS For the selective killing of SKBR3 cells the following radiolabelled c-
 XX erb-B2 oligonucleotides were used: (1) the antisense oligonucleotide
 CC given in AAQ40911, complementary to the non-transcribed sequence at the
 CC 5' end of the gene; (2) the sense oligonucleotide given in AAQ40912,
 CC complementary to the transcribed sequence at the 5' end of the gene; and
 CC (3) the random sequence given in AAQ40913, having the same base compsn.
 CC as the antisense oligonucleotide. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX Sequence 17 BP; 4 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 360 GAGCCTGGCGCCTTG 376
 DB 17 GAGCTGGCGCCTTG 1
 RESULT 366
 AAT05984/c
 ID AAT05984 standard; DNA; 17 BP.
 XX AAT05984;
 AC AAT05984;
 XX 31-MAY-1996 (first entry)
 DT COX II forward primer binds 60 bp upstream of COX II gene.
 DE Human; mitochondrial cytochrome C oxidase; COX; subunit I; subunit II;
 KW subunit III; mutation; Alzheimer's disease; AD; sporadic form;
 KW diabetes mellitus; IDDM; detection; PCR; amplify; primer; ss.
 XX Synthetic.
 OS WO9526973-A1.
 PN 12-OCT-1995.
 PD 30-MAR-1995; 95WO-US004063.
 XX 30-MAR-1994; 94US-00219842.
 PR 03-MAR-1995; 95US-00397808.
 XX (GENE-) APPLIED GENETICS INC..
 PA Herrnstadt C, Parker WD, Davis RE, Miller SW;
 XX WPI; 1995-358577/46.
 DR Mutant mitochondrial cytochrome C oxidase genes - useful for generating
 XX probes for diagnosing and treating e.g. Alzheimer's disease and new cell
 PT lines for screening for drugs.
 XX Example 1; Page 78; 149pp; English.
 PS The sequences given in AAT05976-81 are primers which were used in the
 XX amplification of the human mitochondrial cytochrome C oxidase (COX)
 CC

CC subunit I, II and III genes. These primers were targetted 100 bp upstream
 CC and downstream of each gene. The amplified sequences were cloned and
 CC further amplified using the primers given in AAT05982-87. COX genes from
 CC normal individuals and patients with Alzheimer's disease were sequenced
 CC and compared. The COX subunit I and II genes were found to be mutated in
 CC patients with Alzheimer's disease (AD) and comparison between wildtype
 CC and mutated sequences can lead to the identification of recurrent
 CC mutations. Knowledge of these mutations allows the detection of the
 CC sporadic form of AD. Mutations within the COX I and II genes have also
 CC been found to segregate with diabetes mellitus. Oligomers which are
 CC antisense to the positions of mutations can be used in the therapy of AD
 XX SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 562 TGGCTTTTAAATACCT 578
 DB 17 TGGCTTTTAAATACCT 1
 RESULT 367
 AAA18772
 ID AAA18772 standard; RNA; 17 BP.
 XX AAA18772;
 AC AAA18772;
 XX 19-JUN-2000 (first entry)
 DT Human TIE-2 substrate sequence SEQ ID NO:1998.
 DE Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytotstatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS WO9950403-A2.
 PN 07-OCT-1999.
 PD 24-MAR-1999; 99WO-US006507.
 PF 27-MAR-1998; 98US-0079678P.
 PR (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 PI WPI; 1999-591315/50.
 DR Novel ribozymes for modulating the synthesis, expression and/or stability
 XX of an mRNA encoding an angiogenic factors.
 PT Claim 56; Page 116; 305pp; English.
 PS The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC

CC AA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA22476 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, psoriasis, verruca vulgaris,
 CC neovascular glaucoma, myopic degeneration, pot-wine stains, Sturge Weber
 CC angioblastoma of tuberous sclerosis, and arthritis, as well as
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 7 A; 6 C; 2 G; 0 T; 2 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 339 CAGATCTGAGCCCA 955
 Db 1 CAGAAUCUCAAAGCACCA 17
 RESULT 368
 AAF04220
 ID AAF04220 standard; DNA; 17 BP.
 XX
 AC AAF04220;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1736.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 4; Page 95; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 396 TTTTCCTTACAATTCAA 412
 Db 1 TTTTCCTTACAATTCCA 17
 RESULT 370
 ABK02567/c
 ID ABK02567 standard; RNA; 17 BP.
 XX
 AC ABK02567;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Hammerhead ribozyme substrate #2184.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 4; Page 105; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 396 TTTTCCTTACAATTCAA 412
 Db 1 TTTTCCTTACAATTCCA 17
 RESULT 369
 AAF04668
 ID AAF04668 standard; DNA; 17 BP.
 XX
 AC AAF04668;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #2184.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 4; Page 105; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 396 TTTTCCTTACAATTCAA 412
 Db 1 TTTTCCTTACAATTCCA 17
 RESULT 370
 ABK02567/c
 ID ABK02567 standard; RNA; 17 BP.
 XX
 AC ABK02567;
 XX
 DT 12-MAR-2002 (first entry)
 XX

DE Human NIGO Amberyze #239.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme;

KW DNzyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

OS WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797B.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX Claim 88; Page 136; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NIGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-

CC targeting nucleic acid is used to cleave RNA of the NIGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NIGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NIGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NIGO-targetting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC

CC states which respond to the modulation of NIGO expression. The present

CC sequence is an amberyze molecule of the invention

XX Sequence 17 BP; 11 A; 2 C; 2 G; 0 T; 2 U; 0 Other;

XX Query Match 1.2%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 2e+02;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 413 GGGTTTTTCCCTTATT 429

Db 17 GAGTTTTTCCCTTATT 1

RESULT 371

AAF69066/C

ID AAF69066 standard; DNA; 17 BP.

XX AAF69066;

AC AAF69066;

XX 12-APR-2001 (first entry)

DT COXII PCR primer #13.

XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;

XX ss.

XX Homo sapiens.

XX US6171959-B1.

XX 09-JAN-2001.

XX 30-MAR-1995; 95US-00413740.

XX 30-MAR-1994; 94US-00219842.

XX (MITO-) MITOKOR.

XX Herrnstadt C, Parker WD;

XX WPI; 2001-136875/14.

XX Targeting conjugate molecule to mitochondria having defective cytochrome

PT C oxidase activity for diagnosing Alzheimer's disease, involves

PT contacting mitochondria with a conjugate of targeting molecule and toxin.

XX Example 2; Col 41-42; 88pp; English.

XX The present invention relates to a method for selectively accumulating a

CC mitochondrial disabling or destructive amount of a conjugate molecule in

CC mitochondria having defective cytochrome C oxidase (COX) activity or

CC displaying increased membrane potential. The method involves contacting

CC mitochondria with a conjugate molecule comprising a targeting molecule

CC conjugated to a toxin, where the conjugate or targeting molecule selected

CC accumulates in the mitochondria. The method is useful for diagnosis of

CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is

CC a PCR primer used in the method of the present invention

XX Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 2e+02;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTAAACCTT 579

Db 17 GGGTTTTTAAACCTT 1

RESULT 372

AAF69029/C

ID AAF69029 standard; DNA; 17 BP.

CC mitochondria having defective cytochrome C oxidase (COX) activity or
 CC displaying increased membrane potential. The method involves contacting
 CC mitochondria with a conjugate molecule comprising a targeting molecule
 CC conjugated to a toxin, where the conjugate or targeting molecule selected
 CC accumulates in the mitochondria. The method is useful for diagnosis of
 CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
 CC a PCR primer used in the method of the present invention
 XX
 SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTCTTAATACCTT 579
 DB 17 GGGTTTCTTAATACCTT 1

RESULT 375
 AAF69018/c
 ID AAF69018 standard; DNA; 17 BP.

XX
 AC AAF69018;

DT 12-APR-2001 (first entry)

DE COXII PCR primer #3.

XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
 KW ss.

OS Homo sapiens.

XX US6171859-B1.

PN 09-JAN-2001.

XX 30-MAR-1995; 95US-00413740.

XX 30-MAR-1994; 94US-00219842.

XX (MITO-) MITOKOR.

XX Herrnsstadt C, Parker WD;

XX WPI; 2001-136875/14.

XX Targeting conjugate molecule to mitochondria having defective cytochrome
 PT C oxidase activity for diagnosing Alzheimer's disease, involves
 PT contacting mitochondria with a conjugate of targeting molecule and toxin.
 XX Example 1; Col 38; 89pp; English.

XX The present invention relates to a method for selectively accumulating a
 CC mitochondrial disabling or destructive amount of a conjugate molecule in
 CC mitochondria having defective cytochrome C oxidase (COX) activity or
 CC displaying increased membrane potential. The method involves contacting
 CC mitochondria with a conjugate molecule comprising a targeting molecule
 CC conjugated to a toxin, where the conjugate or targeting molecule selected
 CC accumulates in the mitochondria. The method is useful for diagnosis of
 CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
 CC a PCR primer used in the method of the present invention
 XX

SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTCTTAATACCTT 578
 DB 17 TGGTTTCTTAATACCTT 1

RESULT 376

ABL46970
 ID ABL46970 standard; RNA; 17 BP.

XX
 AC ABL46970;

DT 27-JUN-2003 (first entry)

XX Human GRID zinzyme substrate oligonucleotide #54.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.

OS Homo sapiens.

XX WO200162911-A2.

PN 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005957.

XX 24-FEB-2000; 2000US-0184594P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (GLAX) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 72; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX

SQ Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 2e+02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 105 TCAGTGGGGCTATTGGA 121

DB 1 UCAGUGGGGCGUGGGA 17

RESULT 377

AAI65652
 ID AAI65652 standard; DNA; 17 BP.

XX
 AC AAI65652;

DT 03-JAN-2002 (first entry)

XX Primer for studying biallelic polymorphic markers in the IBD1 region.

XX Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox;

XX intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;

XX inflammatory disease; immune disease; cryptogenetic inflammation;

XX hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.

XX OS Homo sapiens.
 XX FR2806739-A1.
 XX PD 28-SEP-2001.
 XX PF 27-MAR-2000; 2000FR-00003832.
 XX PR 27-MAR-2000; 2000FR-00003832.
 XX PA (DAUS-) FOND DAUSSET-CEPH JEAN.
 XX PI Hugot JP, Thomas G, Zouali M, Lesage S, Chamailard M;
 XX WPI; 2001-608364/70.
 XX PT New human nucleic acids associated with intestinal inflammatory disease,
 XX related proteins.
 XX PS Example 4; Page 85; 97pp; French.
 XX CC Primers A165647-78 were used to characterise biallelic polymorphic
 CC markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory
 CC bowel disease 1 (IBD1) polypeptide, which is associated with intestinal
 CC inflammatory disease. The specification also describes a polypeptide
 CC which is in proximity to IBD1, and is designated IBD1prox. The IBD1 gene
 CC is probably involved in regulation of apoptosis and activation of NF-
 CC kappa B. The IBD1 and IBD1prox polynucleotides are useful as source of
 CC probes and primers, as source of (anti)sense oligonucleotides, for
 CC recombinant production of polypeptides, and in screening for interactive
 CC compounds. The polypeptides are used to raise specific antibodies which
 CC useful for diagnostic detection or purification of IBD1 and IBD1prox, to
 CC screen for specific binding agents, potential therapeutic agents. The
 CC IBD1 and IBD1prox polynucleotides and polypeptides are useful for
 CC treatment and prevention of inflammatory and/or immune diseases or
 CC cancer, where associated with mutations in genes corresponding to IBD1
 CC and IBD1prox, especially cryptogenic inflammation of the intestines
 CC (hemorrhagic rectocolitis, Crohn's disease and Blau syndrome)
 XX
 XX SQ Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 197 GCCATCTCTCCCATCC 213
 DB 1 GCCATCTCTCCCATCC 17
 RESULT 378
 ABN06757
 ID ABN06757 standard; DNA; 17 BP.
 AC ABN06757;
 XX
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6749.
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX OS Homo sapiens.
 XX WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (ABOM-) ABOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 WPI; 2002-179446/23.
 DR
 XX
 XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX PS Disclosure; SEQ ID NO 6749; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 XX SQ Sequence 17 BP; 5 A; 2 C; 9 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 836 AGGAGGCCCGGTGGA 852
 DB 1 AGGAGGCCCGGTGGA 17
 RESULT 379
 ABN02571/C
 ID ABN02571 standard; DNA; 17 BP.
 AC ABN02571;
 XX
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2563.
 XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 PT
 XX Disclosure; SEQ ID NO 2563; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 XX Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 745 GCAGCTGCCACCTTATG 761
 Db 17 GCAGCTGCCACCTTATG 1

RESULT 380
 ABN02572/c
 ID ABN02572 standard; DNA; 17 BP.
 XX
 AC ABN02572;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2564.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 PT
 XX Disclosure; SEQ ID NO 2564; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX

XX SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 744 GGCAGCTGCCACCTTAT 760
 |||||
 Db 17 GGCAGCTGCCGCTTCT 1

RESULT 381
 ABV82997
 ID ABV82997 standard; DNA; 17 BP.
 XX AC ABV82997;
 XX DT 03-JAN-2003 (first entry)
 XX DE Human HTPL scanning oligonucleotide SEQ ID 4243.
 XX KW Human: gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX OS Homo sapiens.
 XX FN EP1229046-A2.
 XX PD 07-AUG-2002.
 XX PF 28-JAN-2002; 2002EP-00001167.
 XX PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX PA (ABOM-) ABOMICA INC.
 XX PI Zhan J;
 XX WPI; 2002-676582/73.
 XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 XX PS Example 2; Page 620; 718pp; English.
 XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for

CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX SQ Sequence 17 BP; 3 A; 1 C; 3 G; 10 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 673 AAATTATGTTACTTGT 689
 |||||
 Db 1 AGATTATGTTCTTGT 17

RESULT 382
 ABK19408
 ID ABK19408 standard; RNA; 17 BP.
 XX AC ABK19408;
 XX DT 09-APR-2002 (first entry)
 XX DE Human ERG Amberzyme target sequence Seq ID No 2055.
 XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 XX OS Homo sapiens.
 XX FN WO200188124-A2.
 XX PD 22-NOV-2001.
 XX PF 16-MAY-2001; 2001WO-US015866.
 XX PR 16-MAY-2000; 2000US-00572021.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI (GLAX) GLAXO GROUP LTD.
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082995/11.
 XX DR Novel polynucleotide which down regulates expression of Ets-related gene,
 XX PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 XX PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX PS Claim 4; Page 128; 149pp; English.
 XX CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 2e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 960 GGACCCAGGACATTTTG 976
 Db 1 GGACUCAGGACAUUGG 17

RESULT 383

ABL31405
 ID ABL31405 standard; DNA; 17 BP.

AC ABL31405;

XX

DT 21-MAR-2002 (first entry)

XX Human HLA genotyping oligonucleotide SEQ ID NO 894.

DE

XX Human; human leukocyte antigen; HLA; genotype; polymorphism;

KW immunogenetic; transplantation; genetic disease; ss.

KW Homo sapiens.

OS

XX WO200192572-A1.

PN 06-DEC-2001.

PD

XX 01-JUN-2001; 2001WO-JP004662.

PF 01-JUN-2000; 2000JP-00164798.

PR (NISR) NISSHINBO IND INC.

XX (SYST-) SYSTEM RES INC.

PA Inoko H, Kagiya T, Ichihara T, Mateumura Y, Moriya S, Nishida M;

XX WPI; 2002-122074/16.

DR

XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of

PT individuals e.g. by determining immunogenetic differences when

PT transplanting between them.

XX Claim 10; Page 262; 345pp; Japanese.

PS

XX The invention relates to a typing kit for judging human leukocyte antigen

CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base

CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of

CC genes e.g. belonging to HLA class I antigens on human genome and

Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 404 ACAATTCAAGGGTTTTT 420

Db 1 ACAATTACAGGGTTTTT 17

RESULT 384

ADA49961/C

ID ADA49961 standard; DNA; 17 BP.

XX

AC ADA49961;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human mitochondrial COX gene primer #9.

XX

KW Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;

KW segregation; neutropic; neuroprotective; primer; ss.

XX

OS Homo sapiens.

XX

PN US2003087858-A1.

XX

PD 08-MAY-2003.

XX

PF 15-OCT-2001; 2001US-00978600.

XX

PR 30-MAR-1994; 94US-00219842.

PR 30-MAR-1995; 95US-00413740.

PR 23-NOV-1999; 99US-00448312.

XX

PA (MITO-) MITOKOR.

XX

PI Hernstadt C, Ghosh SS;

XX

XX WPI; 2003-597110/56.

DR

XX Compositions and methods for the treatment and diagnosis of Alzheimer's

PT disease using nucleic acids related in sequence to (mutants of) the

PT cytochrome c oxidase gene.

XX

PS Example 1; Page 24; 93pp; English.

XX

The present invention relates to compositions and method for the treatment and diagnosis of Alzheimer's disease (AD). The method comprises the use of genetic mutations in the human mitochondrial cytochrome c oxidase (COX) gene and their segregation with AD. Also disclosed are antisense sequences specific to mutant human cytochrome c oxidase genes that are designed to bind and inhibit transcription or translation of the target mutant COX genes without inhibiting transcription or translation of wild-type cytochrome c oxidase genes. Also disclosed are probes for detecting a disease state associated with one or more mutations in the mitochondrial COX genes, and a kit comprising a probe for detection of an Alzheimer's disease genotype which is complementary to the sense or antisense strands of a mitochondrial COX gene. Definitive diagnosis of Alzheimer's disease can currently only be accomplished by pathological examination at autopsy, the new method provides a non-invasive diagnostic that is reliable at or before the earliest manifestations of AD symptoms. There is at present no effective therapy for AD other than certain palliative treatments. The new therapeutic compositions and methods provide an effective therapy that addresses the primary cause of AD. The present sequence represents a primer for the human mitochondrial COX gene.

SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTTATACCT 578

KW HLA-B*5701; C4A6; HLA-DR7; HLA-DQ3; Human immunodeficiency virus; HIV;
 KW immune system; acquired immune deficiency syndrome; AIDS;
 KW peripheral nervous system; antiviral compound; HIV replication inhibitor;
 KW antiretroviral; nucleoside reverse transcriptase inhibitor; NRTI;
 KW antiretroviral drug; abacavir; human; sequencing primer; primer; PCR; ss;
 KW 90835.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068985-A1.
 XX
 PD 21-AUG-2003.
 XX
 PF 12-FEB-2003; 2003WO-AU000183.
 XX
 PR 12-FEB-2002; 2002AU-00000464.
 XX
 PA (EPIP-) EPIPOP PTY LTD.
 XX
 PI Mallal S;
 XX
 DR WPI; 2003-697530/66.
 XX
 XX Method for the identification of subjects hypersensitive to abacavir,
 PT useful for excluding patients from treatment, comprises detecting the
 PT presence of the 57.1 ancestral haplotype.
 XX
 PS Example 2; Page 21; 43pp; English.
 XX
 CC This invention relates to a method for determining whether a patient will
 CC show a hypersensitivity, or similar, reaction to abacavir by typing the
 CC patient for presence of the 57.1 ancestral haplotype of the Major
 CC Histocompatibility Complex (MHC). The ancestral haplotype is defined by
 CC presence of the human leukocyte antigen (HLA) subtypes HLA-B*5701, C4A6,
 CC HLA-DR7 and HLA-DQ3. Human immunodeficiency virus (HIV) is the
 CC aetiological agent of a complex disease that includes progressive
 CC destruction of the immune system (acquired immune deficiency syndrome,
 CC AIDS) and degeneration of the peripheral nervous system. It is known that
 CC some antiviral compounds which act as inhibitors of HIV replication are
 CC effective agents in the treatment of AIDS. Treatment with an antiviral to
 CC a person with hypersensitivity may lead to a range of ailments and
 CC occasionally death. Patients who have the 57.1 ancestral haplotype are at
 CC a high risk of developing a hypersensitive reaction to abacavir, a
 CC nucleoside reverse transcriptase inhibitor (NRTI) antiretroviral drug
 CC often used to treat HIV and AIDS. The identification method of the
 CC invention may be useful for identifying patients who need to be excluded
 CC from treatment with abacavir. The present sequence is that of a human
 CC sequencing and PCR amplification primer which was used for identifying
 CC the presence or absence of the 57.1 ancestral haplotype of the MHC of the
 CC invention.
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 245 TCAGATCGACACGATAG 261
 |||||
 Db 1 TCAGCTGCACACGAG 17
 RESULT 390
 ADL46684/C
 ID ADL46684 standard; RNA; 17 BP.
 XX
 AC ADL46684;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human NOGO receptor inozyme substrate sequence #117.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;

KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis;
 KW NOGO receptor inozyme; substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 XX
 PR 29-MAY-2001; 2001US-0294412P.
 XX
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fornaugh K;
 XX WPI; 2003-058513/05.
 DR
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 XX Claim 9; SEQ ID NO 217; 317pp; English.
 PS
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human NOGO
 CC receptor inozyme substrate sequence.
 XX
 SQ Sequence 17 BP; 1 A; 9 C; 6 G; 0 T; 1 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 15 GGCTGCCCGGCGCGTGG 31
 |||||
 Db 17 GGCGGCCCGGCGCGTGG 1
 RESULT 391
 ADM09493/C
 ID ADM09493 standard; RNA; 17 BP.
 XX
 AC ADM09493;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human NOGO receptor amberzyme substrate sequence #48.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;

KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor; substrate; ss.
OS Unidentified.
XX WO200281628-A2.
PN 17-OCT-2002.
XX 03-APR-2002; 2002WO-US010512.
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX (RIBO-) RIBOZYME PHARM INC.
PA Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX Claim 9; SEQ ID NO 888; 317pp; English.
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human NOGO
CC receptor amberzyme substrate sequence.
XX Sequence 17 BP; 1 A; 8 C; 6 G; 0 T; 2 U; 0 Other;
SQ Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 14 AGCGTCCCGCCGCG 30
DB ||||| ||||| ||||| ||||| |||||
17 AGCGCGCCCGCGCGCG 1
RESULT 392
ADW54293
ID ADM54293 standard; mRNA; 17 BP.
XX ADM54293;
AC 03-JUN-2004 (first entry)
XX Human GRID mRNA substrate sequence #603.
DE Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW

KW NCH ribozyme; G-cleaver ribozyme; Zinzyyme; DNAszyme; amberzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
OS Homo sapiens.
PN US2003134806-A1.
XX 17-JUL-2003.
XX 23-FEB-2001; 2001US-00792818.
XX 10-FEB-2000; 2000US-0181594P.
XX (JARV/) JARVIS T.
PA (CARL/) CARLOWITZ I V.
PA (MCSW/) MCSWIGGEN J.
PA (HAMB/) HAMBLIN P A.
PA (ELLI/) ELLIS J H.
XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
PI WPI; 2003-829646/77.
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX Claim 4; SEQ ID NO 603; 74pp; English.
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyyme, DNAszyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
SQ Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 105 TCAGTGGGGCGCTATTGGA 121
DB :|||:|||||: :|||
1 UCAGUGGGGCGUGGGA.17
RESULT 393
ADL82299
ID ADL82299 standard; DNA; 17 BP.
XX ADL82299;
AC 20-MAY-2004 (first entry)
XX Human ER+ breast cancer differentially expressed sequence #269.
DE gene therapy; ds; breast cancer; human; ER+ breast cancer.
KW Homo sapiens.
OS

PN US2003166026-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 08-JAN-2003; 2003US-00339782.
 XX
 PR 09-JAN-2002; 2002US-0348053P.
 XX
 XX (LYNX-) LYNX THERAPEUTICS INC.
 PA Goodman LJ, Bowen BA;
 XX WPI; 2004-069003/07.
 DR
 XX Vector containing nucleic acid associated with breast cancer, useful for
 PT treating, diagnosing and characterizing breast cancer, also related
 PT polypeptides and antibodies.
 PT
 PS Claim 1; SEQ ID NO 270; 61pp; English.
 XX
 CC The invention relates to a composition which contains at least one vector
 CC (B) containing a nucleic acid (I) associated with breast cancer. The
 CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
 CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
 CC -specific antibodies (Ab) are used to predict characteristics (e.g.
 CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
 CC used to modulate characteristics of such cells; to identify breast cancer
 CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
 CC or its products). The present sequence represents a human ER+ breast
 CC cancer differentially expressed sequence.
 XX
 SQ Sequence 17 BP; 7 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 898 GACCAAGAGCCTCAACA 914
 DB 1 GATCAAGACCCTCAACA 17
 RESULT 394
 ACN69847
 ID ACN69847 standard; DNA; 17 BP.
 XX
 AC ACN69847;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPLP-1 probe SEQ ID NO:6749.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-026680P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 PA (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 XX
 DR Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 6749; 0pp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (SI) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (SI), 95% deviation from (SI) which are conservative substitutions, and
 CC 65% identity to (SI). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmacological composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 5 A; 2 C; 9 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 836 AGGAAGCCCGGGTGA 852
 DB 1 AGGAAGCCCGTGGAGGA 17
 RESULT 395
 ACN65662/c
 ID ACN65662 standard; DNA; 17 BP.
 XX
 AC ACN65662;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPLP-1 probe SEQ ID NO:2564.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 PA (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 2564; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 744 GGCAGCTGCCACTTATG 760
 DB |||||
 17 GGCAGCTGCCGCTTCT 1
 RESULT 396
 ACN65661/c
 ID ACN65661 standard; DNA; 17 BP.
 XX
 AC ACN65661;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPL-1 probe SEQ ID NO:2563.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;
 KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.

XX US2004137589-A1.
 XX 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 PA (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 2563; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 745 GCAGCTGCCACTTATG 761
 DB |||||
 17 GCAGCTGCCGCTTCTG 1
 RESULT 397
 AAV44608/c
 ID AAV44608 standard; DNA; 18 BP.
 XX
 AC AAV44608;
 XX
 DT 24-NOV-1998 (first entry)

```

XX DE Human uncoupling protein-2 UCP2 gene reverse primer hUCP2g.e6r1.
XX KW Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
XX KW obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
XX KW hypothermia; wasting; cachexia; anorexia; inflammation; fever;
XX KW hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9831396-A1.
XX XX 23-JUL-1998.
XX PD
XX PF 22-APR-1997; 97WO-US006864.
XX XX 15-JAN-1997; 97US-0034960P.
XX PR
XX PA (UYDU-) UNIV DUKE.
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (CNRS ) CENT NAT RECH SCI.
XX XX
XX PI Surwit RS, Collins SA, Warden CH, Seldin MF, Ricquier D;
XX PI Bouillaud F;
XX XX
XX DR WPI; 1998-413823/35.
XX XX
XX PT Method for treating disease associated with altered UCP-2 expression - by
XX PT administering agent which enhances or inhibits UCP-2 activity,
XX PT effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
XX PT etc.
XX PS
XX PS Example IX; Page 47; 98pp; English.
XX CC
XX CC Primer hUCP2g.e6r1 is used with forward primer hUCP2g.e6f1 (see AAV44607)
XX CC in the PCR amplification of bp 3147-3416 in exon 6 of the human
XX CC uncoupling protein-2 (UCP2) gene. Primers (see AAV44603-18) were designed
XX CC to amplify hUCP2 exons 4, 6, 7 and 8 from genomic DNA. Common amino acid
XX CC variants (see AAW69166) are present in exons 4, 6 and 8; A55V in exon 4,
XX CC N190S in exon 6, and L294M in exon 8 (see also AAV44595). Restriction
XX CC enzymes have been identified that would differentially digest each
XX CC of the alleles. The invention relates to a method for treating disease
XX CC associated with altered UCP2 expression, such as obesity, diabetes,
XX CC syndrome X, hypothermia, hyperinsulinaemia, glucose intolerance, wasting,
XX CC anorexia, inflammation, cachexia, fever or hyperthermia
XX XX
XX SQ Sequence 18 BP; 5 A; 1 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 201 TCTCCCCCATCCCCCAT 217
Db ||||| ||||| |||||
17 TCTCACCCTTCCCCCAT 1

RESULT 198
AAZ00111
ID AAZ00111 standard; DNA; 18 BP.
XX AC
XX AC AAZ00111;
XX XX
XX DT 12-OCT-1999 (first entry)
XX XX
XX DE HEV US-1 amplifying primer.
XX XX
XX KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
XX KW vaccine; passive immunisation; PCR primer; ss.
XX OS Synthetic.
XX OS Hepatitis E virus.

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XX WO9919732-A1.
XX PN
XX PD 22-APR-1999.
XX XX
XX PF 15-OCT-1998; 98WO-US021941.
XX XX
XX PR 15-OCT-1997; 97US-0061199P.
XX XX
XX PA (ABBO ) ABBOTT LAB.
XX XX
XX PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX PI WPI; 1999-288017/24.
XX DR
XX DR Detection of United States isolates of hepatitis E virus.
XX PT
XX PS Example 2; Page 141; 260pp; English.
XX XX
XX CC The invention provides a method for detecting a US (subtype hepatitis E
XX CC virus (US-HEV), or its naturally occurring variants in a sample by
XX CC treatment with a binding partner specific for a marker of the virus, and
XX CC then detecting any complex formed. The method is used to diagnose
XX CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
XX CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
XX CC are useful in vaccines or for passive immunisation. The polypeptides are
XX CC also used to raise specific antibodies (useful as immunoassay reagents).
XX CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
XX CC usual hybridisation and amplification assays for detecting infection. The
XX CC present sequence represents a HEV specific primer
XX XX
XX SQ Sequence 18 BP; 6 A; 8 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1035 TAAACATCACACCCCAAC 1051
Db ||||| ||||| |||||
2 TGAACATCACGCCCAAC 18

RESULT 399
AAAX76902/c
ID AAAX76902 standard; DNA; 18 BP.
XX AC
XX AC AAAX76902;
XX XX
XX DT 17-OCT-2003 (revised)
XX DT 05-AUG-1999 (first entry)
XX XX
XX DE Hz-1 Pag1 gene direct repeat sequence.
XX XX
XX KW Hz-1 pag1 promoter; persistence-associated gene 1; insect cell;
XX KW constitutive expression promoter; direct repeat; ss.
XX XX
XX OS Heliothis zea virus 1.
XX XX
XX PN US5911982-A.
XX XX
XX PD 15-JUN-1999.
XX XX
XX PF 18-APR-1996; 96US-00634350.
XX XX
XX PR 06-OCT-1995; 95US-0004894P.
XX PR 11-OCT-1995; 95US-0005128P.
XX XX
XX PA (NASC-) NAT SCI COUNCIL.
XX XX
XX PI Chao Y;
XX XX
XX DR WPI; 1999-357167/30.
XX XX

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Query Match 1.2%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 CCCCCATCCCCCATTC 220
 Db 18 CCTCATCCCCCATTC 2

RESULT 402
 AAZ70376/C
 ID AAZ70376 standard; DNA; 18 BP.
 XX AC AAZ70376;
 XX DT 10-SEP-2001 (first entry)
 XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4732.
 XX KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX OS Homo sapiens.
 XX PN WO9954500-A2.
 XX PD 28-OCT-1999.
 XX PF 21-APR-1999; 99WO-IB000822.
 XX PR 21-APR-1998; 98US-0082614P.
 XX PR 23-NOV-1998; 98US-0109732P.
 XX PR (GBST) GENSET.
 XX PI Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium
 map of the human genome.
 PS Claim 8; Page 1240; 2745pp; English.
 XX AAZ65854 to AAZ69578 represent human biallelic markers from the present
 invention, which contain a polymorphic base at position 24 of their
 nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 primers for the biallelic markers. The biallelic markers of the invention
 have a variety of uses: they can be used for high density mapping of the
 human genome, and in complex association studies and haplotyping studies
 which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 identification of the targets for the development of pharmaceutical
 agents and diagnostic methods, as well as the characterisation of the
 differential efficacious responses to and side effects from
 pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. the SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 3367, are not actually given a sequence in the Sequence Listing from the
 present invention
 XX Sequence 18 BP; 5 A; 2 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 905 AGCCTCACATTCCTA 921
 Db 17 AGCCTCAGCATTCATA 1

RESULT 403
 ABL54891
 ID ABL54891 standard; DNA; 18 BP.
 XX AC ABL54891;
 XX DT 31-MAY-2002 (first entry)
 XX DE PCR primer BV-b5.
 XX KW PCR primer; gap vector; Escherichia coli; stop codon assay;
 KW truncating mutation; ss.
 XX OS Synthetic.
 XX PN KR2001016649-A.
 XX PD 05-MAR-2001.
 XX PF 02-AUG-1999; 99KR-00031647.
 XX PR 02-AUG-1999; 99KR-00031647.
 XX PA (KWAN-) KWANGMYUNG SUNGAE MEDICAL FOUND.
 XX WPI; 2001-495301/54.
 XX Gap vector for Escherichia coli stop codon assay used for assaying
 heterozygous truncating mutation.
 PS Disclosure; Page 19; 33pp; Korean.
 XX This sequence represents a PCR primer used within the scope of the
 invention. The invention relates to a gap vector (GV) for assaying
 Escherichia coli (E.coli) stop codon. The invention also relates to a
 method for assaying heterozygous truncating mutation using the GV
 comprising the following steps: (1) multiplying exon fragments showing
 truncating mutation by polymerase chain reaction (PCR) and cloning the
 exon fragments with a plasmid for E. coli having a low copy number; (2)
 using the plasmid having cloned exon gene as a template and performing
 PCR with a primer having 50-200 bp of 5' and 3' terminals of the exon
 gene to make a gap vector for E. coli stop codon assay; (3) multiplying
 the same genetic fragment as the multiplied exon fragment through RT-PCR
 or PCR using RNA obtained from a sample to be measured or cDNA as a
 template; and (4) transforming the gap vector obtained from step (2) and
 the genetic fragment obtained from step (3) into E. coli at the same time
 XX Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 CACATGAAGTTTGAGA 1016
 Db 1 CACATGCAAGTTTGAAA 17

RESULT 404
 ACF63028/C
 ID ACF63028 standard; DNA; 18 BP.
 XX AC ACF63028;
 XX DT -09-OCT-2003 (first entry)
 XX DE Human progesterone receptor PCR primer SEQ ID NO:277.
 XX KW Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
 KW progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
 KW characterisation; classification; diagnosis; differentiation;
 KW colon cell proliferative disorder; PCR primer; ss.

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XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003014388-A2.
XX PD 20-FEB-2003.
XX XX
XX PF 09-AUG-2002; 2002WO-EP008939.
XX XX
XX PR 09-AUG-2001; 2001DE-01039283.
XX XX
XX PA (EPITG-) EPIGENOMICS AG.
XX XX
XX PI Distler J, Model F, Taubert H;
XX XX
XX PS WPI; 2003-256600/25.
XX DR
XX CC Determining methylation status of CpG dinucleotides using modified
XX PT genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
XX PT characterization, grading, staging and/or diagnosis of colon cancer.
XX XX
XX PS Claim 26; Page 171; 219pp; English.
XX XX
XX CC The present invention describes a method for determining the methylation
XX CC status of CpG dinucleotides within the genes for oestrogen receptor, p21,
XX CC p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erbB2, p53
XX CC and/or CEA, which comprises contacting the target nucleic acid with a
XX CC reagent that distinguishes between methylated and non-methylated CpG
XX CC dinucleotides, and determining from the methylation status of the CpG
XX CC nucleic acid (PNA)-oligomers can be used as probes for determining the
XX CC positions the presence of a colon cancer. A set of oligomers or peptide
XX CC cytosine methylation state and/or single nucleotide polymorphisms (SNP)
XX CC of a corresponding genomic DNA by analysis of a chemically pretreated
XX CC genomic DNA. The pretreated genomic DNA is useful for the determination
XX CC of the methylation status of a corresponding genomic DNA and/or detection
XX CC of SNPs. The methods and pretreated genomic DNA are also useful for the
XX CC characterisation, classification, diagnosis and differentiation of colon
XX CC cell proliferative disorders. ACF62752 to ACF63278 represent sequences
XX CC used in the exemplification of the present invention
XX XX
XX SQ Sequence 18 BP; 8 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 TAGGAGATCAGTTTAT 632
Db 17 TAGGAGATCAGATTTT 1

RESULT 405
ACF63026
ID ACF63026 standard; DNA; 18 BP.
XX
XX AC ACF63026;
XX XX
XX DT 09-OCT-2003 (first entry)
XX XX
XX DE Human progesterone receptor PCR primer SEQ ID NO:275.
XX XX
XX KW Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
XX KW progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
XX KW characterisation; classification; diagnosis; differentiation;
XX KW colon cell proliferative disorder; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN WO2003014388-A2.
XX PD 20-FEB-2003.

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XX 09-AUG-2002; 2002WO-EP008939.
XX PF
XX PR 09-AUG-2001; 2001DE-01039283.
XX XX
XX PA (EPITG-) EPIGENOMICS AG.
XX XX
XX PI Distler J, Model F, Taubert H;
XX XX
XX PS WPI; 2003-256600/25.
XX DR
XX CC Determining methylation status of CpG dinucleotides using modified
XX PT genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
XX PT characterization, grading, staging and/or diagnosis of colon cancer.
XX XX
XX PS Claim 26; Page 170; 219pp; English.
XX XX
XX CC The present invention describes a method for determining the methylation
XX CC status of CpG dinucleotides within the genes for oestrogen receptor, p21,
XX CC p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erbB2, p53
XX CC and/or CEA, which comprises contacting the target nucleic acid with a
XX CC reagent that distinguishes between methylated and non-methylated CpG
XX CC dinucleotides, and determining from the methylation status of the CpG
XX CC nucleic acid (PNA)-oligomers can be used as probes for determining the
XX CC positions the presence of a colon cancer. A set of oligomers or peptide
XX CC cytosine methylation state and/or single nucleotide polymorphisms (SNP)
XX CC of a corresponding genomic DNA by analysis of a chemically pretreated
XX CC genomic DNA. The pretreated genomic DNA is useful for the determination
XX CC of the methylation status of a corresponding genomic DNA and/or detection
XX CC of SNPs. The methods and pretreated genomic DNA are also useful for the
XX CC characterisation, classification, diagnosis and differentiation of colon
XX CC cell proliferative disorders. ACF62752 to ACF63278 represent sequences
XX CC used in the exemplification of the present invention
XX XX
XX SQ Sequence 18 BP; 5 A; 0 C; 5 G; 8 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 TAGGAGATCAGTTTAT 632
Db 2 TAGGAGATCAGATTTT 18

RESULT 406
ADM06379/c
ID ADM06379 standard; DNA; 18 BP.
XX
XX AC ADM06379;
XX XX
XX DT 20-MAY-2004 (first entry)
XX XX
XX DE Human PCR primer SEQ ID NO:5064.
XX XX
XX KW human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.
XX XX
XX OS Homo sapiens.
XX XX
XX PN EP1347046-A1.
XX XX
XX PD 24-SEP-2003.
XX XX
XX PF 12-APR-2002; 2002EP-00008400.
XX XX
XX PR 22-MAR-2002; 2002JP-00137785.
XX XX
XX PS (REAS-) RES ASSOC BIOTECHNOLOGY.
XX XX
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX XX

```

DR WPI; 2003-723558/69.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX Example 8; SEQ ID NO 5064; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents an

CC oligonucleotide used in the invention.

XX Sequence 18 BP; 9 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2;

Qy 295 TGGATTGTTGTTCTG 311

Db 18 TGGATTGTTGTTCTG 2

RESULT 407

ADJ65208

ID ADJ65208 standard; DNA; 18 BP.

XX

AC ADJ65208;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human connexin gene 26 Cx26 235 Del mutant primer seq id 10.

XX

KW hereditary hearing loss; connexin 26; Cx26; mitochondrial gene;

KW Cytomegalovirus gene; CMV; human; PCR; primer; ss; mutant.

XX

OS Homo sapiens.

XX

PN US2004038266-A1.

XX

XX 26-FEB-2004.

XX

XX 22-MAY-2003; 2003US-00443545.

XX

XX 28-MAY-2002; 2002US-0370762P.

XX

PA (DOBR/) DOBROWOLSKI S F.

PA (LINZ/) LIN Z.

XX

PI Dobrowolski SF, Lin Z;

XX

DR WPI; 2004-213937/20.

XX

PT Genetically screening for detecting hereditary hearing loss by detecting

PT connexin 26, a mitochondrial or Cytomegalovirus nucleic acids by

PT hybridization and/or PCR.

XX

PS Claim 6; SEQ ID NO 10; 22pp; English.

XX

XX The invention describes a method of genetically screening for detecting

CC hereditary hearing loss. The method comprises detecting a nucleic acid

CC from a connexin 26 (Cx26), a mitochondrial gene and/or a Cytomegalovirus

CC (CMV) gene by hybridisation and/or PCR. The methods of the invention are

CC used for detecting causes of hereditary hearing loss. This sequence

CC represents a primer used in the isolation of DNA encoding the human

CC connexin 26 (Cx26) mutant Cx26 235 Del.

XX

XX Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2;

Qy 196 CGCCATCTCCCATCC 212

Db 1 CCCCATCTCCCATCC 17

RESULT 408

ADN35818/C

ID ADN35818 standard; DNA; 18 BP.

XX

AC ADN35818;

XX

DT 01-JUL-2004 (first entry)

XX

DE Human NSCLC gene antisense-s oligonucleotide #39.

XX

KW ss; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC;

KW diagnosis; cancer; URLC1; antisense.

XX

OS Homo sapiens.

XX

PN WO2004031413-A2.

XX

XX 15-APR-2004.

XX

XX 22-SEP-2003; 2003WO-JP012072.

XX

XX 30-SEP-2002; 2002US-0414673P.

XX

XX 28-FEB-2003; 2003US-0451374P.

XX

XX 28-APR-2003; 2003US-0466100P.

XX

PA (ONCO-) ONCOTHERAPY SCI INC.

PA (UVTY) UNIV TOKYO.

XX

PI Nakamura Y, Daigo Y, Nakatsuru S;

XX

DR WPI; 2004-330206/30.

XX

PT Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)

PT comprises determining an expression level of an NSCLC-associated gene in

PT a sample.

XX

PS Disclosure; SEQ ID NO 499; 394pp; English.

XX

XX The invention relates to a method of diagnosing non-small cell lung

CC cancer (NSCLC) or a predisposition to developing NSCLC in a subject by

CC determining the expression level of a NSCLC-associated gene in a

CC biological sample derived from the subject, where an increase or decrease

CC of the level compared to a normal control level of the gene indicates

CC that the subject suffers from or is at risk of developing NSCLC. The

CC method is useful in diagnosing NSCLC or a predisposition to developing

CC NSCLC in a subject. The compound, polynucleotide and the encoded

CC polypeptide and composition are useful in treating or preventing NSCLC.

CC This sequence corresponds to an antisense oligonucleotide of genes that

CC are differentially expressed in NSCLC cells.

XX

SQ Sequence 18 BP; 5 A; 7 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2;

Qy 432 GAAGAGGAGATGATTTT 448

Db 18 GAGGAGGAGATGATTTT 2

```

RESULT 409
ADS90119
ID ADS90119 standard; DNA; 18 BP.
XX
AC ADS90119;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:1135.
XX
KW ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Unidentified.
XX
PN WO2004035803-A2.
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model P;
PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
WPI; 2004-348468/32.
XX
PT Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject..
XX
PS Disclosure; SEQ ID NO 1135; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 18 BP; 3 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 152 GAGGATTATGCGGTTTA 168
DB 1 GAGGGTTATCGGTTTA 17
|||||
|||||

RESULT 410
AAA83453/c
ID AAA83453 standard; DNA; 19 BP.
XX
AC AAA83453;
XX
DT 04-DEC-2000 (first entry)
XX

```

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XX cdk8 ribozyme binding site #173.
DE
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KW
XX Mammalia.
OS
WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI
XX WPI; 2000-412314/35.
DR
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
XX Disclosure; Page 62; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 10 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 415 GTTTTCCTTATATTG 431
DB 19 GTTTTCCTTATATTG 3
|||||
|||||

RESULT 411
AAA83063/c
ID AAA83063 standard; DNA; 19 BP.
XX
AC AAA83063;
XX
DT 04-DEC-2000 (first entry)
XX
DE cdk6 ribozyme binding site #123.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX

```


DR WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves

PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,

PT PCNA and Cyclin B1.

XX Disclosure; Page 56; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme,

CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase

CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

CC Representative examples of ribozyme recognition sites are given in

CC AA82415 to AA86787. The ribozyme of the invention is useful for

CC inhibiting restenosis by introduction of the ribozyme into cells. The

CC ribozyme is resistant to endonuclease activity and hence is efficient in

CC restenosis treatment

XX

SQ Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 603 AAGACTTCATCAAGTAGG 619

Db 19 AACACTTCAGAGTAGG 3

RESULT 412

AAH56706/C

ID AAH56706 standard; DNA; 19 BP.

XX

AC AAH56706;

XX

DT 06-SEP-2001 (first entry)

XX

XX Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:354.

XX

XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;

XX microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;

XX Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;

XX antibacterial; antiviral; antiproliferative; antisense therapy;

XX microbial infection; ss.

XX

OS Streptococcus pyogenes.

XX

PN WO200136625-A2.

XX

PD 25-MAY-2001.

XX

XX 20-NOV-2000; 2000WO-CA001347.

XX

XX 18-NOV-1999; 99US-0166249P.

XX

PA (GENE-) GENESENSE TECHNOLOGIES INC.

XX

PI Wright JA, Young AH, Dugourd D;

XX

XX WPI; 2001-355633/37.

DR

XX Novel antisense compounds targeting nucleic acid encoding groEL or groES

PT gene of microorganism, which hybridize with and inhibit expression of the

PT genes, useful to inhibit growth of microorganism having the genes.

XX

PS Claim 3; Page 50; 110pp; English.

XX

XX The present invention specifically claims AAH56368 to AAH56832 which are

CC antisense oligonucleotides to nucleotide sequences encoding groE. More

CC generally, antisense compounds (I) comprising antisense oligonucleotides

CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat

CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a

CC microorganism, where the antisense compound is complementary to GL or GS

CC of a microorganism and specifically hybridizes with and inhibits the

expression of GL or GS, is claimed. (I) have antibacterial, antiviral and

antiproliferative activities, and can be used in antisense therapy and

for inhibiting expression of groES or groEL. (I) are useful for

inhibiting expression of GL or GS in cells or tissues in vitro. (I) are

also useful for inhibiting the growth of a microorganism, or inhibiting

the expression of GL or GS gene in a microorganism (a bacterial cell or a

virus) having a GL or GS gene which involves administering to the

microorganism or to a cell infected with the microorganism, (I). (I) are

also useful for treating a mammalian pathological condition mediated by

the microorganisms which involves identifying a eukaryotic organism

having a pathological condition mediated by microorganisms having a GL or

GS gene and administering (I) such that the growth of microorganism is

inhibited. The antisense compounds are utilised for diagnostics,

therapeutics, prophylaxis and as research reagents and kits, e.g., to

prevent or delay microbial infections in humans. They are also useful as

molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854

represent PCR primers for groE sequences which are used in the

exemplification of the present invention. AAH56855 to AAH56870 represent

groE nucleotide sequence given in the present invention

XX

SQ Sequence 19 BP; 8 A; 2 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 567 TTTTAAATACCTTTATA 583

Db 18 TTTTAAACCTTTAGA 2

RESULT 413

AAH58225/C

ID AAH58225 standard; DNA; 19 BP.

XX

AC AAH58225;

XX

DT 10-SEP-2001 (first entry)

XX

XX Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:649.

XX

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

XX recognition site; target; ribozyme binding site; eye disease; vulnary;

XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;

XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;

XX antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;

XX antipsoriasis; ophthalmological; keratolytic; gene therapy; viral wart;

XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;

XX basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;

XX sickle cell retinopathy; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200130362-A2.

XX

PD 03-MAY-2001.

XX

XX 26-OCT-2000; 2000WO-US029500.

PF

XX 26-OCT-1999; 99US-0161532P.

PR

XX (IMMU-) IMMUSOL INC.

PA

XX Robbins JM, Tritz R;

PI

XX WPI; 2001-300427/31.

DR

XX Treating proliferative skin or eye diseases and scarring, using ribozymes

PT that cleave RNA encoding cytokines involved in inflammation, matrix

PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX

```

PS      Example 1; Page 119; 408pp; English.
XX
CC      The present invention describes a method for treating a proliferative
CC      skin or eye disease and scarring. The method involves administering a
CC      ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC      inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC      dependent kinase, growth factor or a reductase, or administering a
CC      nucleic acid molecule (II) comprising a promoter operably linked to a
CC      nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC      dermatological, cytostatic, antiseborrheic, antidiabetic, anti-itching,
CC      ophthalmological, vulnary, keratolytic and virucide activities, and
CC      cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC      in gene therapy. (I) and (II) are useful for treating proliferative skin
CC      diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC      squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC      also be used for treating proliferative eye diseases such as diabetic
CC      retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC      prematurity and retinal detachment, and for treating and preventing
CC      scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC      scar. AAH57577 to AAH62099 represent sequences used in the
CC      exemplification of the present invention
XX
SQ      Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

      Query Match      1.2%; Score 13.8; DB 1; Length 19;
      Best Local Similarity 88.2%; Pred. No. 2.1e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      603 AAGACTTCATTAAGTAGG 619
DB      || ||||| |||||
      19 AACACTTCAGAGTAGG 3

RESULT 414
AAH58615/c
ID      AAH58615 standard; DNA; 19 BP.
XX
AC      AAH58615;
XX
DT      10-SEP-2001 (first entry)
XX
DE      Cell-cycle dependent kinase cd8 ribozyme binding site SEQ ID NO:1039.
XX
KW      Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW      recognition site; target; ribozyme binding site; eye disease; vulnary;
KW      proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW      cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW      matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW      antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW      anti-itching; ophthalmological; keratolytic; gene therapy; viral wart;
KW      atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW      basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW      sickle cell retinopathy; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200130362-A2.
XX
PD      03-MAY-2001.
XX
XX      26-OCT-2000; 2000WO-US029500.
XX
XX      26-OCT-1999; 99US-0161532P.
XX
XX      (IMMU-) IMMUSOL INC.
XX
XX      Robbins JM, Tritz R;
XX
XX      WPI; 2001-300427/31.
XX
XX      Treating proliferative skin or eye diseases and scarring, using ribozymes
XX      PT that cleave RNA encoding cytokines involved in inflammation, matrix

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```

PT      metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX      Example 1; Page 147; 408pp; English.
XX
CC      The present invention describes a method for treating a proliferative
CC      skin or eye disease and scarring. The method involves administering a
CC      ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC      inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC      dependent kinase, growth factor or a reductase, or administering a
CC      nucleic acid molecule (II) comprising a promoter operably linked to a
CC      nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC      dermatological, cytostatic, antiseborrheic, antidiabetic, anti-itching,
CC      ophthalmological, vulnary, keratolytic and virucide activities, and
CC      cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC      in gene therapy. (I) and (II) are useful for treating proliferative skin
CC      diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC      squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC      also be used for treating proliferative eye diseases such as diabetic
CC      retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC      prematurity and retinal detachment, and for treating and preventing
CC      scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC      scar. AAH57577 to AAH62099 represent sequences used in the
CC      exemplification of the present invention
XX
SQ      Sequence 19 BP; 10 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

      Query Match      1.2%; Score 13.8; DB 1; Length 19;
      Best Local Similarity 88.2%; Pred. No. 2.1e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      415 GTTTTCTTATATTTG 431
DB      ||||| |||||
      19 GTTTTCCATATACTTG 3

RESULT 415
AAF74684
ID      AAF74684 standard; DNA; 19 BP.
XX
AC      AAF74684;
XX
DT      16-MAY-2001 (first entry)
XX
DE      P. furiosus thermophilic glucoamylase PCR primer SEQ ID NO:9.
XX
KW      Pyrococcus furiosus; thermophilic glucoamylase; starch decomposition;
KW      glucose; oligosaccharide; cyclodextrin; genetic engineering; PCR primer;
KW      ss.
XX
OS      Pyrococcus furiosus.
PN      WO200109348-A1.
XX
PD      08-FEB-2001.
XX
XX      26-JUL-2000; 2000WO-JP004956.
XX
XX      02-AUG-1999; 99JP-00218778.
XX
XX      (TAKI) TAKARA SHUZO CO LTD.
XX
XX      Koyama N, Okui T, Takakura H, Asada K, Kato I;
XX
XX      WPI; 2001-168708/17.
XX
XX      Polypeptides with thermophilic glucoamylase activity and high thermal
XX      PT stability, applicable in efficient utilization of biomass e.g. in
XX      PT decomposing starch to produce glucose or oligosaccharides or
XX      PT cyclodextrins.
XX
XX      Example 4; Page 56; 62pp; Japanese.
XX
XX      The present invention describes a protein derived from Pyrococcus

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```

PT infection.
PS Disclosure; SEQ ID NO 63; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents a PCR primer for
CC the Oryza minuta P19 locus.
XX
SQ Sequence 19 BP; 14 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 414 GGTTCCTTCTATATTT 430
Db 19 GGTTCCTTCTATATTT 3

RESULT 420
ADN75775
ID ADN75775 standard; RNA; 19 BP.
XX
AC ADN75775;
XX
DT 01-JUL-2004 (first entry)
XX
DE TCPTP associated siRNA hTCPTP1.5 #2.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
XX
PT 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Claim 1; SEQ ID NO 600; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosolic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 19 BP; 14 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 414 GGTTCCTTCTATATTT 430
Db 19 GGTTCCTTCTATATTT 3

RESULT 420
ADN75775
ID ADN75775 standard; RNA; 19 BP.
XX
AC ADN75775;
XX
DT 01-JUL-2004 (first entry)
XX
DE TCPTP associated siRNA hTCPTP1.5 #2.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
XX
PT 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Claim 1; SEQ ID NO 600; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosolic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 19 BP; 14 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 414 GGTTCCTTCTATATTT 430
Db 19 GGTTCCTTCTATATTT 3

RESULT 421
ADN75774/C
ID ADN75774 standard; RNA; 19 BP.
XX
AC ADN75774;
XX
DT 01-JUL-2004 (first entry)
XX
DE TCPTP associated siRNA hTCPTP1.5 #1.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
XX
PT 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Claim 6; SEQ ID NO 599; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosolic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 19 BP; 5 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 343 GGCTGTGATCAATGGG 359
Db 18 GACTGTGATCATATGGG 2

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RESULT 422
ADQ27278
ID ADQ27278 standard; DNA; 19 BP.
XX
XX
AC ADQ27278;
XX
XX
DT 26-AUG-2004 (first entry)
XX
XX
DE RNA interference target sequence #186.
XX
XX
KW ss; detection; RNA interference; siRNA; gene silencing; gene expression;
KW cytotoxicity.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004048566-A1.
XX
XX
PD 10-JUN-2004.
XX
XX
PF 21-NOV-2003; 2003WO-JP014893.
XX
XX
PR 22-NOV-2002; 2002JP-00340053.
XX
XX
PA (NATO/) NATORI Y.
PA (SAIG/) SAIGO K.
PA (TEIK/) TEI K.
PA (NAIT/) NAITO Y.
XX
XX
PI Saigo K, Tei K, Naito Y;
XX
XX
WPI; 2004-487423/46.
XX
XX
DR Detecting sequence of RNA interference useful for synthesizing siRNA, by
PT detecting regions in sequence fulfilling specific criteria such as base
PT at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
PT guanine or cytosine.
XX
XX
PS Disclosure; SEQ ID NO 200; 325pp; Japanese.
XX
XX
CC The invention relates to a method of detecting the base sequence for RNA
CC interference by detecting the regions in the DNA sequence fulfilling the
CC following requirements such as: (i) the base at 3' terminal is adenine,
CC thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine;
CC (iii) the seven base sequence at 3' terminal is rich in adenine, thymine
CC and uracil, and; (iv) there are bases in a such a number that it causes
CC RNA interference without showing cytotoxicity. The method is used for
CC designing and synthesizing siRNA causing RNA interference. This sequence
CC corresponds to an RNA interference target sequence of the invention.
XX
XX
SQ Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 744 GGCAGCTGCCACCTTAT 760
Db 3 GACAGCTGCCACCTTAT 19

RESULT 423
ADP48850
ID ADP48850 standard; DNA; 19 BP.
XX
XX
AC ADP48850;
XX
XX
DT 09-SEP-2004 (first entry)
XX
XX
DE Mouse Myo1c targeted short inhibitory RNA (siRNA) target DNA SeqID90.
XX
XX
KW short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating;
KW permeabilised cell membrane; antidiabetic; anorectic; gene therapy;
KW type II diabetes; insulin resistance; obesity; Myo1c; ds; mouse; murine.
XX
XX

Mus musculus.
WO2004053103-A2.
24-JUN-2004.
11-DEC-2003; 2003WO-US039774.
11-DEC-2002; 2002US-0432427P.
(UYMA-) UNIV MASSACHUSETTS.
Czech MP, Zhou Q, Jiang Z;
WPI; 2004-468860/44.
Introducing a nucleic acid into an adipocyte, useful for treating type II
diabetes, obesity or insulin resistance, comprises contacting an
adipocyte having a cell membrane with a nucleic acid molecule, thus
forming a mixture.
Disclosure; SEQ ID NO 90; 91pp; English.
This invention relates to a novel method of introducing a nucleic acid
into an adipocyte which comprises contacting an adipocyte having a cell
membrane with a nucleic acid molecule, thus forming a mixture and
electroporating the mixture under conditions such that the cell membrane
becomes permeabilised, such that the nucleic acid is introduced into the
adipocyte. The invention may be useful for the production of compounds
with an antidiabetic or anorectic activity whilst the disclosed sequences
may be useful for gene therapy. The methods are useful for treating type
II diabetes, insulin resistance or obesity. The present sequence is that
of a region of a gene which may be targeted by short inhibitory RNA
(siRNA) used with the method of the invention.
Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1097 TACCTGCTCATTGTTT 1113
Db 2 TACCACCTCATTGTTT 18

RESULT 424
ADP48849
ID ADP48849 standard; DNA; 19 BP.
XX
XX
AC ADP48849;
XX
XX
DT 09-SEP-2004 (first entry)
XX
XX
DE Mouse Myo1c targeted short inhibitory RNA (siRNA) target DNA SeqID89.
XX
XX
KW short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating;
KW permeabilised cell membrane; antidiabetic; anorectic; gene therapy;
KW type II diabetes; insulin resistance; obesity; Myo1c; ds; mouse; murine.
XX
XX
OS Mus musculus.
XX
XX
PN WO2004053103-A2.
XX
XX
PD 24-JUN-2004.
XX
XX
PF 11-DEC-2003; 2003WO-US039774.
XX
XX
PR 11-DEC-2002; 2002US-0432427P.
XX
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
XX

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PI Czech MP, Zhou Q, Jiang Z;
XX WPI; 2004-468860/44.
XX
XX Introducing a nucleic acid into an adipocyte, useful for treating type II
XX diabetes, obesity or insulin resistance, comprises contacting an
XX adipocyte having a cell membrane with a nucleic acid molecule, thus
XX forming a mixture.
XX
XX Disclosure; SEQ ID NO 89; 91pp; English.
XX
XX This invention relates to a novel method of introducing a nucleic acid
XX into an adipocyte which comprises contacting an adipocyte having a cell
XX membrane with a nucleic acid molecule, thus forming a mixture and
XX electroporating the mixture under conditions such that the cell membrane
XX becomes permeabilised, such that the nucleic acid is introduced into the
XX adipocyte. The invention may be useful for the production of compounds
XX with an anti-diabetic or anorectic activity whilst the disclosed sequences
XX may be useful for gene therapy. The methods are useful for treating type
XX II diabetes, insulin resistance or obesity. The present sequence is that
XX of a region of a gene which may be targeted by short inhibitory RNA
XX (siRNA) used with the method of the invention.
XX
XX Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.8; DB 1; Length 19;
XX Best Local Similarity 88.2%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1097 TACTGCTCATTGTTT 1113
Db ||||| ||||| |||||
3 TACCACCTCATTGTTT 19

RESULT 425
ABK15072/C
ID ABK15072 standard; DNA; 15 BP.
XX
XX AC ABK15072;
XX
XX DT 08-MAY-2002 (first entry)
XX
XX DE Human beta actin PCR primer #2.
XX
XX KW Human; PCR; primer; beta actin; molecular beacon;
XX target cell identification; prenatal diagnosis; cystic fibrosis;
XX chromosomal aberration; trisomy 21; Down's syndrome; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1172445-A1.
XX
XX PD 16-JAN-2002.
XX
XX PF 14-JUL-2000; 2000EP-00115268.
XX
XX PR 14-JUL-2000; 2000EP-00115268.
XX
XX PA (PRAE-) PRAENADIA GMBH.
XX
XX PI Wiebusch H, Schmitt-John T, Weidner J;
XX
XX DR WPI; 2002-156652/21.
XX
XX PT Identifying target cell for prenatal diagnosis, by in situ hybridizing
XX target sequence in target cell with complementary labeled sequence and
XX identifying target cell by detecting hybridized sequence by flow
XX cytometry.
XX
XX PS Example 2; Fig 3/4; 28pp; English.
XX
XX This invention relates to a method for identifying a target cell or for
XX allowing direct genetic analysis of target cell, the method involves in

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```

CC situ hybridisation of a target sequence in a target cell with a
CC complementary labeled sequence, and identifying the target cell by
CC detecting the presence of a hybridised sequence by flow cytometry. The
CC method of the invention is useful for distinction of foetal and maternal
CC cells and can be used in prenatal diagnosis for the detection of cystic
CC fibrosis or chromosomal aberrations such as trisomy 21 (Down's syndrome).
CC The method is also useful for the diagnosis of diseases which are due to
CC or characterised by the transcription of genes which are not expressed in
CC the wild type cell, or diseases characterised by the absence of altered
CC expression or expression rates of certain genes or gene fragments. This
CC method improves the identification of foetal cells within a maternal
CC blood sample, and therefore enables the distinction between maternal and
CC foetal cells. The method is less time consuming and required less
CC expertise than common practices and increases the overall sampling rate
CC of target cell within a blood sample. The method also allows simultaneous
CC detection of different cell types or lines in a fast multiplex assay
CC which can be combined with the detection of various genetic differences
CC within the cells at once. The method also allows detection of rare
CC sequences and does not rely on the availability of monoclonal antibodies.
CC The present sequence represents a human beta actin PCR primer used in
CC conjunction with the primer represented in ABK15071 as a control PCR and
CC to allow for normalisation of the number of target cells used in the
CC method of the invention
XX
XX Sequence 15 BP; 1 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 2.2e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 42 GAGCAGCGCGGCC 56
Db ||||| ||||| |||||
15 GAGCAGCGCGTGCC 1

RESULT 426
ADJ82300/C
ID ADJ82300 standard; DNA; 15 BP.
XX
XX AC ADJ82300;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE KLMSY-encoding nucleotide #28.
XX
XX KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX OS Synthetic.
XX
XX PN WO2003045973-A2.
XX
XX PD 05-JUN-2003.
XX
XX PF 30-SEP-2002; 2002WO-US031165.
XX
XX PR 28-NOV-2001; 2001US-0333476P.
XX
XX PA (BECT) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX PI Dean C, Heidaran M, Spargo CA;
XX
XX DR WPI; 2003-505179/47.
XX
XX PT New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX

```

PS Disclosure; SEQ ID NO 81; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGFR-R) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-

CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell

CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,

CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,

CC muscle or bone cell. The peptides are also useful for treating fibrotic

CC disorders, myeloproliferative diseases, and blood vessel proliferative

CC (angiogenic) disorders. This sequence represents a possible nucleotide

CC encoding the P3 peptide.

XX Sequence 15 BP; 5 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

SQ Query Match 1.2%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 615 GTAGGACATGAGTTT 629

DB 15 GTAGGACATGAGTTT 1

RESULT 427

ADJ82292/c

ID ADJ82292 standard; DNA; 15 BP.

XX AC ADJ82292;

XX DT 06-MAY-2004 (first entry)

XX DE KLMSY-encoding nucleotide #20.

XX ss; cytotatic; platelet-derived growth factor receptor; PDGF-R; cancer;

KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;

KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;

KW myeloproliferative disease; blood vessel proliferative disease;

KW angiogenesis.

XX OS Synthetic.

XX PN WO2003045973-A2.

XX PD 05-JUN-2003.

XX PF 30-SEP-2002; 2002WO-US031165.

XX PR 28-NOV-2001; 2001US-0333476P.

XX PA (BECT) BECTON DICKINSON & CO.

XX HAAL/) HAALAND P D.

XX Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor

PT or cancer cell proliferation, or for treating fibrotic disorders,

PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.

XX Disclosure; SEQ ID NO 73; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGFR-R) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

Sequence 15 BP; 5 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 615 GTACGAGATGAGTTT 629
Db 15 GTACGAGATGAGTTT 1

RESULT 429
ADG13597/C
ID ADG13597 standard; RNA; 15 BP.
AC ADG13597;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human HRI-4 hammerhead ribozyme target sequence #2.
DE
XX Human; ss; EGFR; epidermal growth factor receptor; HRI1; HRI2; HRI3;
XX HRI4; hammerhead ribozyme; inozyme; zinzyme; DNazyme; amberszyme; cancer;
XX brain tumour; cytosatic; short interfering RNA; siRNA; RNA interference;
XX prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
XX stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
XX head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
XX multidrug resistant cancer.
XX
XX Homo sapiens.
OS
XX US2003186909-A1.
FN
XX 02-OCT-2003.
PD
XX 21-OCT-2002; 2002US-00277494.
PF
XX 27-JAN-1997; 97US-0036749P.
PR
XX 04-DEC-1997; 97US-00985162.
PR
XX 22-SEP-1999; 99US-00401063.
PR
XX 03-MAY-2001; 2001US-00848754.
PR
XX 25-JUL-2001; 2001US-00916466.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Mcswiggen J;
PI
XX WPI; 2004-032029/03.
DR
XX
XX New double stranded short interfering ribonucleic acid molecule for
PT inhibiting expression of epidermal growth factor receptor gene.
PT
XX
XX Claim 7; SEQ ID NO 24; 113pp; English.
PS
XX
XX The invention relates to a double stranded short interfering RNA (siRNA)
CC molecule that inhibits expression of epidermal growth factor receptor
CC (EGFR) gene (e.g. HRI-4) by RNA interference is new. Also included is an
CC expression vector comprising a nucleic acid sequence encoding siRNA
CC molecule(s) in a manner that allows expression of the nucleic acid
CC molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC amberszymes zinzymes and DNazymes. The invention is used for inhibiting
CC expression of EGFR. It can be used for treatment of cancer, prostate
CC cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC life in vitro, stability, and ease of introduction of oligonucleotide to

target site. The present sequence is an EGFR/HER1-4 target sequence for an siRNA of the invention.

Sequence 15 BP; 1 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 380 GCAGGCAATGCAGTC 394
Db 15 GCAGGCAATGCAGTC 1

RESULT 430
AAH77878
ID AAH77878 standard; DNA; 16 BP.
XX
XX AAH77878;
AC
XX 13-NOV-2001 (first entry)
DT
XX
XX PCR primer used to amplify cDNA encoding a human hB7-H2 polypeptide.
DE
XX hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS;
XX congenital immune deficiency; cellular immune response; PCR primer;
XX inflammatory condition; autoimmune disease; rheumatoid arthritis;
XX multiple sclerosis; insulin-dependent diabetes mellitus; ss.
XX Homo sapiens.
OS
XX WO200164704-A1.
FN
XX 07-SEP-2001.
PD
XX
XX 02-MAR-2001; 2001WO-US006769.
PF
XX
XX 02-MAR-2000; 2000US-0186519P.
PR
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA
XX Chen L;
PI
XX WPI; 2001-514837/56.
DR
XX
XX An isolated DNA encoding a hB7-H2 polypeptide, useful for treating
PT cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, multiple
PT sclerosis or insulin-dependent diabetes mellitus).
XX
XX Example 1; Page 26; 50pp; English.
PS
XX
XX PCR primers AAH77878-79 were used to amplify cDNA encoding a human
CC polypeptide, designated hB7-H2. The hB7-H2 polypeptide co-stimulates T
CC cells. The hB7-H2 proteins and its variants are generally useful as
CC immune response-stimulating therapeutics. For example, the polypeptides
CC can be used for treatment of disease conditions characterized by
CC immunosuppression, e.g., cancer, AIDS or AIDS-related complex, other
CC virally or environmentally-induced conditions, and certain congenital
CC immune deficiencies. They may also be employed to increase immune
CC function that has been impaired by the use of radiotherapy or
CC immunosuppressive drugs such as certain chemotherapeutic agents, and
CC therefore are particularly useful when given in conjunction with such
CC drugs or radiotherapy. The hB7-H2 nucleic acid and polypeptide can be
CC used to treat conditions involving cellular immune responses, e.g.,
CC inflammatory conditions (such as, for example, those induced by
CC infectious agents including Mycobacterium tuberculosis or M. leprae), or
CC other pathologic cell-mediated responses such as those involved in
CC autoimmune diseases (e.g. rheumatoid arthritis), multiple sclerosis, or
XX insulin-dependent diabetes mellitus)
XX
XX Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.2%; Score 13.4; DB 1; Length 16;

```
Best Local Similarity 93.3%; Pred. No. 2.3e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 14; Conservative 0;

QY 49 CCGCGGCCCCAGTTC 63
Db 1 CCGCGGCCCCAGTTC 15

RESULT 431
ADO49843
ID ADO49843 standard; DNA; 16 BP.
XX
AC ADO49843;
XX
DT 29-JUL-2004 (first entry)
XX
DE H. pylori strain J99 genome fragment SEQ ID NO:466.
XX ds; stroke; phosphodiesterase 4D; PDE4D.
XX Helicobacter pylori.
XX US2004091865-A1.
XX 13-MAY-2004.
XX
XX 25-SEP-2002; 2002US-00255120.
XX
XX 19-MAR-2001; 2001US-00811352.
XX 04-FEB-2002; 2002US-00067514.
XX (DECO-) DECODE GENETICS EHF.
XX
XX Gretarsdottir S, Jonasdottir S, Reynisdottir ST, Thorleifsson G;
PI WPI; 2004-374932/35.
XX
XX Diagnosing susceptibility to a stroke in an individual comprising
PT screening for an at-risk haplotype in the phosphodiesterase 4D gene.
XX
XX Disclosure; SEQ ID NO 466; 574pp; English.
XX
XX The invention relates to a method of diagnosing susceptibility to a
CC stroke in an individual comprising screening for an at-risk haplotype in
CC the phosphodiesterase 4D (PDE4D) gene that is more frequently present in
CC an individual susceptible to stroke (affected) compared to a healthy
CC individual (control), where the at-risk haplotype increases risk of
CC stroke significantly. The composition, methods and kit are useful for
CC diagnosing, predicting of clinical course and treating stroke using
CC polymorphisms in the PDE4D gene. These may also be used in identifying
CC agents that enhance or inhibit PDE4D polypeptide expression or activity.
CC The present sequence represents a fragment of H. pylori strain J99 genome
CC which is not referred to at all in the main body of the specification.
XX
XX Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTAGCTGGGA 456
Db 1 TGGTTTTCAGCTGGGA 15

RESULT 432
ADO50267
ID ADO50267 standard; DNA; 16 BP.
XX
AC ADO50267;
XX
DT 29-JUL-2004 (first entry)
XX
DE H. pylori strain J99 genome fragment SEQ ID NO:466.
XX ds; stroke; phosphodiesterase 4D; PDE4D.
XX Helicobacter pylori.
XX US2004091865-A1.
XX 13-MAY-2004.
XX
XX 25-SEP-2002; 2002US-00255120.
XX
XX 19-MAR-2001; 2001US-00811352.
XX 04-FEB-2002; 2002US-00067514.
XX (DECO-) DECODE GENETICS EHF.
XX
XX Gretarsdottir S, Jonasdottir S, Reynisdottir ST, Thorleifsson G;
PI WPI; 2004-374932/35.
XX
XX Diagnosing susceptibility to a stroke in an individual comprising
PT screening for an at-risk haplotype in the phosphodiesterase 4D gene.
XX
XX Disclosure; SEQ ID NO 466; 574pp; English.
XX
XX The invention relates to a method of diagnosing susceptibility to a
CC stroke in an individual comprising screening for an at-risk haplotype in
CC the phosphodiesterase 4D (PDE4D) gene that is more frequently present in
CC an individual susceptible to stroke (affected) compared to a healthy
CC individual (control), where the at-risk haplotype increases risk of
CC stroke significantly. The composition, methods and kit are useful for
CC diagnosing, predicting of clinical course and treating stroke using
CC polymorphisms in the PDE4D gene. These may also be used in identifying
CC agents that enhance or inhibit PDE4D polypeptide expression or activity.
CC The present sequence represents a fragment of H. pylori strain J99 genome
CC which is not referred to at all in the main body of the specification.
XX
XX Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTAGCTGGGA 456
Db 1 TGGTTTTCAGCTGGGA 15

RESULT 433
ADO4357
ID AAF04357 standard; DNA; 17 BP.
XX
AC AAF04357;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1873.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX (RIBO-) RIBOZYME PHARM INC.
PA
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```
DE H. pylori strain J99 genome fragment SEQ ID NO:890.
XX ds; stroke; phosphodiesterase 4D; PDE4D.
XX Helicobacter pylori.
XX US2004091865-A1.
XX 13-MAY-2004.
XX
XX 25-SEP-2002; 2002US-00255120.
XX
XX 19-MAR-2001; 2001US-00811352.
XX 04-FEB-2002; 2002US-00067514.
XX (DECO-) DECODE GENETICS EHF.
XX
XX Gretarsdottir S, Jonasdottir S, Reynisdottir ST, Thorleifsson G;
PI WPI; 2004-374932/35.
XX
XX Diagnosing susceptibility to a stroke in an individual comprising
PT screening for an at-risk haplotype in the phosphodiesterase 4D gene.
XX
XX Disclosure; SEQ ID NO 890; 574pp; English.
XX
XX The invention relates to a method of diagnosing susceptibility to a
CC stroke in an individual comprising screening for an at-risk haplotype in
CC the phosphodiesterase 4D (PDE4D) gene that is more frequently present in
CC an individual susceptible to stroke (affected) compared to a healthy
CC individual (control), where the at-risk haplotype increases risk of
CC stroke significantly. The composition, methods and kit are useful for
CC diagnosing, predicting of clinical course and treating stroke using
CC polymorphisms in the PDE4D gene. These may also be used in identifying
CC agents that enhance or inhibit PDE4D polypeptide expression or activity.
CC The present sequence represents a fragment of H. pylori strain J99 genome
CC which is not referred to at all in the main body of the specification.
XX
XX Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTAGCTGGGA 456
Db 1 TGGTTTTCAGCTGGGA 15

RESULT 433
AAF04357
ID AAF04357 standard; DNA; 17 BP.
XX
AC AAF04357;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1873.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX (RIBO-) RIBOZYME PHARM INC.
PA
```

XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX Claim 4; Page 98; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 851 GATCCCTCTTTGTGT 865
 DB 2 GATACCTCTTTGTGT 16
 RESULT 434
 AAF04805
 ID AAF04805 standard; DNA; 17 BP.
 XX AAF04805;
 AC
 DT 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #2321.
 DE
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 OS
 XX WO200061729-A2.
 PN
 XX 19-OCT-2000.
 PD
 XX 11-APR-2000; 2000WO-US009721.
 PF
 XX 12-APR-1999; 99US-0129390P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 DR
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX Claim 4; Page 108; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC erythropoietin, granulocyte colony stimulating factor protein and

CC interferon alpha
 XX Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 851 GATCCCTCTTTGTGT 865
 DB 2 GATACCTCTTTGTGT 16
 RESULT 435
 AAF04219
 ID AAF04219 standard; DNA; 17 BP.
 XX AAF04219;
 AC
 DT 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #1735.
 DE
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 OS
 XX WO200061729-A2.
 PN
 XX 19-OCT-2000.
 PD
 XX 11-APR-2000; 2000WO-US009721.
 PF
 XX 12-APR-1999; 99US-0129390P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 DR
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX Claim 4; Page 95; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX Sequence 17 BP; 3 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 396 TTTTCCTTACAATTC 410
 DB 2 TTTTCCTTACAATTC 16
 RESULT 436
 AAF04667
 ID AAF04667 standard; DNA; 17 BP.
 XX AAF04667;
 AC

PA	(RIBO-) RIBOZYME PHARM INC.
XX	
XX	Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX	WPI; 2000-647423/62.
XX	
XX	Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT	useful for producing e.g. granulocyte colony stimulating factor protein,
PT	interferon alpha and erythropoietin.
XX	
XX	Claim 37; Page 72; 164pp; English.
XX	
CC	The present invention relates to enzymatic and antisense nucleic acid
CC	molecules that act as inhibitors of the expression of repressor genes
CC	encoding the T92 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC	factor gene, IRF-2 and/or the CAAT Displacement protein (CDP).
CC	Inhibition of the repressors removes prevents inhibition and
CC	consequently increases expression of) genes involved in the production of
CC	erythropoietin, granulocyte colony stimulating factor protein and
CC	interferon alpha
XX	
XX	Sequence 17 BP; 2 A; 2 C; 4 G; 9 T; 0 U; 0 Other;
XX	
XX	Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX	Best Local Similarity 93.3%; Pred. No. 2.3e+02;
XX	Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	
Oy	294 CTGGAATTGTTGTTT 308
Db	2 CTGTAATTGTTGTTT 16
XX	
RESULT 438	
ABK00818	
ID	ABK00818 standard; RNA; 17 BP.
XX	
AC	ABK00818;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Human NOGO Inozyme #88.
XX	
KW	Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW	muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW	DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW	MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW	inflammatory arthropathy; central nervous system injury;
KW	cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW	Parkinson's disease; ataxia; Huntington's disease;
KW	Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200159103-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-US004273.
XX	
PR	11-FEB-2000; 2000US-0181797P.
PR	28-FEB-2000; 2000US-0185516P.
PR	06-MAR-2000; 2000US-0187128P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(BLAT/) BLATT L.
PA	(MCSW/) MCSWIGGEN J.
PA	(CHOW/) CHOWRIRA B M.
XX	

PI Blatt L, Mcswiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 88; Page 79; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 XX Sequence 17 BP; 1 A; 9 C; 5 G; 0 T; 2 U; 0 Other;
 Qy Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2.3e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 49 CCGCGGCCCCAGTTC 63
 2 CCGCGGCCCCAGUGC 16
 RESULT 439
 ABK02566/c
 ID ABK02566 standard; RNA; 17 BP.
 XX
 XX AC ABK02566;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX
 XX DE Human NOGO Amberzyme #328.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob
 KW disease; muscular dystrophy; and/or other neurodegenerative disease.
 KW
 KW Homo sapiens.
 OS Synthetic.
 OS
 XX WO200159103-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR
 XX 28-FEB-2000; 2000US-0185516P.
 PR
 XX 06-MAR-2000; 2000US-0187128P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLATY) BLATT L.
 PA (MCSW) MCSWIGGEN J.
 PA (CHOW) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 CC constructs, which down regulate expression of a CD20 gene or neurite
 CC growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 CC central nervous system injury.
 PT
 XX Claim 88; Page 136; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 XX Sequence 17 BP; 11 A; 1 C; 3 G; 0 T; 2 U; 0 Other;
 Qy Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 415 GTTTTCTCTATATT 429
 |||||

Db 16 GTTTTCCTATT 2

RESULT 440

ABK00819

ID ABK00819 standard; RNA; 17 BP.

XX

AC ABK00819;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human NOGO Inozyme #89.

XX

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IWC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX WO200159103-A2.

XX

XX 16-AUG-2001.

XX

XX 09-FEB-2001; 2001WO-US004273.

XX

XX 11-FEB-2000; 2000US-0181797P.

PR

PR 28-FEB-2000; 2000US-0185516P.

PR

PR 06-MAR-2000; 2000US-0187128P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

XX Blatt L, Mcswiggen J, Chowrira BM;

PI

XX

XX WPI; 2001-607195/69.

DR

XX

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

PT

PT

XX

XX Claim 88; Page 79; 200pp; English.

PS

XX

XX The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a VGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a call to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IWC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC

CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an inozyme of the invention

CC

XX Sequence 17 BP; 1 A; 10 C; 5 G; 0 T; 1 U; 0 Other;

XX

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 2.3e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 49 CCGCGGCCCGCCAGTTC 63

DB 1 CCGCGGCCCGCCAGUC 15

RESULT 441

ABN06296

ID ABN06296 standard; DNA; 17 BP.

XX

XX AC ABN06296;

XX

XX 29-MAY-2002 (first entry)

DT

XX

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6288.

DE

XX

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

KW

XX

XX Homo sapiens.

OS

XX WO200192524-A2.

PN

XX 06-DEC-2001.

PD

XX

XX 25-MAY-2001; 2001WO-US016981.

PF

XX

XX 26-MAY-2000; 2000US-0207456P.

PR

PR 21-SEP-2000; 2000US-0234687P.

PR

PR 27-SEP-2000; 2000US-0236359P.

PR

PR 04-OCT-2000; 2000GB-00024263.

PR

PR 30-JAN-2001; 2001WO-US000661.

PR

PR 30-JAN-2001; 2001WO-US000662.

PR

PR 30-JAN-2001; 2001WO-US000663.

PR

PR 30-JAN-2001; 2001WO-US000664.

PR

PR 30-JAN-2001; 2001WO-US000665.

PR

PR 30-JAN-2001; 2001WO-US000666.

PR

PR 30-JAN-2001; 2001WO-US000667.

PR

PR 30-JAN-2001; 2001WO-US000668.

PR

PR 30-JAN-2001; 2001WO-US000669.

PR

PR 05-FEB-2001; 2001US-0266860P.

XX

XX (AEON-) AEOMICA INC.

XX

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

PI

XX WPI; 2002-179446/23.

DR

XX

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMPLP-1.

PT

XX

PS Disclosure; SEQ ID NO 6288; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX
 SQ Sequence 17 BP; 1 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGGCCCTGGCAGG 35
 ||||| |||||
 Db 2 CCGGGCTGTGGCAGG 16

RESULT 442
 ABN06295
 ID ABN06295 standard; DNA; 17 BP.
 AC ABN06295;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6287.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0268660P.

XX (ABOM-) ABOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or a specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 6287; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX
 SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGGCCCTGGCAGG 35
 ||||| |||||
 Db 3 CCGGGCTGTGGCAGG 17

RESULT 443
 ABN06297
 ID ABN06297 standard; DNA; 17 BP.
 AC ABN06297;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6289.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0268660P.

PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
PA
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 6289; 214pp; English.
PS
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 1 A; 6 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 CCGGGCGTGGCAGG 35
Db 1 CCGGGCGTGGCAGG 15
RESULT 444
ABN02575/c
ID ABN02575 standard; DNA; 17 BP.
XX
XX AC ABN02575;
XX
XX 29-MAY-2002 (first entry)
DT
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2567.
DE
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.

XX WO200192524-A2.
PN
XX 06-DEC-2001.
PD
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 2567; 214pp; English.
PS
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCGCT 1
RESULT 445
ABV82999
ID ABV82999 standard; DNA; 17 BP.
XX


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AC ABV82999;
XX
XX 03-JAN-2003 (first entry)
XX
XX Human HTPL scanning oligonucleotide SEQ ID 4245.
XX
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EPI229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 23-MAY-2001; 2001US-00864761.
XX 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX Example 2; Page 620; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention
XX
XX Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 675 ATTATGTTACTTGT 689
XX |||||
XX Db 1 ATTATGTTCTTGT 15
XX
XX RESULT 446
XX ABV82998

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ID ABV82998 standard; DNA; 17 BP.
XX
XX AC ABV82998;
XX
XX DT 03-JAN-2003 (first entry)
XX
XX DE Human HTPL scanning oligonucleotide SEQ ID 4244.
XX
XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN EPI229046-A2.
XX
XX PD 07-AUG-2002.
XX
XX PF 28-JAN-2002; 2002EP-00001167.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 23-MAY-2001; 2001US-00864761.
XX 09-OCT-2001; 2001US-0327898P.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Zhan J;
XX
XX DR WPI; 2002-676582/73.
XX
XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX PS Example 2; Page 620; 718pp; English.
XX
XX PS The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention
XX
XX SQ Sequence 17 BP; 3 A; 1 C; 3 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 675 ATTATGTTACTTGT 689
XX |||||
XX Db 2 ATTATGTTCTTGT 16
XX
XX RESULT 446
XX ABV82998

```

	Matches	12;	Conservative	2;	Mismatches	1;	Indels	0;	Gaps	0;	
QY	958	CTGGACCCAGGACAT	972								
ID	ABK18400	:- :::									
DB	3	CUGGACUCAGGCAU	17								
XX	ABK18400;										
DT	09-APR-2002	(first entry)									
DE	Human ERG hammerhead ribozyme target sequence,	Seq ID NO 1047.									
KW	Human; hammerhead ribozyme; cytostatic; antitumour; anti-diabetic; ophthalmologic; anti-arthritis; antipsoriasis; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angioblastoma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inosylme; amberzeme. Homo sapiens. WO200188124-A2. 22-NOV-2001. 16-MAY-2001; 2001WO-US015866. 16-MAY-2000; 2000US-00572021. (RIBO-) RIBOZYME PHARM INC. (GLAX) GLAXO GROUP LTD. Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM; WPI; 2002-082995/11. Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Claim 4; Page 77; 149pp; English. The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, arthropitis, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg ⁺⁺ . (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention										
OS	Homo sapiens.										
PN	WO200188124-A2.										
PD	22-NOV-2001.										
PF	16-MAY-2001; 2001WO-US015866.										
PR	16-MAY-2000; 2000US-00572021.										
PA	(RIBO-) RIBOZYME PHARM INC.										
FA	(GLAX) GLAXO GROUP LTD.										
PI	Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;										
DR	WPI; 2002-082995/11.										
PT	Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.										
PS	Claim 4; Page 77; 149pp; English.										
CC	The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, arthropitis, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg ⁺⁺ . (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention										
Query Match	Score 13.4;	DB 1;	Length 17;								
Best Local Similarity	80.0%;	Fred. No. 2.3e+02;									
Matches	14;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;		

Qy 513 ATCTGTATACATGTG 527

```

XX 20-NOV-2003 (first entry)
XX Human MD23 scanning oligonucleotide SEQ ID 767.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 767; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 892 CCCACAGACCAAGAG 906
XX ||||| ||||| |||||
XX Db 2 CCCACAGACCAAGAG 16
XX
XX RESULT 452
XX ADA99779
XX ID ADA99779 standard; DNA; 17 BP.
XX
XX AC ADA99779;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD23 scanning oligonucleotide SEQ ID 768.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX

```

```

KW developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 768; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 892 CCCACAGACCAAGAG 906
XX ||||| ||||| |||||
XX Db 1 CCCACAGACCAAGAG 15
XX
XX RESULT 453
XX ACD52118
XX ID ACD52118 standard; RNA; 17 BP.
XX
XX AC ACD52118;
XX
XX 24-SEP-2003 (first entry)
XX
XX HBV inozyme substrate sequence #248.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis B virus.
XX

```

```

PN WO200281494-A1.
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 154; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC disclosed in the present invention
XX
XX Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 40.0%; Pred. No. 2.3e+02;
XX Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 570 TTAATACCTTTAT 584
XX 1 UUAAGGCCUUUAU 15
XX
XX RESULT 454
XX ACDS3199
XX ID ACDS3199 standard; RNA; 17 BP.
XX
XX AC ACDS3199;
XX
XX DT 24-SEP-2003 (first entry)
XX
XX DE HBV G-cleaver substrate sequence #36.
XX

```

```

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis B virus.
OS
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 165; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC disclosed in the present invention
XX
XX Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 40.0%; Pred. No. 2.3e+02;
XX Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 569 TTTAATACCTTTATA 583
XX 3 UUAAGGCCUUUAU 17
XX
XX

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RESULT 455
ACC68460/c
ID ACC68460 standard; DNA; 17 BP.
XX
XX ACC68460;
AC
DT 01-JUL-2003 (first entry)
XX
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5707.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001PR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 698; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 606 ACTTCATAGTAGGA 620
Db 17 ACTTCATCAGTAGGA 3
|||||
|||||

RESULT 456
ACC64249
ID ACC64249 standard; DNA; 17 BP.
XX
XX ACC64249;
AC
DT 01-JUL-2003 (first entry)
XX
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1496.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW

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KW schizophrenia; ss.
XX
XX Mus musculus.
XX WO2003025176-A2.
PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001PR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 206; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 621 GATCAGTTTATTCT 635
Db 1 GATCAGTTTATTCT 15
|||||
|||||

RESULT 457
ADB42997/c
ID ADB42997 standard; DNA; 17 BP.
XX
XX ADB42997;
AC
XX 18-DEC-2003 (revised)
DT
XX 04-DEC-2003 (first entry)
DE
XX Tumour suppression/reversion associated nucleotide #3320.
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
PN
XX 15-MAY-2003.
PD
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX 17-SEP-2001; 2001PR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA

```

XX Telerman A, Amson R, Tuijndjer M;
 XX WPI; 2003-441574/41.
 XX
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 XX Disclosure; Page 420; 771pp; French.
 XX
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 XX Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. NO. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 588 ATGTTCACTTTAAGA 602
 DB 17 ATGTTCACTTTGAGA 3
 |||||
 RESULT 458
 ADC38464/c
 ID ADC38464 standard; DNA; 17 BP.
 XX
 AC ADC38464;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:813.
 XX
 KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 KW WPI; 2003-430501/40.
 XX
 DR New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 XX Example 2; SEQ ID NO 813; 172pp; English.
 XX
 XX The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 XX Sequence 17 BP; 8 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. NO. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 393 TCATTTTCCTTACAA 407
 DB 16 TCATTTTCCTTACAA 2
 |||||
 RESULT 459
 ADC38465/c
 ID ADC38465 standard; DNA; 17 BP.
 XX
 AC ADC38465;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:814.
 XX
 KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 KW WPI; 2003-430501/40.
 XX
 DR New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 XX Example 2; SEQ ID NO 814; 172pp; English.
 XX
 XX The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 XX Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
 SQ

PT New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 XX Example 2; SEQ ID NO 813; 172pp; English.
 XX
 XX The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 XX Sequence 17 BP; 8 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. NO. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 393 TCATTTTCCTTACAA 407
 DB 16 TCATTTTCCTTACAA 2
 |||||
 RESULT 459
 ADC38465/c
 ID ADC38465 standard; DNA; 17 BP.
 XX
 AC ADC38465;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:814.
 XX
 KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 KW WPI; 2003-430501/40.
 XX
 DR New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 XX Example 2; SEQ ID NO 814; 172pp; English.
 XX
 XX The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 XX Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
 SQ

```

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
DB 15 TCATTTTCCTTCA 1

RESULT 460
ADC38463/c
ID ADC38463 standard; DNA; 17 BP.
XX
AC ADC38463;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:812.
XX
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1b; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
WPI; 2003-430501/40.
XX
DR
XX
FT New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 812; 172pp; English.
XX
CC The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1b, which is used in an example from the
CC present invention.
XX
SQ Sequence 17 BP; 8 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
DB 17 TCATTTTCCTTCA 3

RESULT 461
ADB45002
ID ADB45002 standard; DNA; 17 BP.
XX
AC ADB45002;
XX
DT 18-DEC-2003 (first entry)
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; probe;

Tumour suppression/reversion associated nucleotide #5325.
DE
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
WPI; 2003-441574/41.
XX
DR
XX
FT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 654; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 851 GATCCCTCTTGTGTGT 865
DB 1 GATCCCTCTTGTGTGT 15

RESULT 462
ADI51662/c
ID ADI51662 standard; DNA; 17 BP.
XX
AC ADI51662;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID4165.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; probe;

```


KW primer; PCR; gene chip; antisense; viral disease; tumour;
 XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX OS Homo sapiens.
 XX PN WO2003025177-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004523.
 XX PR 17-SEP-2001; 2001FR-00011980.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; SEQ ID NO 4165; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 588 ATGTTCACTTTAAGA 602
 Db 17 ATGTTCACTTGAAGA 3
 RESULT 463
 ADI49509
 ID ADI49509 standard; DNA; 17 BP.
 AC ADI49509;
 XX 15-APR-2004 (first entry)
 DT Human tumour suppression/reversion-related DNA sequence SeqID2012.
 DE
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX OS Homo sapiens.
 XX PN WO2003025177-A2.
 XX PD 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.
 XX PR 17-SEP-2001; 2001FR-00011980.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; SEQ ID NO 2012; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 1 A; 2 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 556 ATATGCTGGGTTTTT 570
 Db 2 ATCTGCTGGGTTTTT 16
 RESULT 464
 ACC54318/C
 ID ACC54318 standard; DNA; 17 BP.
 XX ACC54318;
 AC 27-JUN-2003 (first entry)
 DT Human tumour suppressor sequence #3085.
 DE
 XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 XX tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 KW Homo sapiens.
 XX OS
 XX FR2826373-A1.
 XX 27-DEC-2002.
 PD 20-JUN-2001; 2001FR-00008139.
 PF 20-JUN-2001; 2001FR-00008139.
 XX 20-JUN-2001; 2001FR-00008139.
 PR (MOLE-) MOLECULAR ENGINES LAB SA.
 XX Tuijnder M, Telerman A, Amson R;
 XX PI

DR WPI; 2003-250498/25.
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 752; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 588 ATGTTCACTTTAAGA 602
Db 17 ATGTTCACTTTGAAGA 3
RESULT 465
ADL82512/C
ID ADL82512 standard; DNA; 17 BP.
XX
AC ADL82512;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ER+ breast cancer differentially expressed sequence #482.
XX
DE Human ER+ breast cancer differentially expressed sequence #482.
XX
KW gene therapy; ds; breast cancer; human; ER+ breast cancer.
XX
OS Homo sapiens.
XX
XX US2003166026-A1.
XX
XX 04-SEP-2003.
XX
XX 08-JAN-2003; 2003US-00339782.
XX
XX 09-JAN-2002; 2002US-0348053P.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Goodman LJ, Bowen BA;
PI
XX WPI; 2004-069003/07.
XX
XX Vector containing nucleic acid associated with breast cancer, useful for
PT treating, diagnosing and characterizing breast cancer, also related
PT polypeptides and antibodies.
XX
XX Claim 1; SEQ ID NO 483; 61pp; English.
XX
CC The invention relates to a composition which contains at least one vector
CC (B) containing a nucleic acid (I) associated with breast cancer. The
CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
CC -specific antibodies (Ab) are used to predict characteristics (e.g.
CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
CC used to modulate characteristics of such cells; to identify breast cancer
CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
CC or its products). The present sequence represents a human ER+ breast
CC cancer differentially expressed sequence.
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 588 ATGTTCACTTTAAGA 602
Db 17 ATGTTCACTTTGAAGA 3
RESULT 466
ADM59349
ID ADM59349 standard; RNA; 17 BP.
XX
AC ADM59349;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #1483.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
XX US2004054156-A1.
XX
XX 18-MAR-2004.
XX
XX 15-JAN-2003; 2003US-00342902.
XX
XX 14-MAY-1992; 92US-00882712.
XX
XX 07-FEB-1994; 94US-00193627.
XX
XX 08-NOV-1999; 99US-00436430.
XX
XX 20-MAR-2000; 2000US-00531025.
XX
XX 09-AUG-2000; 2000US-00636385.
XX
XX 24-OCT-2000; 2000US-00696347.
XX
XX 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP/) DRAPER K.
XX
XX (BLAT/) BLATT L.
XX
XX (MCSW/) MCSWIGGEN J A.
XX
XX (MORR/) MORRISSEY D.
XX
XX Draper K, Blatt L, Mcswiggen JA, Morrissey D;
PI
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 1483; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 1.28; Score 13.4; DB 1; Length 17;

CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 1 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
DB 1 CCGGGCTGTGGCAGG 15

RESULT 469
ACN69386
ID ACN69386 standard; DNA; 17 BP.
XX
AC ACN69386;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:6288.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 6288; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 1 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
DB 2 CCGGGCTGTGGCAGG 16

RESULT 470
ACN69385
ID ACN69385 standard; DNA; 17 BP.
XX
AC ACN69385;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:6287.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX

DR WPI; 2004-533378/51.
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 6287; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 21 CCGGGCCGTGGCAGG 35
 DB 3 CCGGGCTGTGGCAGG 17
 RESULT 471
 ACN65665/c
 ID ACN65665 standard; DNA; 17 BP.
 XX
 AC ACN65665;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPLP-1 probe SEQ ID NO:2567.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 XX (GUYI/) GU Y.
 PA (JIYI/) JI Y.

(PENW/) PENN S G.
 (HANK/) HANZEL D K.
 (RANK/) RANK D.
 (CHEN/) CHEN W.
 (SHAN/) SHANNON M E.
 XX
 Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 WPI; 2004-533378/51.
 XX
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 2567; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 743 AGGCAGCTGCCACCT 757
 DB 15 AGGCAGCTGCCGCT 1
 RESULT 472
 AAZ90709
 ID AAZ90709 standard; DNA; 18 BP.
 XX
 AC AAZ90709;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Forward primer for amplifying human KVLQT1 exon 1.
 XX
 KW KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
 KW antiarrhythmic; gene therapy; human; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200006600-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 06-OCT-1998; 98WO-US017838.
 XX
 PR 29-JUL-1998; 98US-0094477P.
 PR 17-AUG-1998; 98US-00135020.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Keating MT, Sanguinetti MC, Splawski I;
 PI WPI; 2000-195262/17.
 DR
 XX Mutant forms of genes encoding minK protein and KVLQT1 protein involved
 PT in cardiac potassium channel formation useful for screening drugs, for
 PT preventing and treating cardiac arrhythmia.

XX Example 11; Page 70; 167pp; English.

PS The invention relates to KVLQT1 and KCNE1 genes, associated with long QT

CC (LQT) syndrome. It provides a mink protein comprising a mutation which

CC substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and

CC Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening

CC KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and

CC treating LQT. The ability to predict LQT enables physicians to prevent

CC the diseases with medical therapy such as beta blocking agents and opts

CC for better treatments. Sequences AA290707-290740 represent PCR primers

CC for amplifying human KVLQT1 exons

XX

XX Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGGCGCCCGAGTT 62

DB 2 GCCGGCGCCCGAGTT 16

RESULT 473

AAZ71388

ID AAZ71388 standard; DNA; 18 BP.

XX

AC AAZ71388;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human biallelic marker upstream amplification primer SEQ ID NO:5744.

XX

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO9954500-A2.

XX

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX

PS Claim 8; Page 1455; 2745pp; English.

XX

CC AA265654 to AA269578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AA269579 to AA277440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX

SQ Sequence 18 BP; 7 A; 0 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 TAAGTAGGAGATGAG 626

DB 3 TAAGTAGGAGATGAG 17

RESULT 474

AAZ71139/C

ID AAZ71139 standard; DNA; 18 BP.

XX

AC AAZ71139;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human biallelic marker upstream amplification primer SEQ ID NO:5495.

XX

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO9954500-A2.

XX

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX

PS Claim 8; Page 1402; 2745pp; English.

XX

CC AA265654 to AA269578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AA269579 to AA277440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX

SQ Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;

```

Best Local Similarity 93.3%; Pred. NO. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1060 CTTTCCAGTGGCTAA 1074
Db 18 CTTACCACTGGCTAA 4

RESULT 475
AAZ98939
ID AAZ98939 standard; DNA; 18 BP.
XX
AC AAZ98939;
XX
XX 06-JUN-2000 (first entry)
XX
XX Human long QT syndrome-associated KVLQT1 exon 1 forward primer #2.
XX
XX KVLQT1; mutation; human; cardiac I (ke) potassium channel; KCNE1; ss;
XX
XX cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
XX
XX chromosome 11p15.5; PCR primer.
XX
XX Homo sapiens.
XX
XX WO200006199-A1.
XX
XX 10-FEB-2000.
XX
XX 12-MAY-1999; 99WO-US010260.
XX
XX 29-JUL-1998; 98US-0094477P.
XX
XX 17-AUG-1998; 98US-00135010.
XX
XX (UTAH ) UNIV UTAH RES FOUND.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Keating MT, Sanguinetti MC, Curran ME, Landes GM, Connors TD;
XX
XX Burn TC, Splawski I;
XX
XX WPI; 2000-195199/17.
XX
XX New isolated mutant KVLQT1 nucleic acids, useful for developing products
XX
XX for the diagnosis, prevention and treatment of long QT syndrome.
XX
XX Claim 27; Page 73; 178pp; English.
XX
XX The invention relates to KVLQT1 nucleic acids which have a mutation
XX
XX compared to wild-type KVLQT1 (AAZ98901) The KVLQT1 gene encodes a protein
XX
XX of 676 amino acids which forms a cardiac I(ks) potassium channel with the
XX
XX KCNE1 protein (AAZ90563). The KVLQT1 gene contains 15 introns and encodes
XX
XX a protein containing 6 putative transmembrane segments and a pore forming
XX
XX region. The gene has been mapped to the chromosomal location 11p15.5. The
XX
XX sequences AAZ98937-298970 represent primers used to PCR amplify the
XX
XX KVLQT1 exon sequences. Mutations in the KVLQT1 or KCNE1 genes result in
XX
XX cardiac arrhythmias observed as a prolonged QT curve in
XX
XX electrocardiograms (long QT syndrome). The genes and proteins can be used
XX
XX for the diagnosis of subjects with long QT syndrome. They can also be
XX
XX used to screen for drugs which can be used for treating or preventing
XX
XX long QT syndrome. The KVLQT1 nucleic acids can be used for gene therapy,
XX
XX and KVLQT1 peptides can be used for peptide therapy
XX
XX Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. NO. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCGAGTT 62
Db 2 GCCGCGGCCCGAGTT 16

RESULT 476

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```

AAA66260/c
ID AAA66260 standard; DNA; 18 BP.
XX
AC AAA66260;
XX
XX 09-OCT-2000 (first entry)
XX
XX Dog genomic marker oligonucleotide sequence SEQ ID NO:122.
XX
XX Dog; genome; genomic marker; radiation hybrid map; identification;
XX
XX chromosome location; gene marker; polymorphic microsatellite marker;
XX
XX phenotype; behaviour; pedigree; ss.
XX
XX Canis familiaris.
XX
XX WO200029615-A2.
XX
XX 25-MAY-2000.
XX
XX 15-NOV-1999; 99WO-IB001907.
XX
XX 13-NOV-1998; 98US-0108193P.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Galibert F, Andre C;
XX
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX
XX for e.g. identifying genes implicated in phenotypic and behavioral traits
XX
XX or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 58; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
XX
XX familiaris) genome comprising the genome location of a marker selected
XX
XX from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX
XX identifying and localising dog genes, since it covers approximately 80 %
XX
XX of the dog genome and provides a dense map integrating different types
XX
XX (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX
XX (or complementary sequences) are especially useful to identify genes
XX
XX responsible for phenotypic and behavioural traits in dogs, to identify
XX
XX morbid genes, to analyse diseases and identify implicated genes in such
XX
XX diseases and their alleles, and to study dog pedigrees. They may also be
XX
XX useful for isolating corresponding human gene sequences e.g. genes
XX
XX involved in genetic diseases
XX
XX Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. NO. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 523 ATGTGCATCGCGC 537
Db 17 ATGTGCATCTGGCGC 3

RESULT 477
AAC89949
ID AAC89949 standard; DNA; 18 BP.
XX
XX AAC89949;
XX
XX 08-MAR-2001 (first entry)
XX
XX Human KVLQT1 exon 1 PCR primer #3.
XX
XX Human; KVLQT1; antiarrhythmic; cardiac; gene therapy; PCR primer;
XX
XX cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
XX
XX chromosome 11p15.5; long QT syndrome; ss.
XX

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OS Homo sapiens.
XX US6150104-A.
XX 21-NOV-2000.
XX
XX 17-AUG-1998; 98US-00135021.
XX
XX 13-JUN-1997; 97US-00874655.
XX 29-JUL-1998; 98US-0094477P.
XX (UTAH ) UNIV UTAH RES FOUND.
XX
XX Keating MT, Splawski I;
XX WPI; 2001-060013/07.
XX
XX DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
XX syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
XX or diagnosing or prognosing JLN.
XX
XX Example 5; Col 45-46; 58pp; English.
XX
XX KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
XX cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to chromosome
XX 11p15.5. The present invention relates to a mutant KVLQT1 coding sequence
XX (see AAC89314). The mutant KVLQT1 coding sequence is useful in the
XX diagnosis of long QT syndrome and in screening humans for the presence of
XX KVLQT1 gene variants which cause JLN syndrome. The present sequence is a
XX PCR primer used to amplify a KVLQT1 exon
XX
XX Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 18;
XX Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 48 GCGCGGCGCCCAAGT 62
DB 2 GCGCGGCGCCCAAGT 16
XX
RESULT 478
AAS05095/c
ID AAS05095 standard; DNA; 18 BP.
XX
XX AAS05095;
XX
XX 07-SEP-2001 (first entry)
XX
XX Neurofibromatosis (NF1) HA PCR primer #15.
XX
XX Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
XX Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA;
XX frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
XX sequencing primer.
XX
XX Homo sapiens.
XX
XX WO200129251-A2.
XX
XX 26-APR-2001.
XX
XX 18-OCT-2000; 2000WO-EP010255.
XX
XX 18-OCT-1999; 99EP-00870216.
XX 05-JUN-2000; 2000EP-00870122.
XX (UYGE-) UNIV GENT.
XX
XX Messiaen L, Callens T;
XX WPI; 2001-300341/31.
XX
XX Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
XX

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XX Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
XX cell lines formed with lymphocytes of patient with protein synthesis
XX inhibitor, and obtaining peptides by translating amplified RNA from cell
XX line.
XX
XX Claim 9; Page 70; 102pp; English.
XX
XX The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
XX PCR primers and sequencing primers for use in mutation analysis of NF1. A
XX method for mutation analysis of the NF1 gene involves isolating
XX peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-
XX Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated
XX PBL, or short-term culturing of PBL by phytohaemagglutinin (PHA)
XX stimulation, treating the cell line or short-term culture with protein
XX synthesis inhibitor and immediately extracting RNA from the cultures. The
XX RNA is then amplified and peptide fragments are obtained by in vitro
XX transcription/translation of amplified fragments. Mutation analysis of
XX NF1 is used for detection of frame shift, mis-sense and silent mutations
XX in various exons of the gene. This is useful in screening for NF1
XX drug or agent can be identified by a screening process in which the
XX modulation is monitored in vitro using cell systems in which the
XX defective NF1 gene is expressed. The sequences can be used to design
XX drugs which modulate NF1 activity, by using knowledge of the structure of
XX the NF1 protein and of specific defects of the various NF1 mutant
XX proteins. The method allows for reliable analysis of mutations that are
XX difficult to detect due to unstable or wrong-spliced transcripts
XX
XX Sequence 18 BP; 10 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 18;
XX Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 416 TTTTTCCTTATATT 430
DB 18 TTTTTCCTTATAGTT 4
XX
RESULT 479
AAS05039/c
ID AAS05039 standard; DNA; 18 BP.
XX
XX AAS05039;
XX
XX 07-SEP-2001 (first entry)
XX
XX Neurofibromatosis (NF1) genomic DNA sequencing primer #91.
XX
XX Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
XX Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA;
XX frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
XX sequencing primer.
XX
XX Homo sapiens.
XX
XX WO200129251-A2.
XX
XX 26-APR-2001.
XX
XX 18-OCT-2000; 2000WO-EP010255.
XX
XX 18-OCT-1999; 99EP-00870216.
XX 05-JUN-2000; 2000EP-00870122.
XX (UYGE-) UNIV GENT.
XX
XX Messiaen L, Callens T;
XX WPI; 2001-300341/31.
XX
XX Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
XX

```


PT cell lines formed with lymphocytes of patient with protein synthesis
PT inhibitor, and obtaining peptides by translating amplified RNA from cell
PT line.
XX Claim 9; Page 64; 102pp; English.
XX The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A
CC method for mutation analysis of the NF1 gene involves isolating
CC peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-
CC Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated
CC PBL, or short-term culturing of PBL by phytohemagglutinin (PHA)
CC stimulation, treating the cell line or short-term culture with protein
CC synthesis inhibitor and immediately extracting RNA from the cultures. The
CC RNA is then amplified and peptide fragments are obtained by in vitro
CC transcription/translation of amplified fragments. Mutation analysis of
CC NF1 is used for detection of frame shift, mis-sense and silent mutations
CC in various exons of the gene. This is useful in screening for NF1
CC mutations in young children who are often oligosymptomatic. Efficacy of a
CC drug or agent can be identified by a screening process in which the
CC modulation is monitored in vitro using cell systems in which the
CC defective NF1 gene is expressed. The sequences can be used to design
CC drugs which modulate NF1 activity. By using knowledge of the structure of
CC the NF1 protein and of specific defects of the various NF1 mutant
CC proteins. The method allows for reliable analysis of mutations that are
CC difficult to detect due to unstable or wrong-spliced transcripts
XX
SQ Sequence 18 BP; 10 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 416 TTTTCCCTATATT 430
Db 18 TTTTCCCTATATT 4
|||||
RESULT 480
ABV72174
ID ABV72174 standard; DNA; 18 BP.
XX
AC ABV72174;
XX
DT 05-DEC-2002 (first entry)
XX
DE PCR primer used to amplify Heartbreaker (Hbr) loci from maize.
XX
KW Heartbreaker; Hbr; DNA fingerprint; phenotype; polymorphism;
KW miniature inverted repeat transposable element; MITE; molecular marker;
KW PCR; primer; ss.
XX
OS Zea mays.
XX
XX US6420117-B1.
XX
XX 16-JUL-2002.
XX
XX 14-SEP-2000; 2000US-006622402.
XX
XX 14-SEP-1999; 99US-0153812P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX Weasler SR, Casa AM;
XX
XX WPI; 2002-654638/70.
XX
XX Producing a DNA fingerprint of an individual by amplifying fragments
PT containing a miniature inverted repeat transposable element is useful to
PT detect polymorphisms and correlate genotype with phenotype particularly
PT in maize.
XX

PS Example 1; Col 17; 37pp; English.
XX
CC PCR primers ABV72171-90 were used to amplify Heartbreaker (Hbr) loci from
CC maize genomic DNA. The Hbr family of miniature inverted repeat
CC transposable elements (MITEs) is useful to demonstrate the method of the
CC invention. The specification describes a method for producing a DNA
CC fingerprint of an individual. The method comprises generating restriction
CC fragments to which an adaptor is ligated, amplifying fragments containing
CC a MITE and resolving the amplified fragments. The presence of a certain
CC amplified fragment is correlated to a phenotype. The method is used to
CC characterize the DNA of an individual, to detect polymorphisms, to
CC correlate presence of an amplified fragment with phenotype and to
CC generate a set of molecular markers
XX
SQ Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 909 TCACATTTCCTAGA 923
Db 1 TCACGTTCTCTAGA 15
|||||
RESULT 481
ABV76827
ID ABV76827 standard; DNA; 18 BP.
XX
AC ABV76827;
XX
DT 12-FEB-2003 (first entry)
XX
DE PCR primer used to amplify a CD21L gene fragment.
XX
XX Arthritic condition; CD21L; lymphotoxin-beta polypeptide;
KW chemoattractant; arthritis; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200280010-A1.
XX
XX 10-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-US008856.
XX
XX 23-MAR-2001; 2001US-00816814.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Goronzy JJ, Weyand CM;
XX
XX WPI; 2003-058450/05.
XX
XX Determining the severity of arthritic conditions, e.g. rheumatoid
PT arthritis, in a mammal or human by detecting whether a sample contains
PT elevated levels of marker(s), e.g. CD21L polypeptides or lymphotoxin-beta
PT polypeptides.
XX
XX Example 2; Page 13; 27pp; English.
XX
CC The specification describes a method for determining the severity of an
CC arthritic condition in a mammal. The method comprises determining whether
CC or not a sample from the mammal contains at least 1 marker (e.g. an
CC elevated level of a CD21L polypeptide, an elevated level of a lymphotoxin
CC -beta polypeptide, or an elevated level of a chemoattractant
CC polypeptide). The presence of the marker indicates that the arthritis
CC condition is severe. The method is useful for diagnosing the severity of
CC an arthritic condition (e.g. rheumatoid arthritis) in a mammal,
CC particularly a human. PCR primers ABV76826-27 were used to amplify a
CC CD21L gene fragment from a synovial tissue sample. The primers were used
CC in the method of the invention
XX

```
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 277 GGCATATTTCTTCAC 291
||||| |||||||
Db 1 GGCATGTTCTTCAC 15

RESULT 482
ADK13869/c
ID ADK13869 standard; DNA; 18 BP.
XX AC
XX ADK13869;
XX DT
XX 06-MAY-2004 (first entry)
XX PCR primer used to amplify human PSK cDNA - SEQ ID 16.
XX inhibitor; cancer; cytostatic; antiinflammatory; solid lung tumour;
KW colon; breast; prostate; ovary; pancreas; leukaemia; lymphoma;
KW inflammatory disorder; gene therapy; antisense; RNA interference; PCR;
KW primer; ss; human; PSK; prostate-derived STE20-like kinase.
XX OS
XX Homo sapiens.
XX PA
XX WO2004012817-A2.
XX PN
XX 12-FEB-2004.
XX PD
XX 31-JUL-2003; 2003WO-EP008470.
XX PF
XX 31-JUL-2002; 2002EP-00078143.
XX PR
XX 19-AUG-2002; 2002US-00224524.
XX PS
XX (KYL1-) KYLIX BV.
XX PI
XX Van Lohuizen MMS, Berns AJM, Martins CP, Mikkers HMM, Lenz JR;
XX Lund AH, De Koning JP;
XX WPI; 2004-157022/15.
XX DR
XX Inhibitor compounds of expressed proteins of murine genes and/or their
PT human orthologs, useful for treating inflammatory diseases and cancer
PT disorders such as solid tumors, leukemias and lymphomas.
XX PT
XX Example 4; SEQ ID NO 16; 280pp; English.
XX PS
XX The invention relates to a novel inhibitor compound directed against the
CC expressed proteins or the transcription product (mRNA) of a murine gene
CC and/or its human orthologue and useful in the treatment of cancer. The
CC compound of the invention demonstrates cytostatic and antiinflammatory
CC activities and may be useful for the preparation of a therapeutic
CC composition for the treatment of cancer, in particular for the treatment
CC of solid tumours of the lung, colon, breast, prostate, ovary and
CC pancreas, as well as leukaemia and lymphoma. Furthermore, the methods of
CC the invention may be utilised to treat inflammatory disorders, as well as
CC during gene therapy, antisense therapy and RNA interference procedures.
CC The current sequence is that of the PCR primer of the invention which was
CC used to amplify human PSK (prostate-derived STE20-like kinase) cDNA.
XX CC
XX Sequence 18 BP; 1 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 896 CAGACCAAGAGCCTC 910
||||| |||||||
Db 15 CAGCCCAAGAGCCTC 1
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RESULT 483
ADN35810/c
ID ADN35810 standard; DNA; 18 BP.
XX AC
XX ADN35810;
XX DT
XX 01-JUL-2004 (first entry)
XX Human NSCLC gene antisense-S oligonucleotide #35.
XX ss; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC;
KW diagnosis; cancer; URLC1; antisense.
XX OS
XX Homo sapiens.
XX PN
XX WO2004031413-A2.
XX PD
XX 15-APR-2004.
XX PF
XX 22-SEP-2003; 2003WO-JP012072.
XX PR
XX 30-SEP-2002; 2002US-0414673P.
XX PR
XX 28-FEB-2003; 2003US-0451374P.
XX PR
XX 28-APR-2003; 2003US-0466100P.
XX PS
XX (ONCO-) ONCOTHERAPY SCI INC.
XX PA
XX (UVTY) UNIV TOKYO.
XX PI
XX Nakamura Y, Daigo Y, Nakatsuru S;
XX WPI; 2004-330206/30.
XX DR
XX Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)
PT comprises determining an expression level of an NSCLC-associated gene in
PT a sample.
XX PT
XX Disclosure; SEQ ID NO 491; 394pp; English.
XX PS
XX The invention relates to a method of diagnosing non-small cell lung
CC cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
CC determining the expression level of a NSCLC-associated gene in a
CC biological sample derived from the subject, where an increase or decrease
CC of the level compared to a normal control level of the gene indicates
CC that the subject suffers from or is at risk of developing NSCLC. The
CC method is useful in diagnosing NSCLC or a predisposition to developing
CC NSCLC in a subject. The compound, polynucleotide and the encoded
CC polypeptide and composition are useful in treating or preventing NSCLC.
CC This sequence corresponds to an antisense oligonucleotide of genes that
CC are differentially expressed in NSCLC cells.
XX CC
XX Sequence 18 BP; 4 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCAT 210
||||| |||||||
Db 16 CGCCATCTCCCAT 2

RESULT 484
ADO56517/c
ID ADO56517 standard; DNA; 18 BP.
XX AC
XX ADO56517;
XX DT
XX 12-AUG-2004 (first entry)
XX Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #42.
XX DE
XX gene therapy; human; ss; melanoma;
XX KW
```

KW melanoma associated polymorphic variation; SNP;
 KW single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
 XX
 OS Homo sapiens.
 XX
 XX WO2004041164-A2.
 XX
 XX 27-MAY-2004.
 XX
 XX 06-NOV-2003; 2003WO-US035879.
 XX
 XX 06-NOV-2002; 2002US-0424475P.
 PR 23-JUL-2003; 2003US-0489703P.
 XX
 XX (SEQU-) SEQUENOM INC.
 XX
 XX Roth RB, Nelson MR, Braun A, Kammerer SM;
 XX
 XX WPI; 2004-411721/38.
 XX
 XX Identifying a subject at risk of melanoma, useful for treating melanoma,
 PT comprises detecting the presence or absence of one or more polymorphic
 PT variations associated with melanoma in a nucleic acid sample from a
 PT subject.
 XX
 XX Example 5; Page 84; 295pp; English.
 XX
 XX The invention relates to a method of identifying a subject at risk of
 CC melanoma comprising detecting the presence or absence of one or more
 CC polymorphic variations associated with melanoma in a nucleic acid sample
 CC from a subject. Preventing melanoma in a subject comprises detecting the
 CC presence or absence of one or more polymorphic variations associated with
 CC melanoma in a nucleic acid sample from a subject; and administering a
 CC melanoma preventative to a subject in need thereof based upon the
 CC presence or absence of the one or more polymorphic variations in the
 CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
 CC exposure to the subject. The methods, nucleic acids, proteins, and
 CC compositions are useful for treating melanoma. The present sequence
 CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
 XX
 XX Sequence 18 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 1 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 702 TAGTCACGGTCTCT 716
 Db ||||| |||||
 16 TAGTCACGGTCTCT 2
 RESULT 485
 ADR05071
 ID ADR05071 standard; DNA; 18 BP.
 XX
 XX ADR05071;
 XX
 XX 21-OCT-2004 (first entry)
 XX
 XX PCR primer 2 used to amplify human Bcl2 cDNA.
 DE
 XX apoptosis; cytostatic; antiinflammatory; antiasthmatic; respiratory;
 KW antirheumatic; antiarthritic; gynaecological; cardiant; vasotropic;
 KW antiproliferative; antiulcer; gastrointestinal; immunosuppressive;
 KW neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory;
 KW asthma; chronic obstructive pulmonary disease; cystic fibrosis;
 KW rheumatoid arthritis; acute respiratory distress syndrome; preclampsia;
 KW myocardial ischaemia; reperfusion injury; psoriasis; bronchiolitis;
 KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; ss;
 KW quantitative PCR; QPCR; primer; human; Bcl2.
 XX
 XX Homo sapiens.
 OS
 XX

PN WO2004065959-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-GB000271.
 XX
 XX 23-JAN-2003; 2003GB-00001566.
 PR 25-MAR-2003; 2003US-0457533P.
 XX
 XX (EIRX-) EIRX THERAPEUTICS LTD.
 PA
 XX Seery L, Hayes I, Murphy F;
 PI WPI; 2004-593556/57.
 XX
 XX Identifying a modulator of apoptosis-associated polypeptide function,
 PT useful for treating e.g., cancer, comprises incubating a sample
 PT containing an apoptosis-associated polypeptide and a candidate agent to
 PT permit binding.
 XX
 XX Example 3; Page 219; 230pp; English.
 PS
 XX The invention relates to a novel method for identifying an agent that
 CC modulates the function of an apoptosis-associated polypeptide,
 CC particularly a kinase or GPCR (G-protein-coupled receptor). The method
 CC comprises providing a sample containing an apoptosis-associated
 CC polypeptide and a candidate agent and incubating under conditions to
 CC permit binding of the candidate agent to the polypeptide, measuring the
 CC binding and comparing it with the binding of the polypeptide to a control
 CC agent known not to bind to the polypeptide. The method of the invention
 CC has cytostatic, antiinflammatory, antiasthmatic, respiratory,
 CC antirheumatic, antiarthritic, gynaecological, cardiant, vasotropic,
 CC antiproliferative, antiulcer, gastrointestinal, immunosuppressive and
 CC neuroprotective applications. The method and molecules may be useful for
 CC treating a disease or condition characterised by abnormal apoptosis in
 CC mammalian tissue, particularly cancer, such as small cell lung cancer,
 CC cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast,
 CC leukaemias, sarcomas and myelomas. Furthermore, autoimmune,
 CC neurodegenerative and inflammatory conditions may be treated, including
 CC asthma, chronic obstructive pulmonary disease, cystic fibrosis,
 CC rheumatoid arthritis, acute respiratory distress syndrome, preclampsia,
 CC myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis,
 CC Crohn's disease, ulcerative colitis and inflammatory bowel disease. The
 CC current sequence is that of a QPCR (quantitative PCR) primer of the
 CC invention which was used to analyse human apoptosis-associated sequence
 CC expression in the presence or absence of siRNAs (small interfering RNAs).
 XX
 XX Sequence 18 BP; 4 A; 10 C; 1 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 199 CATCTCCCGCATCCC 213
 Db ||||| |||||
 3 CATCTCCCGCATCCC 17
 RESULT 486
 ADS90284
 ID ADS90284 standard; DNA; 18 BP.
 XX
 XX ADS90284;
 XX
 XX 18-NOV-2004 (first entry)
 DT
 XX Oligonucleotide of the invention SEQ ID NO:1300.
 DE
 XX ss; cell proliferative disorder; breast; methylation; cytostatic;
 KW gene therapy; single nucleotide polymorphism; SNP.
 KW
 XX Unidentified.
 OS
 XX

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PN WO2004035803-A2.
XX
PD
XX
XX 29-APR-2004.
XX
XX 01-OCT-2003; 2003WO-EP010881.
XX
XX 01-OCT-2002; 2002DE-01045779.
XX
XX 07-JAN-2003; 2003DE-01000096.
XX
XX 17-APR-2003; 2003DE-01017955.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
XX Nimrich I, Rujan T, Schmitt A, Schmitt M, Look WP, Marx A;
XX WPI; 2004-348468/32.
XX
XX Predicting responsiveness of a subject with breast cell proliferative
XX disorder, useful for treating or differentiating breast cell
XX proliferative disorders comprises analyzing methylation pattern of a
XX genomic DNA from the subject.
XX
XX Disclosure; SEQ ID NO 1300; 104pp; English.
XX
XX The invention relates to a novel method for predicting the responsiveness
XX of a subject with a cell proliferative disorder of the breast tissues to
XX a therapy comprising analysing the methylation pattern of a target
XX nucleic acid by contacting at least one of the target nucleic acids in a
XX biological sample obtained from the subject prior to or during treatment.
XX The method of the invention has cytostatic activity, and may have a use
XX in gene therapy. The set of oligonucleotides comprising at least two of
XX the oligomers are useful for detecting the cytosine methylation state
XX and/or single nucleotide polymorphisms (SNPs) within the sequences. The
XX methods, nucleic acid, oligonucleotide, and kit are useful for the
XX treatment, characterisation, classification and/or differentiation, of
XX breast cell proliferative disorders. The method is also useful for
XX predicting the responsiveness of a subject with a cell proliferative
XX disorder of the breast tissues to a therapy. The present sequence is used
XX in the exemplification of the invention.
XX
XX SQ Sequence 18 BP; 5 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 18;
XX Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 616 TAGGAGATGAGTTT 630
XX |||||
XX 3 TAGGAGATGAGATT 17
XX
XX Db
XX
XX RESULT 487
XX AAV23538
XX ID AAV23538 standard; DNA; 19 BP.
XX
XX AC AAV23538;
XX
XX XX 04-AUG-1998 (first entry)
XX
XX DE Mouse beta defensin-1 gene specific forward primer 2.
XX
XX KW antimicrobial peptide; cystic fibrosis; RT-PCR; emphysema; PCR;
XX beta defensin-1; mbd-1; primer; amplification; ss.
XX
XX XX Synthetic.
XX OS Mus sp.
XX
XX XX WO9807833-A1.
XX
XX XX 26-FEB-1998.
XX
XX XX 20-AUG-1997; 97WO-US014639.
XX
XX XX
XX
XX 22-AUG-1996; 96US-0023424P.
XX 01-OCT-1996; 96US-0027334P.
XX 18-FEB-1997; 97US-0038685P.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
XX (MAGA-) MAGAININ PHARM INC.
XX
XX Wilson JM, Goldman M, Bals R, Stolzenberg ED, Anderson M;
XX Zasloff M;
XX WPI; 1998-179058/16.
XX
XX New isolated mammalian beta defensin-1 gene(s) - used to develop products
XX for treating microbial infections, e.g. respiratory conditions
XX susceptible to microbial infection such as cystic fibrosis.
XX
XX Disclosure; Page 43; 79pp; English.
XX
XX The mouse beta defensin-1 (mbd-1) gene specific forward primer 2 was used
XX with reverse primer 1 (AAV23539) or 2 (AAV23540) in a PCR reaction where
XX mbd-1 cDNA (AAV23528) served as a template. The PCR product was used as a
XX probe to isolate the mbd-1 genomic sequence from a mouse genomic library.
XX The mbd-1 cDNA encodes for the mouse beta defensin-1 (AAW53857) peptide.
XX The mbd-1 peptide was found to be highly salt sensitive and have
XX antimicrobial properties. Expression of mbd-1 and its biological activity
XX renders the mouse as at useful model to investigate the role of
XX antimicrobial peptides in pulmonary microbial infections and in
XX respiratory diseases
XX
XX SQ Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 19;
XX Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 954 CACTCTGGACCCAGG 968
XX |||||
XX 3 CACTCTGGACCCCTGG 17
XX
XX Db
XX
XX RESULT 488
XX AAZ01215/c
XX ID AAZ01215 standard; DNA; 19 BP.
XX
XX AC AAZ01215;
XX
XX DT 27-SEP-1999 (first entry)
XX
XX DE PCR primer for PGI biallelic marker 99-1481-285.
XX
XX KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
XX cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
XX PSA; human; ss.
XX
XX XX Synthetic.
XX OS Homo sapiens.
XX
XX XX WO9932644-A2.
XX
XX XX 01-JUL-1999.
XX
XX XX 22-DEC-1998; 98WO-IB002133.
XX
XX XX 22-DEC-1997; 97US-00996306.
XX
XX XX 09-SEP-1998; 98US-0099658P.
XX
XX XX (GEST ) GENSET.
XX
XX XX Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;
XX WPI; 1999-405178/34.
XX
XX Use of a prostate cancer associated gene and biallelic markers derived
XX

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Qy 351 TCAATGGGAGCCT 365

```

Db      15 TCATAAGGGGAGCCT 1
RESULT 491
AAZ76970
ID      AAZ76970 standard; DNA; 19 BP.
XX
XX      AAZ76970;
AC
XX
XX      10-SEP-2001 (first entry)
DT
XX      Human biallelic marker downstream amplification primer SEQ ID NO:11326.
DE
XX      Human genome; biallelic marker; high density disequilibrium map;
KW      genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW      haplotyping; hybridisation; identification; characterisation;
KW      amplification; single nucleotide polymorphism; SNP; PCR primer;
KW      diagnosis; ss.
XX
XX      Homo sapiens.
OS
XX      WO9954500-A2.
PN
XX
XX      28-OCT-1999.
PD
XX
XX      21-APR-1999; 99WO-1B000822.
PF
XX
XX      21-APR-1998; 98US-0082614P.
PR
XX      23-NOV-1998; 98US-0109732P.
XX
XX      (GEST ) GENSET.
PA
XX
XX      Cohen D, Blumenfeld M, Chumakov I;
PI
XX      WPI; 2000-013267/01.
XX
XX      Novel biallelic markers used to construct a high density disequilibrium
XX      map of the human genome.
PT
XX
XX      Claim 9; Page 2645; 2745pp; English.
PS
XX
XX      AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX      invention, which contain a polymorphic base at position 24 of their
XX      nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX      primers for the biallelic markers. The biallelic markers of the invention
XX      have a variety of uses: they can be used for high density mapping of the
XX      human genome, and in complex association studies and haplotyping studies
XX      which are useful in determining the genetic basis for disease states.
XX      Compositions and methods of the invention can also be useful for the
XX      identification of the targets for the development of pharmaceutical
XX      agents and diagnostic methods, as well as the characterisation of the
XX      differential efficacious responses to and side effects from
XX      pharmaceutical agents acting on a disease as well as other treatment.
XX      N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX      3367, are not actually given a sequence in the Sequence Listing from the
XX      present invention
XX
XX      Sequence 19 BP; 4 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
SQ
XX      Query Match 1.2%; Score 13.4; DB 1; Length 19;
XX      Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      394 CATTTCCTTACAAAT 408
Db      4 CATTTCCTTACAAAT 18
RESULT 492
ABA95463/C
ID      ABA95463 standard; DNA; 19 BP.
XX
XX      ABA95463;
AC
XX
XX      11-MAR-2002 (first entry)
DT
XX      Thermus thermophilus dnaQ gene PCR primer P133-A1237.
DE
XX      DNA polymerase III; holoenzyme; enzyme; thermophilic; replicase;
KW      PCR primer; ss.
KW
XX      Thermus thermophilus.
OS
XX      WO200173052-A2.
PN
XX      04-OCT-2001.
PD
XX
XX      28-MAR-2001; 2001WO-US009950.
PF
XX
XX      28-MAR-2000; 2000US-0192736P.
PR
XX      (MCHE/) MCHENRY C S.
XX
XX      Mchenry CS;
XX      PI
XX      WPI; 2001-611633/70.
XX
XX      Isolated DNA polymerase III holoenzyme subunits and accessory proteins
XX      useful for synthesizing DNA, e.g. in the polymerase chain reaction.
XX
XX      Example 14; Page 171; 249pp; English.
XX
XX      The present invention relates to DNA polymerase III holoenzyme subunits
XX      and accessory proteins and their coding sequences from Thermus
XX      thermophilus. The various subunits may be useful in PCR assays and for
XX      synthesising DNA, since the subunits provide a thermophilic replicase
XX      capable of rapid replication and highly processive properties at elevated
XX      temperatures compared to the prior art that is limited by relatively non-
XX      processive repair-like DNA polymerases. The present sequence is a PCR
XX      primer, which was used in an example from the present invention
XX
XX      Sequence 19 BP; 3 A; 10 C; 3 G; 3 T; 0 U; 0 Other;
SQ
XX      Query Match 1.2%; Score 13.4; DB 1; Length 19;
XX      Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      835 CAGGAAGCCCGGGGT 849
Db      15 CTGGAAGCCCGGGGT 1
RESULT 493
AAH61247
ID      AAH61247 standard; DNA; 19 BP.
XX
XX      AAH61247;
AC
XX
XX      10-SEP-2001 (first entry)
DT
XX
XX      Cdc25 hs ribozyme binding site SEQ ID NO:3671.
DE
XX
XX      Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW      recognition site; target; ribozyme binding site; eye disease; vulvovag;
KW      proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW      cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW      matrix metalloproteinase; growth factor; reductase; scarring; cytotatic;
KW      antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
KW      antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
KW      atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW      basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW      sickle cell retinopathy; ss.
XX
XX      Homo sapiens.
OS
XX      Synthetic.

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PN WO200130362-A2.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-US029500.
XX 26-OCT-1999; 99US-0161532P.
XX (IMMU-) IMMUSOL INC.
XX Robbins JM, Tritz R;
XX WPI; 2001-300427/31.
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX Example 1; Page 339; 408pp; English.
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 238 CTATGACTCAGATGC 252
Db ||||| ||||| ||||| ||||| |||||
2 CTATGACTCAGATGC 16

RESULT 494
ABL43540/C
ID ABL43540 standard; DNA; 19 BP.
XX ABL43540;
XX 11-APR-2002 (first entry)
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:584.
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX Homo sapiens.
XX JP2001321190-A.
XX 20-NOV-2001.
XX 12-MAR-2001; 2001JP-00068285.
XX 10-MAR-2000; 2000JP-00066716.

PN WO200130362-A2.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-US029500.
XX 26-OCT-1999; 99US-0161532P.
XX (IMMU-) IMMUSOL INC.
XX Robbins JM, Tritz R;
XX WPI; 2001-300427/31.
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX Example 1; Page 339; 408pp; English.
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 238 CTATGACTCAGATGC 252
Db ||||| ||||| ||||| ||||| |||||
2 CTATGACTCAGATGC 16

RESULT 494
ABL43540/C
ID ABL43540 standard; DNA; 19 BP.
XX ABL43540;
XX 11-APR-2002 (first entry)
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:584.
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX Homo sapiens.
XX JP2001321190-A.
XX 20-NOV-2001.
XX 12-MAR-2001; 2001JP-00068285.
XX 10-MAR-2000; 2000JP-00066716.

XX (RIKA ) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX WPI; 2002-144136/19.
XX Arraying genome clones.
XX Claim 4; Page 16; 528pp; Japanese.
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
XX Sequence 19 BP; 8 A; 5 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 406 AATTCAGGGGTTTTT 420
Db ||||| ||||| ||||| ||||| |||||
16 AATTCAGGGGTTATT 2

RESULT 495
ADF85077
ID ADF85077 standard; RNA; 19 BP.
XX ADF85077;
XX 26-FEB-2004 (first entry)
XX Human ERG2-targeted siRNA - SEQ ID 1371.
XX short interfering nucleic acid; siRNA; breakpoint cluster region;
KW v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL;
KW cytostatic; leukaemia; lymphoma; human; ss; siRNA; ERG2;
KW v-ets erythroblastosis virus E26 oncogene like (avian).
XX Homo sapiens.
XX WO2003070972-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005234.
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 15-AUG-2002; 2002US-0404039P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

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PR 14-JAN-2003; 2003US-0439922P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-679889/64.
XX
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
XX and diagnosis of leukemia and lymphoma, downregulates the breakpoint
XX cluster region-Abelson (BCR-ABL) gene.
XX
XX Example 7; SEQ ID NO 1371; 197pp; English.
XX
XX The invention relates to a novel double-stranded short interfering
XX nucleic acid (siRNA) that downregulates expression of the breakpoint
XX cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1
XX (BCR-ABL) gene. The siRNA of the invention demonstrates cytostatic
XX activity and may be useful for modulating expression of the BCR-ABL gene,
XX as well as for treating leukaemia or lymphoma and in diagnosis, drug
XX screening, target identification and validation, genetic engineering,
XX gene function studies and gene mapping. The current sequence is that of
XX the human ERG2 (v-ets erythroblastosis virus E26 oncogene like (avian))-
XX targeted siRNA of the invention.
XX
XX Sequence 19 BP; 7 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 19;
XX Best Local Similarity 80.0%; Pred. No. 2.4e+02;
XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
QY 958 CTGGACCCAGGACAT 972
DB 5 CUGGACUCAGGACAU 19
XX
XX RESULT 496
XX ADF85253/C
XX ID ADF85253 standard; RNA; 19 BP.
XX
XX ADF85253;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human ERG2-targeted siRNA - SEQ ID 1547.
XX
XX short interfering nucleic acid; siRNA; breakpoint cluster region;
XX v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL;
XX cytostatic; leukaemia; lymphoma; human; ss; siRNA; ERG2;
XX v-ets erythroblastosis virus E26 oncogene like (avian).
XX
XX Homo sapiens.
XX
XX WO2003070972-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005234.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-0386782P.
XX 15-AUG-2002; 2002US-0404039P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 14-JAN-2003; 2003US-0439922P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-679889/64.
XX
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
XX and diagnosis of leukemia and lymphoma, downregulates the breakpoint
XX cluster region-Abelson (BCR-ABL) gene.
XX
XX Example 7; SEQ ID NO 1371; 197pp; English.
XX
XX The invention relates to a novel double-stranded short interfering
XX nucleic acid (siRNA) that downregulates expression of the breakpoint
XX cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1
XX (BCR-ABL) gene. The siRNA of the invention demonstrates cytostatic
XX activity and may be useful for modulating expression of the BCR-ABL gene,
XX as well as for treating leukaemia or lymphoma and in diagnosis, drug
XX screening, target identification and validation, genetic engineering,
XX gene function studies and gene mapping. The current sequence is that of
XX the human ERG2 (v-ets erythroblastosis virus E26 oncogene like (avian))-
XX targeted siRNA of the invention.
XX
XX Sequence 19 BP; 7 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 19;
XX Best Local Similarity 80.0%; Pred. No. 2.4e+02;
XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
QY 958 CTGGACCCAGGACAT 972
DB 5 CUGGACUCAGGACAU 19
XX
XX RESULT 497
XX ADF75949/C
XX ID ADF75949 standard; RNA; 19 BP.
XX
XX ADF75949;
XX
XX 01-JUL-2004 (first entry)
XX
XX TCPTP2 siRNA #1.
XX
XX small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
XX cytostatic; immunomodulator; antimicrobial; antiinflammatory;
XX antidiabetic; anorectic; cancer; autoimmune disease; infection;
XX inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
XX Homo sapiens.
XX
XX WO2004016735-A2.
XX
XX 26-FEB-2004.
XX
XX 23-MAY-2003; 2003WO-US016632.
XX
XX 23-MAY-2002; 2002US-0383249P.
XX 14-APR-2003; 2003US-0462942P.
XX
XX (CEPT-) CEPTYR INC.
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
XX WPI; 2004-203773/19.
XX
XX New isolated small interfering RNA (siRNA) polynucleotide useful for
XX treating diseases with aberrant activity of the protein tyrosine
XX phosphatase, such as cancer, autoimmune disease, infection, inflammation,
XX diabetes and obesity.
XX
XX Disclosure; SEQ ID NO 774; 392pp; English.
XX
XX This invention describes novel small interfering RNA (siRNA)
XX polynucleotides capable of interfering with expression of a polypeptide

```


CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
 CC invention have cytosolic, immunomodulator, antimicrobial,
 CC antiinflammatory, antidiabetic and anorectic activity. The methods and
 CC compositions of the present invention are useful for treating diseases or
 CC conditions associated with aberrant expression or activity of the protein
 CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
 CC inflammation, diabetes and obesity. This sequence represents a siRNA
 CC directed against dual specificity phosphatase (DSP) expression.

XX Sequence 19 BP; 7 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 345 CTGTGATCAAAATGGG 359
 DB 18 CTGTGATCATATGGG 4

RESULT 498

ADN75950
 ID ADN75950 standard; RNA; 19 BP.

AC ADN75950;

DT 01-JUL-2004 (first entry)

DE TCPTP2 siRNA #2.

XX small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
 KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
 KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
 KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.

XX Homo sapiens.

XX WO2004016735-A2.

XX 26-FEB-2004.

XX 23-MAY-2003; 2003WO-US016632.

XX 23-MAY-2002; 2002US-0383249P.

XX 14-APR-2003; 2003US-0462942P.

XX (CEPT-) CEPTVR INC.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;

XX WPI; 2004-203773/19.

XX New isolated small interfering RNA (siRNA) polynucleotide useful for
 FT treating diseases with aberrant activity of the protein tyrosine
 FT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
 FT diabetes and obesity.

XX Disclosure; SEQ ID NO 775; 392pp; English.

XX This invention describes novel small interfering RNA (siRNA)
 CC polynucleotides capable of interfering with expression of a polypeptide
 CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
 CC invention have cytosolic, immunomodulator, antimicrobial,
 CC antiinflammatory, antidiabetic and anorectic activity. The methods and
 CC compositions of the present invention are useful for treating diseases or
 CC conditions associated with aberrant expression or activity of the protein
 CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
 CC inflammation, diabetes and obesity. This sequence represents a siRNA
 CC directed against dual specificity phosphatase (DSP) expression.

XX Sequence 19 BP; 4 A; 3 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 345 CTGTGATCAAAATGGG 359
 DB 2 CUGUGAUCUAUGGG 16

RESULT 499

ADO18480

ID ADO18480 standard; DNA; 19 BP.

XX ADO18480;

DT 15-JUL-2004 (first entry)

DE Analytical probe chip of the invention #239.

XX analytical chip; bacterial 16S-rRNA; genotypic characterization; probe;
 KW ss.

XX Synthetic.

XX WO2004033720-A2.

XX 22-APR-2004.

XX 24-SEP-2003; 2003WO-EP010626.

XX 09-OCT-2002; 2002EP-00022631.

XX (UYGE-) UNIV GENEVE HOPITAUX.

XX Schrenzel J, Francois P, Charbonnier Y, Jacquet JG, Uttinger D;
 PI Kresbach GM, Abel A, Ehrat M;

XX WPI; 2004-375537/35.

XX Analytical chip useful for simultaneous determination of one or more
 FT different bacterial 16S-rRNA in liquid sample, comprising evanescent
 FT field measurement platform as solid carrier and several specific
 FT recognition elements.

XX Claim 1; SEQ ID NO 239; 82pp; English.

XX The present invention relates to an analytical chip for simultaneous
 CC determination of one or more different bacterial 16S-rRNA in liquid
 CC sample. The chip is useful for detecting one or more bacterial 16S-rRNA,
 CC derived from bacteria such as *Achromobacter xylosoxidans*, *Acinetobacter*
 CC *baumannii*, *Actinomyces israelii*, *Aerococcus viridans*, *Aeromonas*
 CC *hydrophilia*, *Agrobacterium radiobacter*, *Bacillus* sp., *Bacteroides*
 CC *ovatus*, *Campylobacter fetus*, *Citrobacter freundii*, *Enterococcus avium*
 CC, *Escherichia coli*, *Flavobacterium breve*,
 CC *Haemophilus influenzae*, *Gemella morbillorum*, *Gardnerella vaginalis*,
 CC *Haemophilus influenzae*, *Hafnia alvei*, *Kingella* sp., *Klebsiella oxytoca*
 CC, *Lactobacillus acidophilus*, *Legionella pneumophila*, *Moraxella*
 CC *catarrhalis*, *Mycobacterium avium*, *Neisseria cinerea*, *Nocardia* sp.,
 CC *Ochrobactrum anthropi*, *Pasteurella multocida*, *Peptostreptococcus magnus*
 CC, *Salmonella typhi*, *Shigella sonnei*, *Veillonella parvula*, *Veillonella*
 CC sp. or *Yersinia enterocolitica*. The chip is useful for detecting
 CC clinically relevant bacteria. The chip enables determination of one or
 CC more different bacterial 16S-rRNA in a liquid sample, simultaneously and
 CC enables rapid, accurate, easy and reliable identification of bacteria by
 CC genotypic characterization in a provided sample and also enables
 CC identification of a bacterium even in a complex biological sample. The
 CC chip which is produced at reduced cost, enables determination of 16S-rRNA
 CC in a sample with reduced experimental error and variation. The present
 CC sequence represents a probe of the invention used as an analytical chip.

XX Sequence 19 BP; 4 A; 4 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;

Fri Aug 19 11:00:00 2005

Best Local Similarity 93.3%; Pred. No. 2.4e+02; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 466 GCACCTTTATTCGAT 480
 DB 3 GCACCTTTATTCGAT 17

RESULT 500
 ADO18573
 ID ADO18573 standard; DNA; 19 BP.
 XX
 AC
 XX ADO18573;
 DT 15-JUL-2004 (first entry)
 XX
 DE Analytical probe chip of the invention #332.
 XX
 KW analytical chip; bacterial 16S-rRNA; genotypic characterization; probe;
 KW ss.
 XX Synthetic.
 OS
 XX WO2004033720-A2.
 PN
 XX 22-APR-2004.
 XX
 XX 24-SEP-2003; 2003WO-BP010626.
 XX
 XX 09-OCT-2002; 2002EP-00022631.
 PR
 XX (UYGE-) UNIV GENEVE HOPITAUX.
 PA
 XX
 XX Schrenzel J, Francois P, Charbonnier Y, Jacquet JG, Uttinger D;
 PI Kresbach GM, Abel A, Ehrat M;
 XX
 XX WPI; 2004-375537/35.
 DR
 XX Analytical chip useful for simultaneous determination of one or more
 PT different bacterial 16S-rRNA in liquid sample, comprising evanescent
 PT field measurement platform as solid carrier and several specific
 PT recognition elements.
 XX
 XX Claim 45; SEQ ID NO 332; 82pp; English.
 PS
 XX The present invention relates to an analytical chip for simultaneous
 CC determination of one or more different bacterial 16S-rRNA in liquid
 CC sample. The chip is useful for detecting one or more bacterial 16S-rRNA,
 CC derived from bacteria such as *Achromobacter xylosoxidans*, *Acinetobacter*
 CC *baumannii*, *Actinomyces israelii*, *Aerococcus viridans*, *Aeromonas*
 CC *hydrophila*, *Agrobacterium radiobacter*, *Bacillus* sp., *Bacteroides*
 CC *ovatus*, *Campylobacter fetus*, *Citrobacter freundii*, *Enterococcus avium*
 CC *Fusobacterium lentum*, *Escherichia coli*, *Flavobacterium breve*,
 CC *Gardnerella vaginalis*, *Gemella morbillorum*, *Kingella* sp., *Klebsiella oxytoca*
 CC *Haemophilus influenzae*, *Hafnia alvei*, *Legionella pneumophila*, *Moraxella*
 CC *Lactobacillus acidophilus*, *Legionella cinerea*, *Nocardia* sp.,
 CC *Ochrobactrum anthonii*, *Pasteurella multocida*, *Peptostreptococcus magnus*
 CC *Salmonella typhi*, *Shigella sonnei*, *Veillonella parvula*, *Veillonella*
 CC *sp.* or *Yersinia enterocolitica*. The chip is useful for detecting
 CC clinically relevant bacteria. The chip enables determination of one or
 CC more different bacterial 16S-rRNA in a liquid sample, simultaneously and
 CC enables rapid, accurate, easy and reliable identification of bacteria by
 CC genotypic characterization in a provided sample and also enables
 CC identification of a bacterium even in a complex biological sample. The
 CC chip which is produced at reduced cost, enables determination of 16S-rRNA
 CC in a sample with reduced experimental error and variation. The present
 CC sequence represents a probe of the invention used as an analytical chip.
 XX
 XX Sequence 19 BP; 4 A; 4 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 466 GCACCTTTATTCGAT 480
 DB 3 GCACCTTTATTCGAT 17
 RESULT 501
 ADR79444
 ID ADR79444 standard; DNA; 19 BP.
 XX
 AC ADR79444;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human apolipoprotein B (ApoB) oligonucleotide seqid 3929.
 XX
 KW antilipemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cyostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2004080406-A2.
 PN
 XX 23-SEP-2004.
 PD
 XX
 XX 08-MAR-2004; 2004WO-US007070.
 PF
 XX 07-MAR-2003; 2003US-0452682P.
 PR 12-MAR-2003; 2003US-0454285P.
 PR 13-MAR-2003; 2003US-0454962P.
 PR 13-MAR-2003; 2003US-0455050P.
 PR 14-APR-2003; 2003US-0462894P.
 PR 17-APR-2003; 2003US-0463772P.
 PR 25-APR-2003; 2003US-0465665P.
 PR 25-APR-2003; 2003US-0465802P.
 PR 09-MAY-2003; 2003US-0469612P.
 PR 08-AUG-2003; 2003US-0493986P.
 PR 11-AUG-2003; 2003US-0494597P.
 PR 26-SEP-2003; 2003US-0506341P.
 PR 09-OCT-2003; 2003US-0510246P.
 PR 10-OCT-2003; 2003US-0510318P.
 PR 07-NOV-2003; 2003US-0518453P.
 XX (ALNY-) ALNYLAM PHARM.
 PA
 XX Manoharan M, Bumcrot D;
 PI
 XX WPI; 2004-677362/66.
 DR
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 XX disease, diabetes, cancer or neurological disease, comprises sense
 XX sequence and antisense sequence which has specific modifications.
 XX
 XX Example 5; SEQ ID NO 3929; 378pp; English.
 PS
 XX The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequence have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its

activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted levels of cholesterol, and/or dysregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant disease (CAD), coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.

XX SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 830 TGACCCAGGAAGGCC 844
 |||||
 Db 2 TGACTCAGGAAGGCC 16

RESULT 502
 ADR77809
 ID ADR77809 standard; DNA; 19 BP.
 XX AC ADR77809;
 XX DT 16-DEC-2004 (first entry)
 XX DE Human apolipoprotein B (ApoB) oligonucleotide seqid 2294.
 KW antilipemic; cardiast; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cycostatic; anticonvulsant; nootropic; muscular; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.

XX OS Homo sapiens.
 XX WO2004080406-A2.
 XX 23-SEP-2004.
 XX 08-MAR-2004; 2004WO-US007070.
 XX 07-MAR-2003; 2003US-0452682P.
 XX 12-MAR-2003; 2003US-0454265P.
 XX 13-MAR-2003; 2003US-0454962P.
 XX 13-MAR-2003; 2003US-0455050P.
 XX 14-APR-2003; 2003US-0462894P.
 XX 17-APR-2003; 2003US-0463772P.
 XX 25-APR-2003; 2003US-0465665P.
 XX 25-APR-2003; 2003US-0465802P.
 XX 09-MAY-2003; 2003US-0469612P.
 XX 08-AUG-2003; 2003US-0493986P.
 XX 11-AUG-2003; 2003US-0494597P.
 XX 26-SEP-2003; 2003US-0506341P.
 XX 09-OCT-2003; 2003US-0510246P.
 XX 10-OCT-2003; 2003US-0510318P.
 XX 07-NOV-2003; 2003US-0518453P.

XX PA (ALNY-) ALNYLAM PHARM.
 XX PI Manoharan M, Bumcrot D;
 XX WPI; 2004-677362/66.
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
 XX Example 5; SEQ ID NO 2294; 378pp; English.
 XX The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2'-O alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100 levels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1) The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted levels of cholesterol, and/or dysregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant disease (CAD), coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.

XX SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 830 TGACCCAGGAAGGCC 844
 |||||
 Db 2 TGACTCAGGAAGGCC 16

RESULT 503
 AAQ91053/c
 ID AAQ91053 standard; DNA; 18 BP.
 XX AC AAQ91053;
 XX DT 30-JAN-1996 (first entry)
 XX DE HHV-6 associated MS genetic marker 38E internal primer 38E6.
 XX KW Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; 38E;
 XX internal primer 38E6; diagnosis; ss.
 XX OS Synthetic.
 XX WO9512313-A1.
 XX 11-MAY-1995.
 XX 04-NOV-1994; 94WO-US012655.

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XX 05-NOV-1993; 93US-00149176.
PR 24-MAR-1994; 94US-00218029.
PR 05-AUG-1994; 94US-00287942.
PR 04-NOV-1994; 94US-00334482.
XX (PATH-) PATHOGENESIS CORP.
XX Burmer GC, Challoner PB, Smith KT, Brown JP, Parker JD;
PI Nowinski RC;
PI WPI; 1995-215032/28.
XX Treatment of human herpes-virus-6-associated multiple sclerosis - using
PT an antiviral agent, e.g. a nucleoside analogue, administered to the
PT cerebrospinal fluid.
XX Disclosure; Page 35; 116pp; English.
XX AAQ91052 and AAQ91053 are an internal primer pair for the human herpes
CC virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, 38E
CC (AAQ91054). The primers can be used in the diagnosis of MS
XX Sequence 18 BP; 7 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GCTATTGGACTGCTGCTTTT 130
DB 18 GCTGTGGACTGGCATT 1

RESULT 504
AAAT60161/C
ID AAAT60161 standard; DNA; 18 BP.
XX AAAT60161;
XX 01-DEC-1997 (first entry)
DT
DE Collagen gene promoter region binding oligomer Oligo 158 APS.
XX Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_feature 1..18
FT /*tag= a
FT /note= "Phosphorothioate linkages"
XX
XX WO9710254-A1.
XX
XX 20-MAR-1997.
XX
XX 12-SEP-1996; 96WO-US014640.
XX
XX 11-SEP-1995; 95US-00528836.
XX 11-SEP-1996; 96US-00712357.
XX
XX (GUNT/) GUNTAKA R V.
XX
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 1997-202172/18.
XX Triplex forming oligomer binds to collagen gene promoter region - used to
PT impede pathological fibrosis etc.
PT

XX Claim 18; Page 36; 52pp; English.
XX An oligomer has been produced which is capable of inhibiting expression
XX of a collagen gene. The present sequence represents a specifically
XX claimed oligomer Oligo 158 APS, which binds to the polypurine
XX polypyrimidine region of the rat alpha1(I) collagen gene promoter region.
XX The oligomer may be used to impede pathological fibrosis which is
XX associated with myocardial fibrosis in hypertensive heart diseases,
XX atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
XX fibrosis found in scleroderma, in hypertrophic scars and in skin
XX following burn injury. The oligomer inhibits expression of a collagen
XX gene after insertion into a cell by causing an intracellular reaction
XX which inhibits gene expression. The oligomer is preferably a triplex
XX forming oligomer (TFO) which is targeted to a 30-mer polypurine
XX oligonucleotide corresponding to the noncoding strand of the promoter
XX between -170 and -140. This section was chosen due to its binding
XX stability at physiological pH
XX
XX Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 202 CTCGCCCATCCCCCATTT 219
DB 18 CTCGCCCATCCCCCATTT 1

RESULT 505
AAV48417/C
ID AAV48417 standard; DNA; 18 BP.
XX AAV48417;
XX 15-OCT-1998 (first entry)
DT
DE Transforming growth factor beta-1 antisense oligonucleotide N5.
XX Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
KW modulate; gene expression; ss.
XX Synthetic.
XX Homo sapiens.
XX EP856579-A1.
XX 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX 31-JAN-1997; 97EP-00101531.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen K, Brysch W;
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX Example 1; Fig 3a; 286pp; English.
XX AAV48412-84 represent antisense oligonucleotides directed against
XX transforming growth factor beta-1 (TGF beta-1). The oligonucleotides
XX exemplify the invention. The specification describes oligonucleotides
XX that contain 8-30 nucleotides, which contain at most 8 nucleotides that
XX can each form three hydrogen bonds to cytosine; do not contain four
XX

```

CC consecutive nucleotides able to form three H-bonds each to four
 CC consecutive cytosines; do not contain two sequences of three consecutive
 CC nucleotides each able to form three H-bonds to three consecutive
 CC cytosines, and the ratio between residues able to form two H-bonds each
 CC (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The
 CC oligonucleotides are used to modulate expression of genes, particularly
 CC the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or beta 2 to control
 CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
 CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
 CC oligonucleotides can also be used to analyse function of proteins (by
 CC altering their expression or activity) and therapeutically, e.g. in cases
 CC of cancer or (targeting TGF) for stimulating the immune system
 XX

SQ Sequence 18 BP; 2 A; 3 C; 12 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 196 CGCCATCTCCCCCATGCC 213
 ||||| ||||| ||||| |||||
 Db 18 CGCCGCTCTCCCCCATGCC 1

RESULT 506

AAAX76549
 ID AAX76549 standard; DNA; 18 BP.

XX AC AAX76549;

XX DT 06-AUG-1999 (first entry)

XX DE Human WISP-2 PCR primer SEQ ID NO:131.

XX KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
 KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
 KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;
 KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
 KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
 KW connective tissue disorder; catabolic state; inflammation;
 KW testicular-related disorder; angiogenesis; immunological disorder; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9921998-A1.

XX PD 06-MAY-1999.

XX PF 29-OCT-1998; 98WO-US022991.

XX PR 29-OCT-1997; 97US-0063704P.

XX PR 03-FEB-1998; 98US-0073612P.

XX PR 14-APR-1998; 98US-0081695P.

XX PA (GETH) GENENTECH INC.

XX PI Botstein DA, Cohen RL, Gurney AL, Hillan K, Lawrence DA;

XX PI Levine AJ, Pennica D, Roy MA, Goddard A, Wood WI;

XX DR WPI; 1999-337420/28.

XX PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3.

XX PS Example 11; Page 272; 284pp; English.

XX CC The present invention describes Wnt-1 induced secreted polypeptides, WISP
 CC -1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and
 CC WISP-3 have homology to connective tissue growth factor (CTGF). Products
 CC from the present invention can be used to treat WISP-related disorders
 CC such as breast, ovarian, and colon cancer or melanoma. The products can
 CC be used to treat arteriosclerosis. The products can also be used to treat
 CC other diseases e.g. benign and malignant tumours, leukaemia and lymphoid

CC malignancies, neuronal, glial, astrocytal, hypothalamic and other
 CC glandular, macrophagal, epithelial, stromal, and blastocoeic disorders,
 CC haematopoiesis-related disorders, tissue-growth disorders, skin
 CC disorders, desmoplasia, fibrotic lesions, kidney disorders, bone-related
 CC disorders such as osteoporosis, trauma such as burns, incisions, and
 CC other wounds, connective tissue disorders, catabolic states, testicular-
 CC related disorders, and inflammatory, angiogenic and immunologic disorders
 CC including arteriosclerosis. The products can also be used for detection
 CC and diagnosis especially of individuals with neoplastic cell growth or
 CC proliferation. The products can be used in the production of transgenic
 CC or knock-out animals. Antibodies can be used to induce death in WISP-1, 2
 CC or 3 overexpressing cells
 XX

SQ Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 897 AGACCAAGAGCCTCAACA 914
 ||||| ||||| ||||| |||||
 Db 1 AGTCCAAGAGTCTCAGCA 18

RESULT 507

AAZ22179/C
 ID AAZ22179 standard; DNA; 18 BP.

XX AC AAZ22179;

XX DT 26-NOV-1999 (first entry)

XX DE Human c-IAP-1 mRNA inhibiting antisense oligo ISIS #23361.

XX KW Cellular Inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
 KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5958772-A.

XX PD 28-SEP-1999.

XX PF 03-DEC-1998; 98US-00205204.

XX PR 03-DEC-1998; 98US-00205204.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Cowsett LM, Ackermann EJ;

XX DR WPI; 1999-561047/47.

XX PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1
 useful for e.g. diagnostics, therapeutics, and as research reagents.

XX PS Claim 3; Col 39; 32pp; English.

XX CC The invention provides antisense compounds of 8-30 nucleotides that
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-
 CC 1). The antisense compounds may be used for diagnostics, therapeutics
 CC (for modulating the expression of c-IAP-1), prophylaxis (e.g. to prevent
 CC or delay infection, inflammation, or tumor formation), as research
 CC reagents (e.g. to distinguish between members of a biological pathway)
 CC and in kits. Sequences AAZ22150-189 represent phosphorothioate
 CC oligonucleotides used for antisense inhibition of cellular inhibitor of
 CC apoptosis-1
 XX

SQ Sequence 18 BP; 6 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 TTGATGAGATCCAAAGGA 991
 |||||
 Db 18 TTGATGAGATCCAGGTA 1

RESULT 508
 AAX22147
 ID AAX22147 standard; tRNA; 18 BP.
 XX AC
 XX AAX22147;
 XX 20-MAR-2003 (revised)
 DT 26-MAY-1999 (first entry)
 XX Murine tRNA gene fragment.
 XX Murine Leukaemia virus; MLV; retroviral transfer vector; retrovirus;
 KW modified tRNA primer; antiviral agent; pathogenic; virus; HIV-1; HTLV-1;
 KW cellular tropism; murine; ss.
 XX OS
 XX Mus musculus.
 XX US5886166-A.
 XX 23-MAR-1999.
 XX 15-NOV-1996; 96US-00749495.
 XX 08-SEP-1995; 95US-00525849.
 XX (LUND/) LUND A H.
 PA (PEDE/) PEDERSEN P S.
 PA (JORG/) JORGENSEN P.
 PA (LOVM/) LOVMAND J.
 PA (DUCH/) DUCH M.
 XX Pedersen FS, Jorgensen P, Lovmand J, Lund AH, Duch M;
 PI WPI; 1999-228613/19.
 XX Murine leukaemia virus retroviral vector - whose transfer is dependent on
 XX the presence of specific tRNA-like primer.
 XX Disclosure; Col 10; 26pp; English.

CC The invention relates to a modified tRNA primer for reverse transcription
 CC of a Murine Leukaemia virus (MLV) retroviral transfer vector. The vector
 CC comprises (i) a retrovirus in which at least part of the genomic RNA
 CC sequences carrying information for the production of viral proteins have
 CC been replaced by one or more sequences carrying information to be
 CC introduced in a target cell chromosome; (ii) a primer binding site (PBS)
 CC which has been modified to a sequence that does not allow strong base
 CC pairing with the 3' end of any naturally occurring tRNA, and the three 5'
 CC nucleotides of the PBS are UGG, where the modified tRNA primer has been
 CC modified to allow strong base pairing with the PBS of the transfer
 CC vector. The retroviral vectors can be used as antiviral agents. Such vectors
 CC can be directed against pathogenic viruses, e.g. HIV-1 or HTLV-1, related
 CC to the type used for construction of the vector, thus having the same
 CC host range and cellular tropism. The use of a modified tRNA primer
 CC reduces the risk of uncontrolled regeneration of complete virus, or of
 CC virus spread. Only specialised packaging cells provided with appropriate
 CC artificial primers allow vector propagation. Sequences AAX22147-167
 CC represent published murine tRNA sequences based on which the modified
 CC tRNA primer is synthesised. (Updated on 20-MAR-2003 to correct PF field.)
 XX

SQ Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 192 TCCACGCCATCTCCCCA 209
 :||| |||:|:|
 Db 1 UCCCGGCAUCCUCCACCA 18

RESULT 510
 AAC66251
 ID AAC66251 standard; tRNA; 18 BP.
 XX AC
 XX AAC66251;
 XX

QY 192 TCCACGCCATCTCCCCA 209
 :||| |||:|:|
 Db 1 UCCCGGCAUCCUCCACCA 18

RESULT 509
 AAX01825
 ID AAX01825 standard; tRNA; 18 BP.
 XX AC
 XX AAX01825;
 XX 13-APR-1999 (first entry)
 DT Mouse tRNA-Ala(g) primer tRNA.
 XX tRNA; transfer vector; viral protein; replication; primer binding site;
 KW PBS; gene therapy; antisense; ribozyme; pathogenic; primer; tRNA-ala; ss.
 XX Murine leukemia virus.
 OS US5866411-A.
 XX 02-FEB-1999.
 XX 08-SEP-1995; 95US-00525849.
 XX 08-SEP-1995; 95US-00525849.
 XX (JORG/) JORGENSEN P.
 PA (LUND/) LUND A H.
 PA (PEDE/) PEDERSEN P S.
 PA (LOVM/) LOVMAND J.
 PA (DUCH/) DUCH M.
 XX Lund AH, Jorgensen P, Lovmand J, Pedersen FS, Duch M;
 PI WPI; 1999-141937/12.
 XX Murine leukaemia virus transfer vector - with modified primer binding
 XX site requiring artificial primer.
 XX Disclosure; Col 10; 31pp; English.

CC AAX01825-X01845 are primers used in a method for the construction of a
 CC transfer vector in which the genomic RNA sequences encoding viral
 CC proteins required in trans for MLV replication have been at least partly
 CC replaced by at least 1 sequence carrying information to be introduced
 CC into a target cell chromosome, where the primer binding site (PBS) has
 CC been modified to a sequence that does not allow strong base-pairing with
 CC the 3' end of any naturally occurring tRNA. The transfer vector can be
 CC used for gene therapy, e.g. for carrying antisense or ribozyme constructs
 CC targeted to the PBS of a pathogenic virus such as HIV or HTLV-1. The
 CC modified PBS reduces the risk of uncontrolled regeneration of whole virus
 CC by interaction of the vector with various engineered or endogenous cis-
 CC or trans-acting components
 XX Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 192 TCCACGCCATCTCCCCA 209
 :||| |||:|:|
 Db 1 UCCCGGCAUCCUCCACCA 18

RESULT 510
 AAC66251
 ID AAC66251 standard; tRNA; 18 BP.
 XX AC
 XX AAC66251;
 XX

DT 20-FEB-2001 (first entry)
 XX Murine Ala tRNA 3' nucleotide sequence.
 DE tRNA primer; retroviral transfer vector; primer binding site; ss.
 XX Mus sp.
 XX US6107478-A.
 XX 22-AUG-2000.
 XX 09-OCT-1998; 98US-00169248.
 PF 08-SEP-1995; 95US-00525849.
 XX 15-NOV-1996; 96US-00749495.
 XX (LOVM/) LOVMAND J.
 PA (PEDE/) PEDERSEN F S.
 PA (LUND/) LUND A H.
 PA (JORG/) JORGENSEN P.
 PA (DUCH/) DUCH M.
 XX Duch M, Lovmand J, Lund AH, Pedersen FS, Jorgensen P;
 XX WPI; 2000-586220/55.
 XX New modified tRNA primer for reverse transcribing a retroviral transfer
 PT vector comprising a primer binding site modified to a sequence which does
 PT not allow strong base pairing with the 3' end in any occurring tRNA.
 XX Disclosure; Col 10; 27pp; English.
 XX This invention relates to a new tRNA primer for reverse transcribing a
 CC retroviral transfer vector comprising a primer binding site (PBS) that
 CC has been modified to a sequence that does not allow strong base pairing
 CC with the 3' end of any naturally occurring tRNA and comprises three 5'
 CC nucleotides of UGG. The new tRNA primer is modified to allow strong base
 CC pairing with the modified PBS of a transfer vector; reverse transcribes
 CC the retroviral transfer vector which comprises a retrovirus in which at
 CC least part of the genomic RNA sequences necessary for production of viral
 CC proteins required in for retroviral replication have been replaced by
 CC sequences that have been introduced in a target cell chromosome; and has a PBS
 CC that has been modified to a sequence that does not allow strong base
 CC pairing with the 3' end of any naturally occurring tRNA and the three 5'
 CC nucleotides are UGG. The primer is used for reverse transcribing the
 CC retroviral vector comprising a retrovirus with infectivity for birds
 CC and/or mammals in which a part of the genomic RNA sequences necessary for
 CC production of viral proteins required in trans for retroviral replication
 CC have been replaced by sequences to be introduced in a target cell
 CC chromosome. The present sequence represents a murine tRNA sequence used
 CC in the design of the primer of the invention
 XX Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;
 SQ Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 192 TCACGCGCATCTCCCCA 209
 Db 1 UCCCGCGCAUCUCCACCA 18
 RESULT 511
 AAA35959/c
 ID AAA35959 standard; DNA; 18 BP.
 XX AAA35959;
 AC AAA35959;
 XX 26-JUL-2000 (first entry)
 DT Human genomic SNP allele specific oligonucleotide SEQ ID NO:16.
 DE

XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.
 XX Homo sapiens.
 OS WO200018960-A2.
 PN 06-APR-2000.
 PD 24-SEP-1999; 99WO-US022283.
 PF 25-SEP-1998; 98US-0101757P.
 PR (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Landers JB, Jordan B, Housman DE, Charest A;
 PI WPI; 2000-293181/25.
 DR Detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs.
 XX Disclosure; Page 53; 111pp; English.
 XX A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a SNP
 CC allele. The method can be used to characterise a tumour, to generate a
 CC genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be used
 CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences
 CC used in the exemplification of the present invention. AAA35948 to
 CC AAA36632 represent nucleotide sequences containing SNPs
 XX Sequence 18 BP; 9 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 568 TTTTAAATACCTTATATA 585
 Db 18 TTTTATACCTTCATAAA 1
 RESULT 512
 AAZ98709/c
 ID AAZ98709 standard; DNA; 18 BP.
 XX AAZ98709;
 AC AAZ98709;
 XX 20-JUN-2000 (first entry)
 DT Collagen promoter inhibitory oligonucleotide Oligo Col 158 APS.
 XX Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
 KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
 KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
 XX Rattus sp.
 OS WO200008213-A1.
 PN 17-FEB-2000.
 PD 06-AUG-1999; 99WO-US017824.
 XX

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XX 07-AUG-1998; 98US-00130888.
PR (GUNTAKA R V.
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 2000-205739/18.
DR
XX Inhibitors of collagen gene useful for treating fibrosis associated with
PT atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
PA comprises oligomers capable of inhibiting collagen gene.
PT
XX Claim 19; Fig 8; 77pp; English.
PS
XX This sequence represents an oligomer which is capable of inhibiting the
CC expression of the collagen gene. The oligomer is capable of binding to
CC the promoter region of the collagen gene. Collagen is a family of fibrous
CC proteins, and is the major element of skin, bone, tendon, cartilage,
CC blood vessels and teeth. The oligomers are useful for inhibiting
CC expression of the collagen gene, comprising inserting the oligomers into
CC a cell and causing an intracellular reaction to inhibit the gene
CC expression. The collagen inhibitory oligomers of the invention are useful
CC for treating pathological fibrosis associated with myocardial fibrosis in
CC hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
CC lung fibrosis, peritoneal fibrosis and skin fibrosis found in
CC scleroderma, hypertrophic scars and burn injury
XX
XX Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 202 CTCCTCCCTCCCTCCCTTT 219
DB 18 CTCCTCCCTCCCTCCCTTT 1
XX
RESULT 513
AAA97374
ID AAA97374 standard; DNA; 18 BP.
XX
AC AAA97374;
XX
DT 29-JAN-2001 (first entry)
XX
XX CMV GlyB detection oligonucleotide SA-B1.
XX
XX Cytomegalovirus GlyB gene; detection oligonucleotide; detection;
KW target-associated detectable structure; signal amplification; ss.
XX
XX Human herpesvirus 5.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /*note= "Biotinylated"
FT
XX
XX WO200055365-A1.
XX
XX 21-SEP-2000.
XX
XX 13-MAR-2000; 2000WO-GB000921.
XX
XX 12-MAR-1999; 99GB-00005580.
XX
XX (TEPN-) TEPNEL MEDICAL LTD.
XX
XX Mulrooney C, Oultram JD;
PI
XX WPI; 2000-638207/61.
DR
XX
XX Detecting a target molecule by enzymatically catalyzed amplification of
PT target associated detectable structures comprises contacting a sample
PA with a locator probe, amplifying the structure bound and detecting bound
PT locator probes.
XX
XX Example 5; Page 72; 75pp; English.
PS
XX The invention relates to a novel method of detecting a target nucleic
CC acid molecule. The method involves contacting a sample with a locator
CC probe comprising a binding moiety specific for the target molecule and an
CC amplification nucleic acid sequence. An amplification structure which is
CC bound to the target molecule-locator probe complex is produced via
CC amplification of the sample and locator probe using a single stranded
CC amplification template (comprising, in the 5' to 3' direction, an
CC extension nucleic acid sequence, a hybridisation nucleic acid sequence
CC and an amplification moiety); a polymerase; and a separating agent
CC capable of removing sufficient of the extension nucleic acid sequence of
CC the amplification template when hybridised to the complementary strand to
CC allow subsequent hybridisation of the hybridisation nucleic acid sequence
CC of the amplification template to the complementary strand. After
CC optionally repeating amplification of this structure, any additional
CC locator probes or amplification template is detected, and the result is
CC correlated with the presence of a target molecule. The method is used to
CC detect target molecules in a sample by using an enzymatically catalysed
CC amplification of the target-associated detectable structures. As a small
CC number of inexpensive components are utilised, the new method is more
CC economical than previous methods. The method utilises signal
CC amplification rather than target amplification, thus overcoming
CC contamination problems. It is an enzymatically catalysed process that
CC actively assembles the signal generating structure rather than relying on
CC the passive hybridisation-based methods of non-enzymatic methods such as
CC bDNA. Unlike prior art techniques such as polymerase chain reaction
CC (PCR), the method has the ability to address RNA and DNA targets with
CC equal efficiency without pretreatments. The present sequence represents a
CC detection oligonucleotide SA-B1, used with amplification template SA-EX1
CC (AAA97373) in an exemplification of the invention to detect the CMV GlyB
XX target oligonucleotide CMV-002 (AAA97372)
XX
XX Sequence 18 BP; 2 A; 6 C; 2 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1056 TTATCTTTCCAGTGGCTA 1073
DB 1 TTCTCTTCCAGTTGCTA 18
XX
XX RESULT 514
AAA08213
ID AAA08213 standard; tRNA; 18 BP.
XX
XX AAA08213;
XX
XX 28-JUN-2000 (first entry)
XX
XX Murine tRNA oligonucleotide sequence SEQ ID NO:3.
XX
XX Retroviral vector; antiviral; retrovirus; infection; primer binding site;
KW PBS; human immunodeficiency virus; human T-cell lymphotropic virus-1;
XX HIV; ss.
XX
XX Mus musculus.
OS
XX US6037172-A.
XX
XX 14-MAR-2000.
PD
XX 09-OCT-1998; 98US-00169078.
PF
XX 08-SEP-1995; 95US-00525849.
XX
XX

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XX (PBDE/) PEDERSEN F S.
PA (LUND/) LUND A H.
PA (LOVM/) LOWMAND J.
PA (JORG/) JORGENSEN P.
PA (DUCH/) DUCH M.
XX
PI Lund AH, Lowmand J, Pedersen FS, Duch M, Jorgensen P;
XX WPI; 2000-282226/24.
XX
XX Retroviral vector for gene transfer, useful as antiviral agent, has a
PT primer binding site modified to prevent base pairing with natural
XX transfer RNA.
XX
PS Disclosure; Col 10; 27pp; English.
XX
XX The present invention describes a retroviral vector (I) comprising a
CC retrovirus in which at least part of the genomic RNA sequences carrying
CC information for the production of viral proteins required in trans for
CC retroviral replication have been replaced by one or more sequences
CC carrying information to be introduced in a target cell chromosome, where
CC the primer binding site (PBS) has been modified to a sequence that does
CC not allow strong base pairing with the 3'-end of any naturally occurring
CC tRNA, and where the three 5'-nucleotides of the PBS are UGG. (I) are
CC potentially useful as antiviral agents, e.g. against human immuno-
CC deficiency virus or human T-cell lymphotropic virus-1. (I) depends on a
CC specifically engineered tRNA-like primer for reverse transcription, so
CC only special packaging cells, containing an artificial primer, can
CC support vector propagation. This reduces the risk of uncontrolled
CC regeneration of complete virus if (I) interacts with engineered or
CC endogenous cis- or trans-acting components, particularly transfection
CC efficiency is reduced by a factor of 100000 in normal packaging cells.
CC (I) can be derived from pathogenic viruses of the same type as used for
CC vector construction, i.e. they have the same host range and cell tropism,
CC but the modified PBS means that antiviral activity would not be directed
CC against the vector's own cis-acting elements. The present sequence
CC represents a murine tRNA sequence, which is used in the exemplification
CC of the present invention
XX
SQ Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 192 TCCAGGCATCTCCCCCA 209
:|||||:|:|:|:|:|:|
Db 1 UCCCCGCAUCCUCCACCA 18

RESULT 515
AAZ71352
ID AAZ71352 standard; DNA; 18 BP.
XX
AC AAZ71352;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker upstream amplification primer SEQ ID NO:5708.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB0000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI

PF 21-APR-1999; 99WO-IB0000822.
XX
PR 21-APR-1998; 98US-0082614P;
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 1448; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses; they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 871 TCCATGCTATTAAAGTG 888
|||||:|:|:|:|:|:|
Db 1 TCCATGCTCTTACCAGTG 18

RESULT 516
AAZ75603
ID AAZ75603 standard; DNA; 18 BP.
XX
XX AAZ75603;
AC
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:9959.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB0000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI

XX WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX Claim 8; Page 2354; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterization of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 18 BP; 2 A; 8 C; 0 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 209 ATCCCCCATTTTCATTGCC 226
 Db 1 ATCCCCCTCTTCATTTC 18
 RESULT 517
 AAA91755
 ID AAA91755 standard; DNA; 18 BP.
 AC AAA91755;
 XX 02-JAN-2001 (first entry)
 DT TW7XN1 cDNA antisense PCR primer.
 DE
 XX Tumour; TW7XN1; metastasis; melanoma; seven transmembrane protein;
 KW secretin family; G-protein-coupled peptide hormone receptor; cancer;
 KW chromosome 16q13; tumour suppressor; clydi; cylindromatosis; PCR primer;
 KW human; ss.
 XX Homo sapiens.
 OS AU200013568-A.
 XX 03-AUG-2000.
 XX 25-JAN-2000; 2000AU-00013568.
 PF 29-JAN-1999; 99EP-00101925.
 PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA F Hoffmann- La Roche Ag;
 XX WPI; 2000-572508/54.
 XX Nucleic acid molecule down-regulated during tumor progression and/or
 PT metastasis as prognostic markers in diagnosis of metastatic and
 PT progression potential of tumor cells, and for treating cancer.
 XX Disclosure; Page 17; 48pp; English.
 PS The present invention relates to a novel human integral seven
 XX

CC transmembrane protein with a long N-terminal extracellular domain: TW7XN1
 CC (see AAA91751 and AAB21700). Based on homology comparison, TW7XN1 can be
 CC placed in the secretin family of G-protein-coupled peptide hormone
 CC receptors. TW7XN1 gene expression is down-regulated in metastatic human
 CC melanoma cells, and is down-regulated during tumour progression and/or
 CC metastasis. Therefore, TW7XN1 may be involved in metastasis due to its
 CC down-regulation in melanoma cells. The TW7XN1 gene is localised on
 CC chromosome 16q13, and is therefore a candidate gene for the tumour
 CC suppressor gene clyd1, which is involved in cylindromatosis. The present
 CC sequence is a PCR primer for the coding sequence of TW7XN1. This sequence
 CC was used during the study of mRNA expression of TW7XN1 in various human
 CC cell types
 XX Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 349 GATCAAAATGGGAGCCTG 366
 Db 1 GAGCTGATGGGAGCCTG 18
 RESULT 518
 AAA75986/C
 ID AAA75986 standard; DNA; 18 BP.
 XX AAA75986;
 AC AAA75986;
 XX 08-FEB-2001 (first entry)
 DT PCR primer used to amplify a human PREB gene fragment.
 DE
 XX Prolactin regulatory element binding protein; PREB protein;
 KW kinase-mediated hormonal regulator; transcription factor; 1P element;
 KW prolactin promoter; osteoporosis; cancer; autoimmune disease;
 KW graft-versus-host disease; trisomy 2p; probe; PCR primer; ds.
 XX Homo sapiens.
 OS WO200056756-A2.
 XX 28-SEP-2000.
 PD 23-MAR-2000; 2000WO-US007642.
 PF 23-MAR-1999; 99US-0125728P.
 PR (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 PA Bancroft CF, Fliss M, Clelland CL;
 PI WPI; 2000-638247/61.
 XX New polynucleotide encoding prolactin regulatory element binding protein
 PT useful for treating osteoporosis, cancer and autoimmune diseases.
 XX Example; Page 57; 87pp; English.
 PS The specification describes a prolactin regulatory element binding (PREB)
 CC protein. The protein is a kinase-mediated hormonal regulator of prolactin
 CC gene expression, i.e. a transcription factor. The protein binds to the 1P
 CC element of the prolactin promoter. PREB proteins are useful for treating
 CC osteoporosis. PREB modulators are useful for treating cancer, autoimmune
 CC diseases by inhibiting the expression of prolactin. PREB antisense
 CC sequences are also useful for treating a development defect. Inhibition
 CC of prolactin gene expression is useful for inhibiting graft-versus-host
 CC diseases in transplantations. PREB polynucleotides are useful as a probe
 CC for diagnosing trisomy 2p in a subject. PCR primers AAA75984-87 were used
 CC to amplify a human PREB gene fragment
 XX Sequence 18 BP; 8 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
 SQ

```

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 279 CATATTCTTCTCACTACTG 296
Db 18 CACATTCTTCTCTGCTG 1

RESULT 519
AAC73454/c
ID AAC73454 standard; DNA; 18 BP.
XX
AC AAC73454;
XX
XX 02-FEB-2001 (first entry)
XX
XX Reverse primer #96 used in multiplexing PCR/SBE assay.
XX
XX Oligonucleotide array; genotyping; single base extension reaction; SBE;
XX PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
XX Unidentified.
XX
XX WO200058516-A2.
XX
XX 05-OCT-2000.
XX
XX 27-MAR-2000; 2000WO-US008069.
XX
XX 26-MAR-1999; 99US-0126473P.
XX 23-JUN-1999; 99US-0140359P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (APFY-) AFFYMETRIX INC.
XX
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
XX Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
XX along with locus-specific tagged oligonucleotides useful in genotyping
XX using single base extension reactions.
XX
XX Example 7; Page 58; 70pp; English.
XX
XX The present invention relates to an oligonucleotide array comprising
XX oligonucleotide tags fixed to a solid substrate. The oligonucleotide
XX array is useful for genotyping a nucleic acid sample at one or more loci
XX via single base extension (SBE) reactions. A pair of primers is used to
XX amplify a polymorphic locus in a sample e.g. a single nucleotide
XX polymorphism (SNP). The present sequence is one of the primers used in
XX the method of the present invention to amplify a polymorphic sample. The
XX amplified nucleic acid product is then used as a template in a SBE
XX reaction with an extension primer. The SBE reaction products are used to
XX form the oligonucleotide array
XX
XX Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 93 TGGCATTATCTCTTCAGTG 110
Db 18 TGGCCTTCTCCCTCAGTG 1

RESULT 520
AAF56336/c
ID AAF56336 standard; DNA; 18 BP.

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XX AAF56336;
XX
XX 19-APR-2001 (first entry)
XX
XX Human mGluR1beta GB-PR2:HUMMGLUB antisense oligonucleotide #7.
XX
XX Antisense; metabotropic glutamate receptor type 1; mGluR1; pain;
XX inflammation; arthritis; opioid analgesic; glutamate; neurotoxicity;
XX tumour; human; ss.
XX
XX Homo sapiens.
XX
XX WO200105963-A2.
XX
XX 25-JAN-2001.
XX
XX 17-JUL-2000; 2000WO-CA000824.
XX
XX 15-JUL-1999; 99US-0144004P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Fundytus ME, Coderre TJ, Cohen SR, Henry JL, Vainio A;
XX WPI; 2001-159534/16.
XX
XX New antisense oligonucleotides to metabotropic glutamate receptor type 1
XX gene, which specifically hybridize to mRNA expressed from the gene useful
XX for treating disorders related to elevated glutamate level such as pain.
XX
XX Claim 2; Page 19; 97pp; English.
XX
XX The present invention relates to an antisense oligonucleotide derived
XX from the sequence of metabotropic glutamate receptor type 1 (mGluR1)
XX gene. The antisense oligonucleotide binds to a portion of mRNA expressed
XX from the gene or its splice variant. The binding of the oligonucleotide
XX to the mRNA is effective in decreasing the translation of the mRNA in a
XX host cell expressing the gene. The oligonucleotides are useful for
XX treating chronic pain caused by injury or inflammation of a nerve caused
XX by arthritis. The oligonucleotides may be used with an opioid analgesic.
XX They are also useful for minimizing glutamate neurotoxicity and/or
XX excitotoxicity associated with stroke, ischemia, CNS trauma,
XX neurodegenerative disorders, gastrointestinal disorders or to inhibit
XX tumour formation
XX
XX Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 901 CAAGAGCCTCAACATTTC 918
Db 18 CAAGAGCCTGACCTTTTC 1

RESULT 521
AAD29760
ID AAD29760 standard; DNA; 18 BP.
XX
XX AAD29760;
XX
XX 17-MAY-2002 (first entry)
XX
XX Human HCM1 DNA amplifying antisense primer.
XX
XX Human; hyperpolarisation-activated cyclic nucleotide-gated channel; HCN;
XX therapy; stroke; ischaemia; head injury; epilepsy; Alzheimer's disease;
XX Parkinson's disease; learning disorder; memory; attention disorder; pain;
XX gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic;
XX neuroprotective; cerebroprotective; antiinflammatory; anticonvulsant;
XX tranquilliser; vasotropic; reverse transcription; RT; PCR primer; ss.

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XX OS Homo sapiens.
XX PN WO200202630-A2.
XX PD 10-JAN-2002.
XX PF 03-JUL-2001; 2001WO-GB002959.
XX PR 03-JUL-2000; 2000GB-00016360.
XX PR 03-NOV-2000; 2000GB-00026946.
XX PA (SMK ) SMITHKLINE BEECHAM PLC.
XX PI Strijbos PULM, Bates S, Gloger I, Davies C;
XX PD WPI; 2002-188422/24.
XX PF New HCN channel polypeptides and polynucleotides which encode the
XX PT polypeptides, for the manufacture of compositions to treat stroke,
XX PT ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's
XX PT disease.
XX PS Example 1; Page 21; 68pp; English.
XX CC The invention relates to new uses of human hyperpolarisation-activated,
XX CC cyclic nucleotide-gated (HCN) channel polypeptides and their
XX CC polynucleotides. The HCN channel polypeptides and polynucleotides can be
XX CC used in the manufacture of medicaments to treat stroke, ischaemia, head
XX CC injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or
XX CC memory and attention disorders. These compounds may also be used in
XX CC treating pain, gut disorders, in particular irritable bowel syndrome
XX CC (IBS) or sleep disorders. HCN polynucleotides and polypeptides may also
XX CC be employed as diagnostic reagents for detection of mutations in the
XX CC above stated diseases. The present sequence is a reverse transcription
XX CC (RT)-PCR primer used to amplify human HCN1 channel DNA and it is used in
XX CC the tissue localisation of HCN1 mRNA
XX SQ Sequence 18 BP; 2 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
      Query Match 1.2%; Score 13.2; DB 1; Length 18;
      Best Local Similarity 83.3%; Pred. No. 2.6e+02;
      Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 144 GTGCCTTAGAGGATTATG 161
DB 1 GTGCCTTCGGGATGATG 18
RESULT 522
ACA96836/c
ID ACA96836 standard; DNA; 18 BP.
XX AC ACA96836;
XX XX 24-JUL-2003 (first entry)
XX DE Human glial cell derived neurotrophic factor (GDNF) PCR primer #30.
XX DE Human glial cell derived neurotrophic factor; GDNF; PCR; primer; ss;
XX KW nervous system disease.
XX OS Homo sapiens.
XX XX CN1364812-A.
XX PN 21-AUG-2002.
XX PD 11-JAN-2001; 2001CN-00107450.
XX PF 11-JAN-2001; 2001CN-00107450.
XX PR (YISH-) YISHENG BIOLOGICAL PHARM CO LTD SHUHA1.
XX PA

XX Zhou S, Zheng Z, Feng H;
XX PI WPI; 2003-000523/01.
XX DR Human glial cell derived neurotrophic factor and its derivatives and use.
XX PT Claim 6; Page 3 (Claims); 28pp; Chinese.
XX PS The invention relates to the human glial cell derived neurotrophic factor
XX CC (GDNF) and its derivatives and use. The invention also relates to a
XX CC method of obtaining DNA encoding human glial cell derived neurotrophic
XX CC factor or its active segments and a method of purifying and fining coarse
XX CC GDNF. A composition comprising human glial cell derived neurotrophic
XX CC factor and a medicinal acceptable carrier can be used in the treatment of
XX CC nervous system diseases. Sequences ACA96807-ACA96859 represent PCR
XX CC primers used to amplify human GDNF CDNA
XX SQ Sequence 18 BP; 8 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
      Query Match 1.2%; Score 13.2; DB 1; Length 18;
      Best Local Similarity 83.3%; Pred. No. 2.6e+02;
      Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 645 GACCTGTCAAATTTAGAT 662
DB 18 GACCTGTGTTTATTAGAT 1
RESULT 523
ABZ10992/c
ID ABZ10992 standard; DNA; 18 BP.
XX AC ABZ10992;
XX XX 16-JAN-2003 (first entry)
XX DE Haematopoietic cell proliferation disorder related oligonucleotide #1132.
XX KW Human; haematopoietic cell proliferation disorder; cytostatic;
XX KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX KW cytosine methylation state; probe; primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FN WO20027272-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-EP003401.
XX PR 26-MAR-2001; 2001US-0278333P.
XX PA (EPIG-) EPIGENOMICS AG.
XX XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
XX PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
XX PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
XX PI Schwöpe I, Ziebarth H;
XX XX WPI; 2003-018942/01.
XX DR Detecting and differentiating between hematopoietic cell proliferative
XX PT disorders, comprises contacting a target nucleic acid with a reagent that
XX PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX PS Claim 15; Page 74; 117pp; English.
XX CC The present invention describes a method for detecting and
XX CC differentiating between haematopoietic cell proliferative disorders
XX CC associated with at least 1 gene and/or their regulatory regions in a
XX CC subject. The method comprises contacting a target nucleic acid in a

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CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used; for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1071 CTAACCACTTAACCTCT 1088
 Db 18 CAAAACCACTAACCCCT 1
 RESULT 524
 ABZ10991/c
 ID ABZ10991 standard; DNA; 18 BP.
 AC ABZ10991;
 DT 16-JAN-2003 (first entry)
 XX
 DE Haematopoietic cell proliferation disorder related oligonucleotide #1131.
 KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 OS Homo sapiens.
 OS Synthetic.
 PN WO20027272-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-EP003401.
 XX
 PR 26-MAR-2001; 2001US-0278333P.
 XX
 FA (EPIG-) EPIGENOMICS AG.
 XX
 PI Berlin K, Braun A, Dietler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E,
 PI Lewin A, Liepcher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwoppe I, Ziebarth H;
 XX
 DR WPI; 2003-018942/01.
 XX
 PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 XX distinguishes between methylated and non-methylated CpG dinucleotides.
 PS Claim 15; Page 74; 117pp; English.
 XX
 CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a

CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used; for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 18 BP; 2 A; 1 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1071 CTAACCACTTAACCTCT 1088
 Db 18 CAAAACCACTAACCCCT 1
 RESULT 525
 ABZ14077/c
 ID ABZ14077 standard; DNA; 18 BP.
 AC ABZ14077;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE DNA fragment B amplification primer B1.
 KW vaccine; attenuated virus; recombinant virus; cancer; neoplasm; tumour;
 KW replication-competent virus; carcinoma; viral infection; HIV; rotavirus;
 KW respiratory syncytial virus (RSV); Hepatitis A virus; poliovirus; primer;
 KW papilloma virus; measles virus; influenza virus; bacterial disease; PCR;
 KW Vibrio cholerae; enterotoxigenic Escherichia coli; Shigella; Listeria;
 KW Streptococcus; Salmonella; parasite; Plasmodium falciparum; trypanosome;
 KW ss.
 XX
 OS Poliovirus.
 OS Synthetic.
 XX
 PN WO200278621-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 22-MAR-2002; 2002WO-US008908.
 XX
 PR 28-MAR-2001; 2001US-0279553P.
 XX
 FA (REGC) UNIV CALIFORNIA.
 XX
 PI Andino-Pavlovsky R, Crotty S;
 XX
 DR WPI; 2003-103236/09.
 XX
 PT New population of live attenuated recombinant replication-competent
 PT viruses (e.g. poliovirus, HIV or influenza virus), useful as a vaccine,
 XX particularly for treating or inhibiting cancer, neoplasm, tumor or
 PT carcinoma.
 XX
 PS Example 1; Page 32; 70pp; English.
 XX

CC The invention relates to a population of live attenuated recombinant
 CC replication-competent viruses, which comprise at least two member
 CC viruses. Each of the member viruses comprises a nucleotide sequence
 CC encoding a different antigenic polypeptide from a pathogenic organism
 CC other than a parent virus from which the recombinant virus was derived,
 CC and which is capable of being expressed in a eukaryotic cell. The
 CC replication-competent virus population is useful in a method of inducing
 CC an immune response in a subject. This comprises administering a first
 CC population of replication-competent viruses in a first strain of the
 CC replication-competent viruses; and after a time, administering a second
 CC population in a second strain of the replication-competent viruses. The
 CC second strain is a different strain from the first strain. The population
 CC of live attenuated recombinant replication-competent viruses is useful as
 CC a vaccine, particularly for eliciting an immune response in a subject. In
 CC particular, the population of live attenuated recombinant replication-
 CC competent viruses is useful for treating or inhibiting cancer, neoplasm,
 CC tumour or carcinoma. Also for preventing, reducing, treating, inhibiting
 CC viral infection such as HIV, rotavirus, respiratory syncytial virus
 CC (RSV), Hepatitis A virus, poliovirus, papilloma virus, measles virus and
 CC influenza virus; bacterial diseases caused by e.g. *Vibrio cholerae*,
 CC enterotoxigenic *Escherichia coli*, *Shigella*, *Listeria*, *Streptococcus*,
 CC *Salmonella*; parasites such as *Plasmodium falciparum*, trypanosomes. The
 CC present sequence represents the DNA fragment B amplification primer B1
 CC
 CC Sequence 18 BP; 6 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 650 GTCAAAATTTAGATTATGT 667
 Db 18 GTCAAAATCTCGAATATGT 1

RESULT 526
 AAL55147/c
 ID AAL55147 standard; DNA; 18 BP.
 AC AAL55147;
 XX
 XX 24-APR-2003 (first entry)
 DT
 DE PGC-1 mutational analysis PCR primer #8.
 XX
 XX Peroxisome proliferator-activated receptor-gamma coactivator-1; PGC-1;
 KW type 2 diabetes; antidiabetic; enzyme; PCR; primer; ss.
 XX
 XX Unidentified.
 OS
 XX WO2002100894-A2.
 PN
 XX 19-DEC-2002.
 PD
 XX 06-JUN-2002; 2002WO-DK000382.
 PF
 XX 08-JUN-2001; 2001EP-00610061.
 PR 10-JUL-2001; 2001DK-00001080.
 XX
 XX (NOVO) NOVO NORDISK AS.
 PA
 XX Andersen G, Ek J, Hansen T, Pedersen OB;
 PI WPI; 2003-156949/15.
 XX

XX Novel mutant DNA sequence encoding peroxisome proliferator-activated
 PT receptor coactivator useful for identifying subjects who are at increased
 PT risk of developing type 2 diabetes.
 XX
 XX Example 1; Page 26; 44pp; English.
 PS
 XX The invention relates to an isolated polynucleotide molecule comprising a
 CC nucleotide sequence encoding peroxisome proliferator-activated receptor-

CC gamma coactivator-1 (PGC-1), containing a mutation associated with type 2
 CC diabetes of at least one nucleotide, or comprising a fragment of the
 CC nucleotide sequence including the mutation. The isolated polynucleotide
 CC is useful for detecting the presence of a mutation in the gene encoding the
 CC PGC-1, by obtaining a biological sample from a subject and analysing the
 CC sample for a mutation associated with type 2 diabetes of the nucleotides
 CC in PGC-1 sequence. The biological sample is obtained from a subject, DNA
 CC is isolated from the sample, DNA is amplified and hybridised to the
 CC isolated polynucleotide which contains a mutation associated with type 2
 CC diabetes of at least one nucleotide or comprising a fragment of the
 CC nucleotide sequence including the mutation to be detected, and
 CC hybridisation of the labelled polynucleotide to the DNA is determined.
 CC The amplified DNA is hybridised to a second labelled polynucleotide
 CC comprising a DNA sequence corresponding to a part of the wild-type gene
 CC encoding PGC-1 and hybridisation of the second labelled polynucleotide to
 CC the amplified DNA is determined. The substance with which the labelled
 CC polynucleotide carrying the mutation is labelled is different from the
 CC label substance with which the second labelled polynucleotide
 CC corresponding to a part of the wild-type DNA is labelled. This method is
 CC useful for determining predisposition to type 2 diabetes in a subject.
 CC The polynucleotide of the invention is useful for identifying subjects
 CC who are at an increased risk of developing type 2 diabetes and to
 CC identify subjects with variable response to drugs which act by the
 CC peroxisome proliferator-activated receptor-gamma and for tailoring a
 CC antidiabetic medication. This polynucleotide sequence represents a PCR
 CC primer used for mutational analysis of the peroxisome proliferator-
 CC activated receptor-gamma coactivator-1 (PGC-1) of the invention
 CC
 CC Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 443 GATTTAGCTGGAGCAG 460
 Db 18 GATTTGGCTTGAAGCAG 1

RESULT 527
 ADA41736/c
 ID ADA41736 standard; DNA; 18 BP.
 AC ADA41736;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX TCV RdRP mutagenic PCR primer i120.
 DE
 XX RNA-dependent RNA polymerase; RdRP; plant virus; amplification system;
 KW ss; primer; PCR.
 XX
 XX Synthetic.
 OS Turnip crinkle virus.
 OS
 XX WO2003014366-A2.
 PN
 XX 20-FEB-2003.
 PD
 XX 29-JUL-2002; 2002WO-DE002863.
 PF
 XX 30-JUL-2001; 2001DE-01037444.
 PR
 XX (PROB-) PROBIOGEN AG.
 PA
 XX Sandig V, Jordan I;
 PI WPI; 2003-248302/24.
 XX
 XX Amplifying nucleic acid in animal cells, useful e.g. for gene therapy or
 PT vaccination, uses an RNA-dependent, RNA-polymerase of a plant virus.
 XX
 XX Example 1; Page 17; 39pp; German.
 PS

XX This invention describes a novel method for amplifying nucleic acid in
 CC animal cells by introducing an RNA-dependent RNA polymerase (RdRP) and
 CC it's associated promoters and cis-acting signals from a plant virus into
 CC the cells. RdRP is normally active in plant cells and the gene that
 CC encodes it can be recovered from such cells. Both the RdRP and the
 CC promoter are from plant viruses, particularly turnip crinkle virus and
 CC the amplified RNA is a modified satellite or genomic RNA of this virus.
 CC The method is particularly used for amplification of RNA (which may be
 CC mRNA for protein synthesis; an effector, e.g. antisense RNA or ribozyme,
 CC or genomic RNA) in animal cells, for (i) control of gene expression or
 CC (ii) for gene therapy or vaccination. When the system includes an
 CC inducible promoter, it permits strong and rapid expression of reporter
 CC genes in response to a test substance, especially where the promoter
 CC responds to the human immune deficiency virus or heavy metals, to produce
 CC a diagnostic system or biosensor, respectively. The method of the
 CC invention provides an inducible or constitutive, autonomous RNA-dependent
 CC RNA amplification system for animal cells that requires only one
 CC polymerase and does not use any viral structural genes or helper viruses.
 CC Amplification takes place in the cytoplasm without using any components
 CC potentially infectious for the host cells. Human 293 cells were
 CC transformed with (i) pTJO-39, expressing a turnip crinkle virus 88 kD
 CC protein; (ii) pTJO-60, expressed satellite RNA-C of the same virus in the
 CC sense orientation and a fusion of internal ribosome entry site and green
 CC fluorescent protein in the antisense orientation, and (iii) an expression
 CC vector for T7 RNA polymerase under control of the cytomegalovirus
 CC promoter. Expression of the reporter gene was detected by fluorescence
 CC microscopy. This sequence represents a mutagenic PCR primer, i120, used
 CC to clone the turnip crinkle virus (TCV) RdRP gene into pTJO-39.

XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 39 CCGAAGCAGCGCGGCC 56
 ||| ||||| ||||| |||||
 Db 18 CCGAAGCAGCGCGGCAC 1

RESULT 528

ADBI7690
 ID ADBI7690 standard; DNA; 18 BP.

AC ADBI7690;

XX 20-NOV-2003 (first entry)

XX Xenopus axis duplication assay PCR primer #3.

XX Wnt-1 induced secreted protein; WISP; Wnt-1 induced gene; WIG; WISP-1;
 KW WISP-2; WISP-3; connective tissue growth factor; CTGF; tumour cell;
 KW cell death; atherosclerosis; malignant disorder; breast cancer;
 KW ovarian cancer; colon cancer; melanoma; antiarteriosclerotic; cytostatic;
 KW PCR; primer; ss.

XX Xenopus laevis.

XX US2003068678-A1.

XX 10-APR-2003.

XX 27-MAR-2002; 2002US-00112267.

XX 29-OCT-1997; 97US-0063704P.

PR 04-FEB-1998; 98US-0073612P.

PR 14-APR-1998; 98US-0081695P.

XX 29-OCT-1998; 98US-00182145.

XX (GETH) GENENTECH INC.

XX Levine AJ, Pennica D;

XX WPI; 2003-596689/56.

XX New nucleic acid encoding Wnt-1-Induced Secreted Protein, useful for
 CC preparing a composition for treating a WISP-related disorder in a mammal
 CC comprising atherosclerosis or malignant disorder, e.g., breast, ovarian
 CC or colon cancer.

XX Example 11; Page 39; 205pp; English.

XX The present invention relates to the isolation of novel Wnt-1 induced
 CC secreted proteins (WISPs, previously known as Wnt-1 induced gene (WIG)
 CC polypeptides), and the polynucleotide sequences encoding them. The novel
 CC WISP proteins (WISP-1, WISP-2, WISP-3) show homology to connective tissue
 CC growth factor (CTGF). Also disclosed are vectors and host cells
 CC comprising WISP polynucleotides, chimeric polypeptides comprising WISP
 CC polypeptides fused to heterologous polypeptides, antibodies which bind
 CC WISP polypeptides, and methods for producing the polypeptides. The
 CC antibody may be used in a composition to inhibit the growth of tumour
 CC cells by inducing death of the cells which are overexpressing the WISP
 CC polypeptides. The WISP polynucleotide sequences are useful for preparing
 CC a composition for treating WISP-related disorders such as atherosclerosis
 CC and malignant disorders (e.g. breast, ovarian or colon cancer or
 CC melanoma) in a mammal. The present sequence represents a PCR primer used
 CC in the examples of the present invention.

XX Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 897 AGACCAAGAGCCTCAACA 914
 ||| ||||| ||||| |||||
 Db 1 AGTCCAAGAGTCTCAGCA 18

RESULT 529

ACH00636

ID ACH00636 standard; DNA; 18 BP.

XX ACH00636;

XX 12-FEB-2004 (first entry)

XX Mammalian inverted nipple associated microsatellite PCR primer #90.

XX Inverted nipple; microsatellite; PCR; primer; ss; pig.

XX Mammalia.

XX WO2003066891-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-EP001045.

XX 05-FEB-2002; 2002EP-00002632.

XX (FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE.

XX Hardge T, Schellander K, Wimmers K;

XX WPI; 2003-671539/63.

XX Determining predisposition to inverted nipples useful e.g. for selecting
 CC breeding animals comprises detecting specific microsatellite markers.

XX Disclosure; Page 23; 63pp; German.

XX The present invention relates to the use of a nucleic acid to determine
 CC the predisposition of appearance or inheritance of inverted nipples,
 CC where the nucleic acid is identical to the region of microsatellites

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CC S0200, SW2443, S0097, S0007, SW1301 or S0164 on chromosomes 6, 2, 4, 14,
CC 1 and 3, respectively, in pigs, or homologous positions in the genomes of
CC other mammals. The nucleic acids can be used to select pets, breeding or
CC farm animals that lack inverted nipples, particularly by genomic
CC screening of many related mammals in a population. The present sequence
CC is a PCR primer used in the amplification of the invention to identify
CC microsatellite markers associated with the inverted nipple phenotype
XX
SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 300 TTGTTGTTCTGCTTTG 317
Db 1 TTGCTGTTGCTGCTTTG 18

RESULT 530
ADM06240/c
ID ADM06240 standard; DNA; 18 BP.
AC ADM06240;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PCR primer SEQ ID NO:4925.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
WPI; 2003-723558/69.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Example 8; SEQ ID NO 4925; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM0316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents an
CC oligonucleotide used in the invention.
XX
SQ Sequence 18 BP; 9 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 314 TTGGAATTTCTGTATT 331
```

```
Db 18 TCTGGAGTTGCTGTATT 1
|||||
RESULT 531
ADM96453/c
ID ADM96453 standard; DNA; 18 BP.
XX
AC ADM96453;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CIAP-1 DNA antisense oligonucleotide #30.
XX
KW Human; cellular inhibitor of apoptosis-1; CIAP-1; ss; cellular apoptosis;
KW cancer; antisense oligonucleotide;
KW phosphorothioate internucleoside linkage; 2'-O-methoxyethyl sugar moiety;
KW 5-methylcytosine; autoimmune disorder; viral infection; cytostatic;
KW immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
PN US2004009599-A1.
XX
PD 15-JAN-2004.
XX
PF 18-JUN-2003; 2003US-00464158.
XX
PR 03-DEC-1998; 98US-00205204.
XX
PR 16-JUN-1999; 99WO-US013824.
XX
PR 24-SEP-2001; 2001US-00857278.
XX
PA (BENN/) BENNETT C F.
PA (ACKE/) ACKERMANN E J.
XX
XX Bennett CF, Ackermann EJ;
PI WPI; 2004-090476/09.
XX
DR Inducing cellular apoptosis by administering an antisense modulating the
PT human Cellular Inhibitor of Apoptosis-1, useful in preventing or treating
PT cancer, autoimmune disorders and viral infections.
XX
PS Example 15; SEQ ID NO 37; 25pp; English.
XX
CC The invention relates to a method of inducing cellular apoptosis
CC comprising administering to a cell an effective amount of an antisense
CC compound targeted to a nucleic acid molecule encoding human cellular
CC inhibitor of apoptosis-1 (CIAP-1), so that expression of CIAP-1 is
CC inhibited and apoptosis is induced. The cell used in the method is a
CC cancer cell. The antisense compound is an antisense oligonucleotide that
CC comprises at least one modification of the internucleoside linkage, sugar
CC moiety or nucleobase, wherein the modification is a phosphorothioate
CC internucleoside linkage, a 2'-O-methoxyethyl sugar moiety or a 5-
CC methylcytosine nucleobase. The antisense oligonucleotide is a chimeric
CC oligonucleotide. The methods and compositions are useful for the
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of human CIAP-1, such as cancer,
CC autoimmune disorders and viral infections. This sequence represents a
CC human CIAP-1 DNA antisense oligonucleotide of the invention.
XX
SQ Sequence 18 BP; 6 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 TTGATGAGATCCAAAGGA 991
|||||
Db 18 TTGATGAGATCCAAAGGA 1
|||||

RESULT 532
```


ADP81767/c
 ID ADP81767 standard; DNA; 18 BP.
 XX
 AC ADP81767;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human MD-1 RP105-associated DNA amplifying reverse PCR primer.
 XX
 KW MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
 KW human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2004110146-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 09-DEC-2002; 2002US-00316242.
 XX
 PR 09-DEC-2002; 2002US-00316242.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dobie KW;
 XX
 WPI; 2004-440335/41.
 DR
 PT New oligonucleotide compound that inhibits expression of MD-1 RP105-
 PT associated, useful for preparing a composition for treating autoimmune
 PT disorder.
 XX
 PS Claim 21; SEQ ID NO 6; 63pp; English.
 XX
 CC The invention relates to compounds, compositions and methods for
 CC modulating the expression of MD-1 RP105-associated (also called as MD-1
 CC and MD1) DNA. The composition comprise antisense oligonucleotides
 CC targeted to MD-1 RP105-associated DNA. The compound is useful for
 CC preparing a composition for treating autoimmune disorder. It is also
 CC useful in gene therapy. The present sequence is a PCR primer used for
 CC amplifying human MD-1 RP105-associated DNA. This sequence is used to
 CC illustrate the method of the invention.
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 883 AAAGTGTGGCCACACAC 900
 Db 18 AAAGCTGGCCACACAC 1
 RESULT 533
 ADO80001/c
 ID ADO80001 standard; DNA; 18 BP.
 XX
 AC ADO80001;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE CENPC1 extend primer #52.
 XX
 KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPf3;
 KW CENPC1; SNP; single nucleotide polymorphism; centromere protein C1;
 KW Centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004047514-A2.
 XX
 PD 10-JUN-2004.
 XX

25-NOV-2003; 2003WO-US037943.
 25-NOV-2002; 2002US-0429136P.
 24-JUL-2003; 2003US-0490234P.
 (SEQU-) SEQUENOM INC.
 Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 WPI; 2004-441037/41.
 Identifying a subject at risk of breast cancer by detecting the presence
 of polymorphic variations in the DLG1, KIAA0783, DPf3 or CENPC1 regions
 which are associated with breast cancer in a nucleic acid sample from a
 subject.
 Example 6; Page 91; 227pp; English.
 The present invention relates to a method for identifying a subject at
 risk of breast cancer. The method comprising detecting the presence or
 absence of one or more polymorphic variations associated with breast
 cancer in a nucleic acid sample from a subject. The nucleic acid sample
 comprises the DLG1 region (ADO79402), KIAA0783 region (ADO79403), DPf3
 region (ADO79404) or CENPC1 region (ADO79405). The gene DLG1 (discs,
 large homolog 1 (Drosophila)) is also known as synapse-associated protein
 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
 gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
 has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
 novel gene with unknown function, however, being a zinc finger protein,
 it likely to be a transcription factor. The gene DPf3 (D4, zinc and
 double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079
 and 2810403B03Rik. DPf3 is a Rho family guanine-nucleotide exchange
 factor. DPf3 has been mapped to chromosomal position 14q24.3-q31.1. The
 gene CENPC1 (centromere protein C1) is also known as Centromere
 autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-
 q13.3. CENPC1 is a centromere autoantigen and a component of the inner
 kinetochore plate. The CENPC1 protein is required for maintaining proper
 kinetochore size and a timely transition to anaphase. The method is
 useful for identifying a subject at risk of breast cancer, for early
 diagnosis, prevention and treatment of breast cancer, to analyze and
 predict a response to a breast cancer treatment, and in clinical drug
 trials. The present sequence was used in an example from the invention.
 Sequence 18 BP; 6 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 398 TTCCTTACAATTCAGGG 415
 Db 18 TTCCTTACAATTCAGG 1
 RESULT 534
 ADP82980/c
 ID ADP82980 standard; DNA; 18 BP.
 XX
 AC ADP82980;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Nitrile hydratase related PCR primer, SEQ ID 32.
 XX
 KW Nitrile hydratase; enzyme; biocatalyst; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO2004056990-A1.
 XX
 PD 08-JUL-2004.
 XX

PF 15-DEC-2003; 2003WO-JP016014.
 XX
 PR 19-DEC-2002; 2002JP-00368360.
 PR 10-NOV-2003; 2003JP-00379280.
 XX
 PA (MITA) MITSUI CHEM INC.
 XX
 PI Yamaki T, Banba S, Matoishi K, Ito K, Kobayashi H, Tanaka E;
 PI Oikawa T;
 XX
 DR WPI; 2004-517682/49.
 XX
 PT Novel nitrile hydratase, useful for producing nitrile and amide
 PT compounds, comprises alpha and beta subunit.
 XX
 PS Disclosure; SEQ ID NO 32; 345pp; Japanese.
 XX
 CC The present invention relates to novel Pseudonocardia thermophila nitrile
 CC hydratase (I) sequences. (I) efficiently converts a nitrile compound into
 CC its corresponding amide compound and is useful for producing biocatalyst
 CC substances. The present sequence is a PCR primer used to illustrate the
 CC invention.
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 17 CTGCTCGTGGCGGCGAG 34
 DB 18 CTGCTCGTGGCGGCGAG 1
 RESULT 535
 ADP83010/c
 ID ADP83010 standard; DNA; 18 BP.
 XX
 AC ADP83010;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Nitrile hydratase related PCR primer, SEQ ID 62.
 XX
 KW Nitrile hydratase; enzyme; biocatalyst; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 FN WO2004056990-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 15-DEC-2003; 2003WO-JP016014.
 XX
 PR 19-DEC-2002; 2002JP-00368360.
 PR 10-NOV-2003; 2003JP-00379280.
 XX
 PA (MITA) MITSUI CHEM INC.
 XX
 PI Yamaki T, Banba S, Matoishi K, Ito K, Kobayashi H, Tanaka E;
 PI Oikawa T;
 XX
 DR WPI; 2004-517682/49.
 XX
 PT Novel nitrile hydratase, useful for producing nitrile and amide
 PT compounds, comprises alpha and beta subunit.
 XX
 PS Example 22; SEQ ID NO 62; 345pp; Japanese.
 XX
 CC The present invention relates to novel Pseudonocardia thermophila nitrile
 CC hydratase (I) sequences. (I) efficiently converts a nitrile compound into
 CC its corresponding amide compound and is useful for producing biocatalyst
 CC substances. The present sequence is a PCR primer used to illustrate the

CC invention.
 XX
 SQ Sequence 18 BP; 1 A; 8 C; 9 G; 0 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 15 GGCTGCGCGGCGCGTGGC 32
 DB 18 GCCGCGCGGCGCGTGGC 1
 RESULT 536
 ADQ80462
 ID ADQ80462 standard; DNA; 18 BP.
 XX
 AC ADQ80462;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE MGB-probe to determine EV1 viral RNA levels.
 XX
 KW echovirus; kagr2; kbgr1; Cytostatic; Immunostimulant; immune response;
 KW cancer; ss; probe.
 XX
 OS Unidentified.
 XX
 FN WO2004054613-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 18-DEC-2003; 2003WO-AU001688.
 XX
 PR 18-DEC-2002; 2002AU-00953436.
 XX
 PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX
 PI Shafren D;
 XX
 DR WPI; 2004-488010/46.
 XX
 PT Treating abnormal cells in a mammal comprises treating the mammal with an
 PT echovirus or its modified forms or combinations, which recognize
 PT alpha2betal for killing at least some of the cells.
 XX
 PS Example 1; Page 23; 67pp; English.
 XX
 CC The present invention relates to treating abnormal cells in a mammal
 CC comprises treating the mammal with an echovirus or its modified forms or
 CC combinations, which recognize kagr; 2 kbgr; 1 for infectivity of the
 CC cells, where at least some of the cells are killed by the virus. The
 CC inoculant for generating echovirus is useful in the manufacture of
 CC medicament for inducing an immune response against cancer cells in a
 CC mammal. The present sequence represents a MGB probe to determine EV1
 CC viral RNA levels.
 XX
 SQ Sequence 18 BP; 7 A; 5 C; 1 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 900 CCAAGAGCTCAACATTT 917
 DB 1 CCATAGCTTCAACATTT 18
 RESULT 537
 ACC67229/c
 ID ACC67229 standard; DNA; 17 BP.
 XX
 AC ACC67229;

```

XX 01-JUL-2003 (first entry)
DT
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 4476.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004210.
XX
PF 17-SEP-2001; 2001FR-00011979.
XX
PR (MOLE-) MOLECULAR ENGINES LAB.
XX
PA Telerman A, Amson R, Tuijnder M;
XX
PI WPI; 2003-333167/31.
XX
DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX Disclosure; Page 554; 738pp; French.
XX
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.1%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 522 CATGTGCACATG 533
Db 16 CATGTGCACATG 5
Search completed: August 19, 2005, 10:56:35
Job time : 11 secs

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